

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:ssspt189dxw

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

\* \* \* \* \* Welcome to STN International \* \* \* \* \*

NEWS	1		Web Page for STN Seminar Schedule - N. America
NEWS	2	JAN 02	STN pricing information for 2008 now available
NEWS	3	JAN 16	CAS patent coverage enhanced to include exemplified prophetic substances
NEWS	4	JAN 28	USPATFULL, USPAT2, and USPATOLD enhanced with new custom IPC display formats
NEWS	5	JAN 28	MARPAT searching enhanced
NEWS	6	JAN 28	USGENE now provides USPTO sequence data within 3 days of publication
NEWS	7	JAN 28	TOXCENTER enhanced with reloaded MEDLINE segment
NEWS	8	JAN 28	MEDLINE and LMEDLINE reloaded with enhancements
NEWS	9	FEB 08	STN Express, Version 8.3, now available
NEWS	10	FEB 20	PCI now available as a replacement to DPCI
NEWS	11	FEB 25	IFIREF reloaded with enhancements
NEWS	12	FEB 25	IMSPRODUCT reloaded with enhancements
NEWS	13	FEB 29	WPINDEX/WPIDS/WPIX enhanced with ECLA and current U.S. National Patent Classification
NEWS	14	MAR 31	IFICDB, IFIPAT, and IFIUIDB enhanced with new custom IPC display formats
NEWS	15	MAR 31	CAS REGISTRY enhanced with additional experimental spectra
NEWS	16	MAR 31	CA/CAPLUS and CASREACT patent number format for U.S. applications updated
NEWS	17	MAR 31	LPCI now available as a replacement to LDPCI
NEWS	18	MAR 31	EMBASE, EMBAL, and LEMBASE reloaded with enhancements
NEWS	19	APR 04	STN AnaVist, Version 1, to be discontinued
NEWS	20	APR 15	WPIDS, WPINDEX, and WPIX enhanced with new predefined hit display formats
NEWS	21	APR 28	EMBASE Controlled Term thesaurus enhanced
NEWS	22	APR 28	IMSRESEARCH reloaded with enhancements
NEWS	23	MAY 30	INPAFAMDB now available on STN for patent family searching
NEWS	24	MAY 30	DGENE, PCTGEN, and USGENE enhanced with new homology sequence search option
NEWS	25	JUN 06	EPFULL enhanced with 260,000 English abstracts
NEWS	26	JUN 06	KOREAPAT updated with 41,000 documents
NEWS	27	JUN 13	USPATFULL and USPAT2 updated with 11-character patent numbers for U.S. applications
NEWS	28	JUN 19	CAS REGISTRY includes selected substances from web-based collections

NEWS EXPRESS FEBRUARY 08 CURRENT WINDOWS VERSION IS V8.3,  
AND CURRENT DISCOVER FILE IS DATED 20 FEBRUARY 2008

NEWS HOURS	STN Operating Hours Plus Help Desk Availability
NEWS LOGIN	Welcome Banner and News Items

NEWS IPC8        For general information regarding STN implementation of IPC 8

Enter NEWS followed by the item number or name to see news on that specific topic.

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\* \* \* \* \* STN Columbus \* \* \* \* \*

FILE 'HOME' ENTERED AT 21:14:36 ON 19 JUN 2008

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION

FULL ESTIMATED COST

0.21	0.21
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INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 21:14:56 ON 19 JUN 2008

69 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0\* with SET DETAIL OFF.

=> s food(p)process? and Enterococcus(p)durans

0*	FILE ADISNEWS
4	FILE AGRICOLA
0*	FILE ANTE
0*	FILE AQUALINE
5*	FILE BIOENG
18	FILE BIOSIS
3*	FILE BIOTECHABS
3*	FILE BIOTECHDS
5*	FILE BIOTECHNO
2	FILE CABA
20	FILE CAPLUS
0*	FILE CEABA-VTB
0*	FILE CIN
4	FILE DGENE
4	FILE EMBASE
6*	FILE ESBIODBASE
0*	FILE FOMAD
0*	FILE FOREGE
32 FILES SEARCHED...	
7*	FILE FROSTI
11*	FILE FSTA
1	FILE HEALSAFE
7	FILE IFIPAT
0*	FILE KOSMET
3	FILE LIFESCI
6	FILE MEDLINE
0*	FILE NTIS
0*	FILE NUTRACEUT
4*	FILE PASCAL
0*	FILE PHARMAML

2 FILE SCISEARCH  
5 FILE TOXCENTER  
60 FILES SEARCHED...  
42 FILE USPATFULL  
9 FILE USPAT2  
0\* FILE WATER  
7 FILE WPIDS  
7 FILE WPINDEX

24 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L1 QUE FOOD(P) PROCESS? AND ENTEROCOCCUS(P) DURANS

=> s l1 and (PTA-475# or PTA-476#)

0\* FILE ADISNEWS  
0\* FILE ANTE  
0\* FILE AQUALINE  
0\* FILE BIOENG  
0\* FILE BIOTECHABS  
0\* FILE BIOTECHDS  
0\* FILE BIOTECHNO  
0\* FILE CEABA-VTB  
0\* FILE CIN  
0\* FILE ESBIODBASE  
0\* FILE FOMAD  
0\* FILE FOREGE  
0\* FILE FROSTI  
0\* FILE FSTA  
1 FILE IFIPAT

37 FILES SEARCHED...  
0\* FILE KOSMET  
0\* FILE NTIS  
0\* FILE NUTRACEUT  
0\* FILE PASCAL  
0\* FILE PHARMAML  
2 FILE USPATFULL  
0\* FILE WATER  
1 FILE WPIDS

68 FILES SEARCHED...  
1 FILE WPINDEX

4 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L2 QUE L1 AND (PTA-475# OR PTA-476#)

=> file ifipat uspatfull

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
2.60	2.81

FULL ESTIMATED COST

FILE 'IFIPAT' ENTERED AT 21:17:15 ON 19 JUN 2008  
COPYRIGHT (C) 2008 IFI CLAIMS(R) Patent Services (IFI)

FILE 'USPATFULL' ENTERED AT 21:17:15 ON 19 JUN 2008  
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

=> s l2

L3 3 L2

=> dup rem l3

PROCESSING COMPLETED FOR L3

L4 3 DUP REM L3 (0 DUPLICATES REMOVED)

=> d 14 1-3

L4 ANSWER 1 OF 3 IFIPAT COPYRIGHT 2008 IFI on STN  
AN 11124117 IFIPAT;IFIUDB;IFICDB  
TI COMPOSITION AND METHOD FOR INHIBITION OF MICROORGANISMS  
IN Doyle Michael P; Zhao Tong  
PA Unassigned Or Assigned To Individual (68000)  
PPA Georgia, University of Research Foundation Inc (Probable)  
PI US 2006073129 A1 20060406  
AI US 2003-535357 20031124  
WO 2003-US37526 20031124  
20050518 PCT 371 date  
20050518 PCT 102(e) date  
PRAI US 2002-428863P 20021125 (Provisional)  
FI US 2006073129 20060406  
DT Utility; Patent Application - First Publication  
FS CHEMICAL  
APPLICATION  
ED Entered STN: 10 Apr 2006  
Last Updated on STN: 10 Apr 2006  
CLMN 35  
GI 1 Figure(s).  
FIG. 1 illustrates the results of analyzing four probiotic isolates for their DNA fingerprinting by pulsed field-gel electrophoresis; lane 1 Lambda ladder DNA standard, lane 2 C-192 (*L. lactis* subsp. *lactis*), lane 3 C-1-152 (*L. lactis* subsp. *lactis*), lane 4 141-1 (*E. durans*), and lane 5 152 (*E. durans*).

L4 ANSWER 2 OF 3 USPATFULL on STN  
AN 2006:86130 USPATFULL  
TI Composition and method for inhibition of microorganisms  
IN Doyle, Michael P, Peachtree City, GA, UNITED STATES  
Zhao, Tong, Peachtree City, GA, UNITED STATES  
PI US 20060073129 A1 20060406  
AI US 2003-535357 A1 20031124 (10)  
WO 2003-US37526 20031124  
20050518 PCT 371 date  
PRAI US 2002-428863P 20021125 (60)  
DT Utility  
FS APPLICATION  
LN.CNT 1238  
INCL INCLM: 424/093.450  
NCL NCLM: 424/093.450  
IC IPCI A61K0035-74 [I,A]; A61K0035-66 [I,C\*]  
IPCR A61K0035-66 [I,C]; A61K0035-74 [I,A]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 3 OF 3 USPATFULL on STN  
AN 2006:79924 USPATFULL  
TI Foaming composition of competitive exclusion microbes and method of using same  
IN Podtburg, Teresa C., Waconia, MN, UNITED STATES  
Schmidt, Bruce, Apple Valley, MN, UNITED STATES  
Cords, Bruce, Inver Grove Heights, MN, UNITED STATES  
Grab, Lawrence A., Dusseldorf, GERMANY, FEDERAL REPUBLIC OF  
Halsrud, David A., Minneapolis, MN, UNITED STATES  
PI US 20060067915 A1 20060330  
AI US 2005-233922 A1 20050922 (11)  
PRAI US 2004-612882P 20040924 (60)  
DT Utility  
FS APPLICATION



LN.CNT 1878  
INCL INCLM: 424/093.400  
INCLS: 435/243.000  
NCL NCLM: 424/093.400  
NCLS: 435/243.000  
IC IPCI A01N0063-00 [I,A]  
IPCR A01N0063-00 [I,A]; A01N0063-00 [I,C]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d hist

(FILE 'HOME' ENTERED AT 21:14:36 ON 19 JUN 2008)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 21:14:56 ON 19 JUN 2008  
SEA FOOD(P)PROCESS? AND ENTEROCOCCUS(P)DURANS

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0\* FILE ADISNEWS  
4 FILE AGRICOLA  
0\* FILE ANTE  
0\* FILE AQUALINE  
5\* FILE BIOENG  
18 FILE BIOSIS  
3\* FILE BIOTECHABS  
3\* FILE BIOTECHDS  
5\* FILE BIOTECHNO  
2 FILE CABA  
20 FILE CAPLUS  
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0\* FILE CIN  
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1 FILE HEALSAFE  
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6 FILE MEDLINE  
0\* FILE NTIS  
0\* FILE NUTRACEUT  
4\* FILE PASCAL  
0\* FILE PHARMAML  
2 FILE SCISEARCH  
5 FILE TOXCENTER  
42 FILE USPATFULL  
9 FILE USPAT2  
0\* FILE WATER  
7 FILE WPIDS  
7 FILE WPINDEX

L1 QUE FOOD(P) PROCESS? AND ENTEROCOCCUS(P) DURANS

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SEA L1 AND (PTA-475# OR PTA-476#)  
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0\* FILE ADISNEWS  
0\* FILE ANTE

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0* FILE BIOTECHDS
0* FILE BIOTECHNO
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1 FILE IFIPAT
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0* FILE NTIS
0* FILE NUTRACEUT
0* FILE PASCAL
0* FILE PHARMAML
2 FILE USPATFULL
0* FILE WATER
1 FILE WPIDS
1 FILE WPINDEX
L2 QUE L1 AND (PTA-475# OR PTA-476#)
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FILE 'IFIPAT, USPATFULL' ENTERED AT 21:17:15 ON 19 JUN 2008
L3 3 S L2
L4 3 DUP REM L3 (0 DUPLICATES REMOVED)

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=> logoff

ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF

LOGOFF? (Y)/N/HOLD:y

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
7.72	10.53

FULL ESTIMATED COST

STN INTERNATIONAL LOGOFF AT 21:17:46 ON 19 JUN 2008

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:ssspt189dxw

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

\* \* \* \* \* Welcome to STN International \* \* \* \* \*

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NEWS 1 Web Page for STN Seminar Schedule - N. America
NEWS 2 AUG 15 CAOLD to be discontinued on December 31, 2008
NEWS 3 OCT 07 EPFULL enhanced with full implementation of EPC2000
NEWS 4 OCT 07 Multiple databases enhanced for more flexible patent
number searching
NEWS 5 OCT 22 Current-awareness alert (SDI) setup and editing
enhanced

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NEWS 6 OCT 22 WPIDS, WPINDEX, and WPIX enhanced with Canadian PCT Applications  
 NEWS 7 OCT 24 CHEMLIST enhanced with intermediate list of pre-registered REACH substances  
 NEWS 8 NOV 21 CAS patent coverage to include exemplified prophetic substances identified in English-, French-, German-, and Japanese-language basic patents from 2004-present  
 NEWS 9 NOV 26 MARPAT enhanced with FSORT command  
 NEWS 10 NOV 26 MEDLINE year-end processing temporarily halts availability of new fully-indexed citations  
 NEWS 11 NOV 26 CHEMSAFE now available on STN Easy  
 NEWS 12 NOV 26 Two new SET commands increase convenience of STN searching  
 NEWS 13 DEC 01 ChemPort single article sales feature unavailable  
 NEWS 14 DEC 12 GBFULL now offers single source for full-text coverage of complete UK patent families

NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,  
 AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

NEWS HOURS STN Operating Hours Plus Help Desk Availability  
 NEWS LOGIN Welcome Banner and News Items  
 NEWS IPC8 For general information regarding STN implementation of IPC 8

Enter NEWS followed by the item number or name to see news on that specific topic.

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\* \* \* \* \* STN Columbus \* \* \* \* \*

FILE 'HOME' ENTERED AT 16:31:09 ON 16 DEC 2008

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	0.21	0.21

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:31:20 ON 16 DEC 2008

69 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0\* with SET DETAIL OFF.

=> s (Enterococcus durans or Lactococcus lactis) and (PTA-4759 or PTA-4758 or PTA-4760 or PTA-4761)

1 FILE IFIPAT  
 53 FILES SEARCHED...  
 2 FILE USPATFULL  
 1 FILE WPIDS  
 1 FILE WPINDEX

4 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L1 QUE (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 OR PTA-4758  
OR PTA-4760 OR PTA-4761)

=> file uspatfull ifipat

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

1.30

1.51

FILE 'USPATFULL' ENTERED AT 16:32:25 ON 16 DEC 2008  
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'IFIPAT' ENTERED AT 16:32:25 ON 16 DEC 2008  
COPYRIGHT (C) 2008 IFI CLAIMS(R) Patent Services (IFI)

=> s l1

L2 3 L1

=> d l2 1-3

L2 ANSWER 1 OF 3 USPATFULL on STN

AN 2006:86130 USPATFULL

TI Composition and method for inhibition of microorganisms

IN Doyle, Michael P, Peachtree City, GA, UNITED STATES

Zhao, Tong, Peachtree City, GA, UNITED STATES

PI US 20060073129 A1 20060406

AI US 2003-535357 A1 20031124 (10)

WO 2003-US37526 20031124

20050518 PCT 371 date

PRAI US 2002-428863P 20021125 (60)

DT Utility

FS APPLICATION

LN.CNT 1238

INCL INCLM: 424/093.450

NCL NCLM: 424/093.450

IC IPCI A61K0035-74 [I,A]; A61K0035-66 [I,C\*]

IPCR A61K0035-66 [I,C]; A61K0035-74 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L2 ANSWER 2 OF 3 USPATFULL on STN

AN 2006:79924 USPATFULL

TI Foaming composition of competitive exclusion microbes and method of  
using same

IN Podtburg, Teresa C., Waconia, MN, UNITED STATES

Schmidt, Bruce, Apple Valley, MN, UNITED STATES

Cords, Bruce, Inver Grove Heights, MN, UNITED STATES

Grab, Lawrence A., Dusseldorf, GERMANY, FEDERAL REPUBLIC OF

Halsrud, David A., Minneapolis, MN, UNITED STATES

PI US 20060067915 A1 20060330

AI US 2005-233922 A1 20050922 (11)

PRAI US 2004-612882P 20040924 (60)

DT Utility

FS APPLICATION

LN.CNT 1878

INCL INCLM: 424/093.400

INCL: 435/243.000

NCL NCLM: 424/093.400

NCL: 435/243.000

IC IPCI A01N0063-00 [I,A]

IPCR A01N0063-00 [I,A]; A01N0063-00 [I,C]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L2 ANSWER 3 OF 3 IFIPAT COPYRIGHT 2008 IFI on STN  
 AN 11124117 IFIPAT;IFIUDB;IFICDB  
 TI Composition and method for inhibition of microorganisms  
 IN Doyle Michael P; Zhao Tong  
 PA Unassigned Or Assigned To Individual (68000)  
 PPA Georgia, University of Research Foundation Inc (Probable)  
 PI US 20060073129 A1 20060406  
 AI US 2003-535357 20031124  
 WO 2003-US37526 20031124  
 20050518 PCT 371 date  
 20050518 PCT 102(e) date  
 PRAI US 2002-428863P 20021125 (Provisional)  
 FI US 20060073129 20060406  
 DT Utility; Patent Application - First Publication  
 FS CHEMICAL  
 APPLICATION  
 ED Entered STN: 10 Apr 2006  
 Last Updated on STN: 10 Apr 2006  
 CLMN 35  
 GI 1 Figure(s).  
 FIG. 1 illustrates the results of analyzing four probiotic isolates for  
 their DNA fingerprinting by pulsed field-gel electrophoresis; lane 1  
 Lambda ladder DNA standard, lane 2 C-1-92 [*L. lactis* subsp. *lactis*], lane  
 3 C-1-152 [*L. lactis* subsp. *lactis*], lane 4 141-1 [*E. durans*], and lane 5  
 152 [*E. durans*].

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
7.72	9.23

FULL ESTIMATED COST

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
 AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
 CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
 DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:33:15 ON 16 DEC 2008

69 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view  
 search error messages that display as 0\* with SET DETAIL OFF.

=> s Enterococcus durans strain 141-1

48 FILES SEARCHED...

0 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L3 QUE ENTEROCOCCUS DURANS STRAIN 141-1

=> s Enterococcus durans strain 152

58 FILES SEARCHED...

0 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L4 QUE ENTEROCOCCUS DURANS STRAIN 152

=> s Enterococcus drans 141-1

0 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L5 QUE ENTEROCOCCUS DRANS 141-1



IN Podtburg, Teresa C., Waconia, MN, UNITED STATES  
 Schmidt, Bruce, Apple Valley, MN, UNITED STATES  
 Cords, Bruce, Inver Grove Heights, MN, UNITED STATES  
 Grab, Lawrence A., Dusseldorf, GERMANY, FEDERAL REPUBLIC OF  
 Halsrud, David A., Minneapolis, MN, UNITED STATES  
 PI US 20060067915 A1 20060330  
 AI US 2005-233922 A1 20050922 (11)  
 PRAI US 2004-612882P 20040924 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 1878  
 INCL INCLM: 424/093.400  
 INCLS: 435/243.000  
 NCL NCLM: 424/093.400  
 NCLS: 435/243.000  
 IC IPCI A01N0063-00 [I,A]  
 IPCR A01N0063-00 [I,A]; A01N0063-00 [I,C]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
3.60	16.73

FULL ESTIMATED COST

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 AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
 CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
 DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:37:29 ON 16 DEC 2008

69 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view  
 search error messages that display as 0\* with SET DETAIL OFF.

=> s Enterococcus durans 152

1 FILE AGRICOLA  
 1 FILE BIOENG  
 1 FILE BIOSIS  
 1 FILE CABA  
 2 FILE CAPLUS  
 1 FILE FROSTI  
 1 FILE FSTA  
 1 FILE HEALSAFE  
 1 FILE LIFESCI  
 1 FILE MEDLINE  
 1 FILE PASCAL  
 1 FILE SCISEARCH  
 2 FILE USPATFULL

67 FILES SEARCHED...

13 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L8 QUE ENTEROCOCCUS DURANS 152

=> file agricola bioeng biosis caba caplus frosti fsta healsafe lifesci medline  
 pascal scisearch uspatfull

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
1.30	18.03

FULL ESTIMATED COST

FILE 'AGRICOLA' ENTERED AT 16:38:26 ON 16 DEC 2008

FILE 'BIOENG' ENTERED AT 16:38:26 ON 16 DEC 2008  
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FILE 'BIOSIS' ENTERED AT 16:38:26 ON 16 DEC 2008  
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FILE 'HEALSAFE' ENTERED AT 16:38:26 ON 16 DEC 2008  
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FILE 'LIFESCI' ENTERED AT 16:38:26 ON 16 DEC 2008  
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FILE 'MEDLINE' ENTERED AT 16:38:26 ON 16 DEC 2008

FILE 'PASCAL' ENTERED AT 16:38:26 ON 16 DEC 2008  
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FILE 'SCISEARCH' ENTERED AT 16:38:26 ON 16 DEC 2008  
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FILE 'USPATFULL' ENTERED AT 16:38:26 ON 16 DEC 2008  
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

=> s l8  
L9 15 L8

=> dup rem l9  
PROCESSING COMPLETED FOR L9  
L10 3 DUP REM L9 (12 DUPLICATES REMOVED)

=> d l10 1-3

L10 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2008 ACS on STN DUPLICATE 1  
AN 2006:299263 CAPLUS  
DN 144:306860  
TI Foaming composition of benign microbes for competitive exclusion of  
undesired microbes  
IN Podtburg, Teresa C.; Schmidt, Bruce; Cords, Bruce; Grab, Lawrence A.;  
Halsrud, David A.  
PA USA  
SO U.S. Pat. Appl. Publ., 21 pp.



CODEN: USXXCO

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI	US 20060067915	A1	20060330	US 2005-233922	20050922
PRAI	US 2004-612882P	P	20040924		

L10 ANSWER 2 OF 3 USPATFULL on STN

AN 2006:86130 USPATFULL

TI Composition and method for inhibition of microorganisms

IN Doyle, Michael P, Peachtree City, GA, UNITED STATES

Zhao, Tong, Peachtree City, GA, UNITED STATES

PI US 20060073129 A1 20060406

AI US 2003-535357 A1 20031124 (10)

WO 2003-US37526 20031124

20050518 PCT 371 date

PRAI US 2002-428863P 20021125 (60)

DT Utility

FS APPLICATION

LN.CNT 1238

INCL INCLM: 424/093.450

NCL NCLM: 424/093.450

IC IPCI A61K0035-74 [I,A]; A61K0035-66 [I,C\*]

IPCR A61K0035-66 [I,C]; A61K0035-74 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L10 ANSWER 3 OF 3 AGRICOLA Compiled and distributed by the National  
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of America. It contains copyrighted materials. All rights reserved.  
(2008) on STN DUPLICATE 2

AN 2006:43066 AGRICOLA

DN IND43806656

TI Control of Listeria spp. by Competitive-Exclusion Bacteria in Floor Drains  
of a Poultry Processing Plant.

AU Zhao, Tong; Podtburg, Teresa C.; Zhao, Ping; Schmidt, Bruce E.; Baker,  
David A.; Cords, Bruce; Doyle, Michael P.

AV DNAL (448.3 Ap5)

SO Applied and environmental microbiology, 2006 May Vol. 72, no. 5 p.  
3314-3320

Publisher: American Society for Microbiology

ISSN: 0099-2240

NTE Includes references

DT Article; (ELECTRONIC RESOURCE)

FS Other US

LA English

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
23.94	41.97

FULL ESTIMATED COST

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:40:04 ON 16 DEC 2008

69 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0\* with SET DETAIL OFF.

=> s Lactococcus lactis C-1-92

```
      1  FILE CAPLUS
34 FILES SEARCHED...
      11  FILE GENBANK
       1  FILE PROMT
       2  FILE USPATFULL
65 FILES SEARCHED...
```

4 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L11 QUE LACTOCOCCUS LACTIS C-1-92

=> file caplus genbank promt uspatfull

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	1.30	43.27

FILE 'CAPLUS' ENTERED AT 16:41:04 ON 16 DEC 2008  
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.  
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.  
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FILE 'GENBANK' ENTERED AT 16:41:04 ON 16 DEC 2008

FILE 'PROMT' ENTERED AT 16:41:04 ON 16 DEC 2008  
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FILE 'USPATFULL' ENTERED AT 16:41:04 ON 16 DEC 2008  
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=> s l11

L12 15 L11

=> rem dup l12

DUP IS NOT VALID HERE

The DELETE command is used to remove various items stored by the system.

To delete a saved query, saved answer set, saved L-number list, SDI request, batch request, mailing list, or user-defined cluster, format, or search field, enter the name. The name may include ? for left, right, or simultaneous left and right truncation.

Examples:

DELETE BIO?/Q	- delete query names starting with BIO
DELETE ?DRUG/A	- delete answer set names ending with DRUG
DELETE ?ELEC?/L	- delete L-number lists containing ELEC
DELETE ANTICOAG/S	- delete SDI request
DELETE ENZYME/B	- delete batch request
DELETE .MYCLUSTER	- delete user-defined cluster
DELETE .MYFORMAT	- delete user-defined display format
DELETE .MYFIELD	- delete user-defined search field
DELETE NAMELIST MYLIST	- delete mailing list

To delete an ordered document or an offline print, enter its number.

Examples:

```
DELETE P123001C      - delete print request
DELETE D134002C      - delete document order request
```

To delete an individual L-number or range of L-numbers, enter the L-number or L-number range. You may also enter DELETE LAST followed by a number, n, to delete the last n L-numbers. RENUMBER or NORENUMBER may also be explicitly specified to override the value of SET RENUMBER.

Examples:

```
DELETE L21           - delete a single L-number
DELETE L3-L6         - delete a range of L-numbers
DELETE LAST 4        - delete the last 4 L-numbers
DELETE L33-          - delete L33 and any higher L-number
DELETE -L55          - delete L55 and any lower L-number
DELETE L2-L6 RENUMBER - delete a range of L-numbers and
                      renumber remaining L-numbers
DELETE RENUMBER       - renumber L-numbers after deletion of
                      intermediate L-numbers
```

Entire sets of saved items, SDI requests, batch requests, user-defined items, or E-numbers can be deleted.

Examples:

```
DELETE SAVED/Q - delete all saved queries
DELETE SAVED/A - delete all saved answer sets
DELETE SAVED/L - delete all saved L-number lists
DELETE SAVED   - delete all saved queries, answer sets,
                  and L-number lists
DELETE SAVED/S - delete all SDI requests
DELETE SAVED/B - delete all batch requests
DELETE CLUSTER - delete all user-defined clusters
DELETE FORMAT  - delete all user-defined display formats
DELETE FIELD   - delete all user-defined search fields
DELETE SELECT  - delete all E-numbers
DELETE HISTORY - delete all L-numbers and restart the
                  session at L1
```

To delete an entire multifile SDI request, enter DELETE and the name of the request. To delete a component from the multifile SDI, enter DELETE and the name of the component.

```
=> dup rem l12
DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L12
L13      14 DUP REM L12 (1 DUPLICATE REMOVED)
```

```
=> d l13 1-14
```

```
L13  ANSWER 1 OF 14  CAPLUS  COPYRIGHT 2008 ACS on STN DUPLICATE 1
AN   2006:299263  CAPLUS
DN   144:306860
TI   Foaming composition of benign microbes for competitive exclusion of
      undesired microbes
IN   Podtburg, Teresa C.; Schmidt, Bruce; Cords, Bruce; Grab, Lawrence A.;
      Halsrud, David A.
PA   USA
SO   U.S. Pat. Appl. Publ., 21 pp.
```

CODEN: USXXCO

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
	-----	----	-----	-----	-----
PI	US 20060067915	A1	20060330	US 2005-233922	20050922
PRAI	US 2004-612882P	P	20040924		

L13 ANSWER 2 OF 14 USPATFULL on STN

AN 2006:86130 USPATFULL

TI Composition and method for inhibition of microorganisms

IN Doyle, Michael P, Peachtree City, GA, UNITED STATES

Zhao, Tong, Peachtree City, GA, UNITED STATES

PI US 20060073129 A1 20060406

AI US 2003-535357 A1 20031124 (10)

WO 2003-US37526 20031124

20050518 PCT 371 date

PRAI US 2002-428863P 20021125 (60)

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IPCR A61K0035-66 [I,C]; A61K0035-74 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L13 ANSWER 3 OF 14 PROMT COPYRIGHT 2008 Gale Group on STN

ACCESSION NUMBER: 2003:81217 PROMT

TITLE: Natural Additives Kill Listeria.

SOURCE: Food Ingredient News, (March 2003) Vol. 11, No. 3.

ISSN: ISSN: 1070-1788.

PUBLISHER: Business Communications Company, Inc.

DOCUMENT TYPE: Newsletter

LANGUAGE: English

WORD COUNT: 391

\*FULL TEXT IS AVAILABLE IN THE ALL FORMAT\*

L13 ANSWER 4 OF 14 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AM286415 GenBank (R)

GenBank ACC. NO. (GBN): AM286415

GenBank VERSION (VER): AM286415.1 GI:122087364

CAS REGISTRY NO. (RN): 917704-63-3

SEQUENCE LENGTH (SQL): 4615899

MOLECULE TYPE (CI): DNA; circular

DIVISION CODE (CI): Bacteria

DATE (DATE): 29 Oct 2008

DEFINITION (DEF): Yersinia enterocolitica subsp. enterocolitica 8081  
complete genome.

KEYWORDS (ST): complete genome

SOURCE: Yersinia enterocolitica subsp. enterocolitica 8081

ORGANISM (ORGN): Yersinia enterocolitica subsp. enterocolitica 8081

Bacteria; Proteobacteria; Gammaproteobacteria;

Enterobacteriales; Enterobacteriaceae; Yersinia

PROJECT (PJID): GenomeProject:190

REFERENCE: 1

AUTHOR (AU): Delihhas, N.

TITLE (TI): Annotation and evolutionary relationships of a small  
regulatory RNA gene micF and its target ompF in

Yersinia species  
 JOURNAL (SO): (er) BMC Microbiol., 3, 13 (2003)  
 REFERENCE: 2  
 AUTHOR (AU): Thomson,N.R.; Howard,S.; Wren,B.W.; Holden,M.T.;  
 Crossman,L.; Challis,G.L.; Churcher,C.; Mungall,K.;  
 Brooks,K.; Chillingworth,T.; Feltwell,T.; Abdellah,Z.;  
 Hauser,H.; Jagels,K.; Maddison,M.; Moule,S.;  
 Sanders,M.; Whitehead,S.; Quail,M.A.; Dougan,G.;  
 Parkhill,J.; Prentice,M.B.  
 TITLE (TI): The complete genome sequence and comparative genome  
 analysis of the high pathogenicity Yersinia  
 enterocolitica strain 8081  
 JOURNAL (SO): PLoS Genet., 2 (12), E206 (2006)  
 REFERENCE: 3 (bases 1 to 4615899)  
 AUTHOR (AU): Thomson,N.R.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (30-JUN-2006) Thomson N.R., Pathogen  
 Sequencing Unit, The Wellcome Trust Sanger Institute,  
 Genome Campus, Hinxton, Cambridge, CB10 1SA, UNITED  
 KINGDOM

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..4615899	/organism="Yersinia enterocolitica subsp. enterocolitica 8081" /mol-type="genomic DNA" /strain="8081" /sub-species="enterocolitica" /db-xref="taxon:393305"
gene	complement(270..710)	/locus-tag="YE0001"
CDS	complement(270..710)	/locus-tag="YE0001" /codon-start=1 /transl-table=11 /product="putative flavoprotein" /protein-id="CAL10146.1" /db-xref="GI:122087365" /db-xref="GOA:A1JHQ8" /db-xref="InterPro:IPR001094" /db-xref="InterPro:IPR008254" /db-xref="InterPro:IPR015702" /db-xref="UniProtKB/TrEMBL:A1JHQ8" /translation="MADITLISGSTLGS AEYVAE HLAEKLEEAGFTTETLHGPELDEL TLDGMWLIITSTHGAGDLPDNLQPLLEQIEQQR DLSQVRFGAVGLGSSEYDTFCGAV RKLDQQLIIQGAIIRVGDILEIDVIKHEIPEDPAE IWVKNWINLL"
misc-feature	complement(273..704)	/locus-tag="YE0001" /inference="protein motif:PFAM:PF00258" /note="Pfam match to entry PF00258 flavodoxin, Flavodoxin, score 117.3, E-value 1.9e-32"
gene	complement(802..1263)	/gene="asnC"
CDS	complement(802..1263)	/locus-tag="YE0002" /gene="asnC" /locus-tag="YE0002" /codon-start=1 /transl-table=11 /product="regulatory protein" /protein-id="CAL10147.1"

		/db-xref="GI:122087366" /db-xref="GOA:A1JHQ9" /db-xref="InterPro:IPR000485" /db-xref="InterPro:IPR011991" /db-xref="UniProtKB/TrEMBL:A1JHQ9" /translation="MSEIYQIDNLD RGILNALME NARTPYAELAKNFGVSPGTIHVRV EKMRQAGIITAACVHVNPKQLGYDVCCFIGIILK SAKDYP SALKKLESLEEVVEAYYT TGHYSIFIKVMCKSIDALQQVLINKIQTIDEIQS TETLISLQNPIMRTIVP"
misc-feature	complement(868..1173)	/gene="asnC" /locus-tag="YE0002" /inference="protein" motif:PFAM:PF01037" /note="Pfam match to entry PF01037 ASNC-trans-reg, AsnC family, score 61.4, E-value 1.2e-15"
misc-feature	complement(1111..1191)	/gene="asnC" /locus-tag="YE0002" /inference="protein" motif:Prosite:PS00519" /note="PS00519 Bacterial regulatory proteins, asnC family signature."
misc-feature	complement(1129..1194)	/gene="asnC" /locus-tag="YE0002" /note="Predicted helix-turn-helix motif with score 1765.000, SD 5.20 at aa 24-45, sequence TPYAELAKNFGVSPGTIHVRVE"
gene	1449..2441	/gene="asnA"
CDS	1449..2441	/locus-tag="YE0003" /gene="asnA" /locus-tag="YE0003" /codon-start=1 /transl-table=11 /product="aspartate-ammonia ligase" /protein-id="CAL10148.1" /db-xref="GI:122087367" /db-xref="GOA:A1JHR0" /db-xref="InterPro:IPR004618" /db-xref="InterPro:IPR006195" /db-xref="UniProtKB/Swiss-Prot:A1J HR0" /translation="MKKQFIQKQQQISFVKSFFS RQLEQQ LGLIEVQAPILSRVGDGT QDNLSGSEKAVQVKVKS LPDATFEVVHSLAKWKR KTLGRFDFGADQGIYTHMKALRPD EDRLSAIHSVYVDQWDWERVMGDGERNLAYLKST VNKIYAAIKETEA AISAEFDIKPF LPEQIHFIHSESLRAKFPDLDAKGRERAI AKELG AVFLIGIGGKLADGKSHDVRAPDY DDWTSPSAEGFAGLNGDIIVWNPVLEDAFEISSM GIRVDAEALKRQLALTSDEDR LKL EWHQSL L NGEMPQTIGGGIGQSRLVMLLLQQQHI GQVQCGVWGPEISEKVEGLL"
misc-feature	1455..2186	/gene="asnA" /locus-tag="YE0003" /inference="protein" motif:PFAM:PF03590"

		/note="Pfam match to entry PF03590 AsnA, Aspartate-ammonia ligase, score 597.7, E-value 4.6e-177" /gene="asnA" /locus-tag="YE0003" /inference="protein motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)." /locus-tag="YE0004" /locus-tag="YE0004" /inference="similar to sequence:INSDC:AE001895" /inference="similar to sequence:INSDC:AL646078" /note="Similar to Ralstonia solanacearum probable transmembrane protein RSP0410 or RS00867 SWALL:Q8XSQ7 (EMBL:AL646078) (224 aa) fasta scores: E(): 7.3e-36, 46.54 38d in 217 aa, and to Deinococcus radiodurans hypothetical protein DR0351 SWALL:Q9RXG2 (EMBL:AE001895) (227 aa) fasta scores: E(): 3.7e-17, 31.67 38d in 221 aa" /codon-start=1 /transl-table=11 /product="putative membrane protein" /protein-id="CAL10149.1" /db-xref="GI:122087368" /db-xref="InterPro:IPR009781" /db-xref="UniProtKB/TrEMBL:A1JHR1" /translation="MARFHPLRHYSHARPRLLS VGAGIIAYFLLPSHFTVLLRVMVS WNIFAWLYLLFLWLQLLRNDPKKIRLIARVQDES ASMVLSIVSMACLASILVILFELS TANQLSGSAKAFHLVLTGMTLLVSWLLLPTAFTM HYAHLFYLSRDESDAVLPLIFPKE VTEPTYWDFLYFSFTIGVASQTADVSTGTSDIRR VVLLQSVLSFIFNMTILGLSINVG AGLLN" /locus-tag="YE0004"
misc-feature	2055..2078	
gene	2595..3266	
CDS	2595..3266	
misc-feature	join(2643..2711, 2721..2777, 2838..2906, 2934..3002, 3192..3260)	/inference="protein motif:TMHMM:2.0" /note="5 probable transmembrane helices predicted for YE0004 by TMHMM2.0 at aa 17-39, 43-61, 82-104, 114-136 and 200-222" /locus-tag="YE0005" /locus-tag="YE0005" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10150.1" /db-xref="GI:122087369" /db-xref="InterPro:IPR002035" /db-xref="UniProtKB/Swiss-Prot:A1J
gene	complement(3276..4742)	
CDS	complement(3276..4742)	

		HR3"
		/translation="MLSLATLDLLLSISESELIE EMVVGLLASPQLAIFFEKFPRIKR ALMKDIPGWKQNLQQRIREAKVPAGLANEFALYQ QSQLEDSPLFYAHLPPQIVVQLQQW HSPFATQAKTLLHTADLERNPQTGDSFQTLFLQR WRVSLTLQTITIIHQLEQEREQL LAELQQRLALSGALEPILATNDGAAGRLWDMSQG HLQRGDYQLLLQYGDFLQQQPELQ QLAEQLGRSRSASAKQPTPDARFEPYTMVVRQPD VPEEVSGIHQSNDILRLLPTELVM LGMSELEFEFYRRLLERRLLTYRLQGDNWQEKTL QRPISLKSHDEQPRGPFIVCVDTS GSMGGFSEQCAKAFCLALLRIALEDNRRCYIMLF ATEIIHYELSSASGIEQAIRFLSQ HFRGGTDLAACLSSSTLSKMEERDWDADAVIISD FIAQRLPEELIRKIKIQQAQHR FHAVAMSAYGKPGIMRIFDHIWRFDTGLKSRLIR RWKR"
misc-feature	complement(4035..4100)	/locus-tag="YE0005" /note="Predicted helix-turn-helix motif with score 997.000, SD 2.58 at aa 215-236, sequence PELQQLAELGRSRSASAKQPTP"
gene	complement(4746..6254)	/locus-tag="YE0006"
CDS	complement(4746..6254)	/locus-tag="YE0006" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10151.1" /db-xref="GI:122087370" /db-xref="GOA:A1JHR5" /db-xref="InterPro:IPR003593" /db-xref="InterPro:IPR011704" /db-xref="UniProtKB/Swiss-Prot:A1J HR5" /translation="MAQSSQLAERISRLSSALES GLYERQEAIRLCLLAALSGESVFL LGPPGIAKSLIARRLKFAFRNARAFEYLMTRFST PEEVFGPLSIQALKEEGRYQRMGTG GYLPEAEIVFLDEIWKAGPAILNTLLTAINERRF RNGDREDSIPMRLLVASNELPDA DSSLEALYDRMLIRLWLDRVQEKQNFRLLSRQ NENHNPVAENLSISDEEFYQWQPL IDKIALPDNCFELIFQLRQQLSAQEQAPYVSDRR WKKALRLLQASAFFSGRDEITPID LILLKDCLWHDLSLKLQQLLEQLLTHEGYQQQ SLLMKLQHIHAQWLKHQQQQSDHQ ALTVTQKQSGMFSRKPQYSLPDHLTDSTLTFLQK PLSLHDIQVNHLLQIEKEMLVQWLN KGGVLRKLNQVGYAQSIDAEVDDQLHITVLQVS RQSSILSQPGASTASVPPELLVEL AELENSLAEQRRFLFSQHQPCLFTPSSWLAKIEAS LLNVAEQVKQLQQKLRGH"
gene	6708..8435	/gene="kup" /locus-tag="YE0007"
CDS	6708..8435	/note="synonym: trkD" /gene="kup" /locus-tag="YE0007" /codon-start=1 /transl-table=11



		/product="potassium transport protein" /protein-id="CAL10152.1" /db-xref="GI:122087371" /db-xref="GOA:A1JHR6" /db-xref="InterPro:IPR003855" /db-xref="UniProtKB/Swiss-Prot:A1J HR6" /translation="MVFGFLSLIFWMLILIVSVK YLTYVMRADNAGEGGILTLMSLAG RNTSSRATSILVILGLIGGSFFYGEVVITPAISV MSAIEGLEIAAPALDPYIVPCSA VLTLLFVIQKHGTGSVGKLFAPVMLVWFLTLALL GLRSIIANPEVLAALNPKWAISFF TEYKSVSFFALGAVVLAITGVEALYADMGHFGKF PIRLAWFTTVLPSLVNLNYFGQGAL LLKNPEAIKNPFFLLAPDWALIPLLILATLATVI ASQAVISGVFSLTRQAVRLGYLPP MRIIHTSEMESGQIYIPVINWTLYLAVVLVIVGF ERSSNLAAAYGIAVTGTMVITSVL FCTVALKNWHWNRRFFVYFLLVALLVIDVPMFSAN ALKLFSGGWLPLSLGLVMFIIMTT WKSERFSLRRMHEHGNSLEAMIASLEKSPVVRV PGTAVYMSRAMNVIPFALLHNLKH NKVLHDRVLLTLRTEDAPYVHNVRVTIEQLSP TFWRVVASYGWRETPNVEEIFHRC GLEGLPCQMMETSFFMSHESLILTKRPWYLFLRG KLFIALSRNALRAADQFEIPPNRV IELGTQVEI" /gene="kup" /locus-tag="YE0007" /inference="protein" motif:PFAM:PF02705" /note="Pfam match to entry PF02705 K-trans, K+ potassium transporter, score 854.9, E-value 1.7e-254" /gene="kup" /locus-tag="YE0007" /inference="protein" motif:TMHMM:2.0" /note="11 probable transmembrane helices predicted for YE0007 by TMHMM2.0 at aa 4-26, 55-77, 87-109, 121-143, 163-185, 198-220, 240-262, 287-309, 319-341, 348-365 and 375-393" /locus-tag="YE0008" /locus-tag="YE0008" /codon-start=1 /transl-table=11 /product="ribose permease" /protein-id="CAL10153.1" /db-xref="GI:122087372" /db-xref="GOA:A1JHR8" /db-xref="InterPro:IPR007721" /db-xref="UniProtKB/Swiss-Prot:A1J HR8"
misc-feature	6711..8432	
misc-feature	join(6717..6785, 6870..6938,6966..7034, 7068..7136,7194..7262, 7299..7367,7425..7493, 7566..7634,7662..7730, 7749..7802,7830..7886)	
gene	8606..9025	
CDS	8606..9025	

		/translation="MKKGALLNSDISAVISRLGH TDQIVIGDAGLPIPATTTTRIDLAL TQGVPGFLQVFEVVTQEMQVESAYLAQEIVKNNP QLHETLLAQLSQLEQHQNQIALH YISHEAFKEQTKQSRVIRSGECSPFANIILCSG VTF"
gene	9033..10535	/gene="rbsA"
		/locus-tag="YE0009"
CDS	9033..10535	/gene="rbsA"
		/locus-tag="YE0009"
		/inference="similar to sequence:INSDC:AL627280"
		/inference="similar to sequence:UniProtKB:P04983"
		/note="Similar to Escherichia coli ribose transport ATP-binding protein RbsA SWALL:RBSA-ECOLI (SWALL:P04983) (501 aa) fasta scores: E(): 2.7e-148, 85.83 38d in 494 aa, and to Salmonella typhi high affinity ribose transport protein STY896 SWALL:Q8Z2R4 (EMBL:AL627280) (501 aa) fasta scores: E(): 1.1e-147, 85.62 38d in 494 aa"
		/codon-start=1
		/transl-table=11
		/product="putative ribose transport ATP-binding protein"
		/protein-id="CAL10154.1"
		/db-xref="GI:122087373"
		/db-xref="GOA:A1JHS1"
		/db-xref="InterPro:IPR003439"
		/db-xref="InterPro:IPR003593"
		/db-xref="InterPro:IPR015861"
		/db-xref="UniProtKB/TrEMBL:A1JHS1"
		/translation="MQPLLQLKGIDKAFPGVKAL SGAALSVYPGRVMALVGENGAGKS TMMKVLTGIYNKDAGSQHFLGKEVVFNGPKESQE AGIGIIHQELNLIPLTLIAENIFL GREFVNHFGGIDWKKMYAEADLLARLNISYSSH RLVGELSIGDQQMVEIAKVLSFES KVIIMDEPTDALTDTETASLFNVIKELKAEGRI VYISHRLKEIFEICDDVTVFRDQ FIAEKPVNLTENALIEMMVGRKLEEQYPRNLNLP RGEKRLQVKQLCGPGVENVNFTLY SGEILGVAGLMGAGRTELMKIIYGALPRKSGFVM LDGREVVTHSPQDGLANGIVYISE DRKRDGLVLGMSVKENMSLTALRYFSRSGGSLKH ADEQQAVADFIRLFNIKTPSMEQP IGLLSGGNQQKVAIARGLMTRPKVLILDEPTRGV DVGAKKEIYQLINQFKQEGLSIIL VSSEMPEVLGMSDRIIVMHEGQLSGEFSIEQATQ EVLMAAVGKRDLLEK"
misc-feature	9120..9683	/gene="rbsA"
		/locus-tag="YE0009"
		/inference="protein"
		motif:PFAM:PF00005"
		/note="Pfam match to entry PF00005 ABC-tran, ABC transporter, score 173.1, E-value 3e-49"
misc-feature	9141..9164	/gene="rbsA"

		/locus-tag="YE0009" /inference="protein" motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)." /gene="rbsA"
misc-feature	9864..10445	/locus-tag="YE0009" /inference="protein" motif:PFAM:PF00005" /note="Pfam match to entry PF00005 ABC-tran, ABC transporter, score 134.4, E-value 1.3e-37" /gene="rbsA"
misc-feature	10218..10262	/locus-tag="YE0009" /inference="protein" motif:Prosite:PS00211" /note="PS00211 ABC transporters family signature." /gene="rbsC"
gene	10623..11588	/locus-tag="YE0010" /gene="rbsC"
CDS	10623..11588	/locus-tag="YE0010" /codon-start=1 /transl-table=11 /product="putative sugar transport system, permease protein" /protein-id="CAL10155.1" /db-xref="GI:122087374" /db-xref="GOA:A1JHS2" /db-xref="InterPro:IPR001851" /db-xref="UniProtKB/TrEMBL:A1JHS2" /translation="MSSQTINTKRWFSSKEWLLEQ KSLIALLVLIHAVVSSLSPNFFTLN NMFNILQQTSVNAIMAVGRTLVLITSGIDLSVGS LLALTGAVAASIVGLEVNALVAVG AALALGAFVGGITGVIVAKGKVQAFIATLVMMLL LRGVTMVYTNGSPINTGFTDVADT FGWFGIGRPLGIPTPIWLMAIVFIAAWYMLHHTR LGRYIYALGGNESATRLSGISVDK VKIIVYSLCGLLAALAGIIEVARLSSAQPTAGTG YELDAIAAVVLGGTSLAGGKGQIV GTLIGALILGFLNGLNLLGVSSYYQMIVKAVVI LLAVLVDNKKQ" /gene="rbsC"
sig-peptide	10623..10748	/locus-tag="YE0010" /note="Signal peptide predicted for YE0010 by SignalP 2.0 HMM (Signal peptide probability 0.969) with cleavage site probability 0.169 between residues 42 and 43" /gene="rbsC"
misc-feature	join(10686..10754, 10815..10883, 10911..10979, 10998..11066, 11124..11192, 11283..11351, 11445..11513)	/locus-tag="YE0010" /inference="protein" motif:TMHMM:2.0" /note="7 probable transmembrane helices predicted for YE0010 by

		TMHMM2.0 at aa 22-44, 65-87, 97-119, 126-148, 168-190, 221-243 and 275-297"
misc-feature	10746..11582	/gene="rbsC" /locus-tag="YE0010" /inference="protein motif:PFAM:PF02653" /note="Pfam match to entry PF02653 BPD-transp-2, Branched-chain amino acid transport system / permease component, score 3.4, E-value 7.7e-07"
gene	11760..12647	/gene="rbsB" /locus-tag="YE0011" /note="synonyms: prlB, rbsP"
CDS	11760..12647	/gene="rbsB" /locus-tag="YE0011" /inference="similar to sequence:UniProtKB:P02925" /inference="similar to sequence:UniProtKB:P02926" /note="Similar to Escherichia coli D-ribose-binding periplasmic protein precursor RbsB or RbsP or PrlB SWALL:RBSB-ECOLI (SWALL:P02925) (296 aa) fasta scores: E(): 1.7e-84, 84.74 38d in 295 aa, and to Salmonella typhimurium, and Salmonella typhi D-ribose-binding periplasmic protein precursor RbsB or RbsP or STM3884 or STY3894 SWALL:RBSB-SALTY (SWALL:P02926) (296 aa) fasta scores: E(): 5.6e-84, 84.06 38d in 295 aa" /codon-start=1 /transl-table=11 /product="putative D-ribose-binding periplasmic protein precursor" /protein-id="CAL10156.1" /db-xref="GI:122087375" /db-xref="InterPro:IPR001761" /db-xref="UniProtKB/TrEMBL:A1JHS3" /translation="MKMKKLATLISVVALSATVS ANALAKDTIALVSTLNNPFFVSM KDGAQKEADKLGYNLVILDSQNNPAKELANVQDL TVRGTKLLLINPTDSDAVGNAVKM ANQANIPVITLDRLANAGTVVSHVASDNRFGGKM AGDYIAKKVGSDAKVQLEGIAGA SAARERGEFGKQSMEKNKFQLLASQPADFDRTKG LNVMQNLLTAHPDVQAVFAQNDEM ALGALRALQTAGKTDVLVVGFDGTDGDIKAVESG KMGATIAQRPDQIGVIGVQTADKV LKGEKVQAVIPVDLKLVTK"
sig-peptide	11760..11834	/gene="rbsB" /locus-tag="YE0011" /note="Signal peptide predicted for YE0011 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.933 between residues 25 and 26"

misc-feature	11835..12641	/gene="rbsB" /locus-tag="YE0011" /inference="protein motif:PFAM:PF00532" /note="Pfam match to entry PF00532 Peripla-BP-like, Periplasmic binding proteins and sugar binding domain of the LacI family, score 63.4, E-value 3.3e-16"
misc-feature	12432..12455	/gene="rbsB" /locus-tag="YE0011" /inference="protein motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	12811..13737	/gene="rbsK" /locus-tag="YE0012"
CDS	12811..13737	/gene="rbsK" /locus-tag="YE0012" /codon-start=1 /transl-table=11 /product="ribokinase" /protein-id="CAL10157.1" /db-xref="GI:122087376" /db-xref="GOA:A1JHS4" /db-xref="InterPro:IPR002139" /db-xref="InterPro:IPR002173" /db-xref="InterPro:IPR011611" /db-xref="InterPro:IPR011877" /db-xref="UniProtKB/TrEMBL:A1JHS4" /translation="METGKLVVLGSINADHILNI EQFPRPGETVVGEQYKVAFGGKGA NQAVAAGRSGANIAFIACVGEDDIGDRVRLQLAS DNIDTAPIEAVAGTTTGVALIFVN GEGENVIGIHAGANSAVTPEYLGRYQQQVIDADA LLMQLESPLGTVIAAAKLAKQHQT QVILNPAPARELPDELLSLVDMITPNETEAERLT GIHIEQDDDAAKAAQILHDKGIAT VIITLGSRGVWLSEQGQKLVAGFKVNAVDTIAA GDTFNGALLTALLEGQAMGSAVRF AHAAAAIAVTRPGAQPSIPWRAEIDSFLQDRV"
misc-feature	12817..13701	/gene="rbsK" /locus-tag="YE0012" /inference="protein motif:PFAM:PF00294" /note="Pfam match to entry PF00294 pfkB, pfkB family carbohydrate kinase, score 298.8, E-value 4.4e-87"
misc-feature	12928..13002	/gene="rbsK" /locus-tag="YE0012" /inference="protein motif:Prosite:PS00583" /note="PS00583 pfkB family of carbohydrate kinases signature 1."
misc-feature	13552..13593	/gene="rbsK" /locus-tag="YE0012" /inference="protein motif:Prosite:PS00584" /note="PS00584 pfkB family of carbohydrate kinases signature 2."
gene	13740..14741	/gene="rbsR"

CDS	13740..14741	<pre> /locus-tag="YE0012A" /gene="rbsR" /locus-tag="YE0012A" /inference="similar to sequence:INSDC:AE008881" /inference="similar to sequence:UniProtKB:P25551" /note="Similar to Escherichia coli, and Escherichia coli O157:H7 ribose operon repressor RbsR or b3753 or z5254 or ecs4695 SWALL:RBSR-ECOLI (SWALL:P25551) (329 aa) fasta scores: E(): 7.1e-94, 73.17 38d in 328 aa and to Salmonella typhimurium transcriptional repressor for rbs operon RbsR or stm3886 SWALL:Q8ZKV7 (EMBL:AE008881) (332 aa) fasta scores: E(): 5.3e-95, 74.09 38d in 332 aa" /codon-start=1 /transl-table=11 /product="ribose operon repressor" /protein-id="CAL10158.1" /db-xref="GI:122087377" /db-xref="GOA:A1JHS5" /db-xref="InterPro:IPR000843" /db-xref="InterPro:IPR001761" /db-xref="UniProtKB/TrEMBL:A1JHS5" /translation="MATMKDVARLAGVSTSTVSH VINKNRFVSDPIRDKVLAAIKQLN YAPSALARSLKLNETRTIGMLVTASSNPFYAEV RGVERSCYERGYSLILCNTEGDID RMSRSIETLMQKRVDGLLLMCTESHRPSQDILRC YPSLP IIMMDWAPFEGVNDVIQDN SLLGEMATSYLIARGYTRIACIAGPQDKTPAKE RLQGFRQAMDRAGLPVLPDYEVAS DFEFGGGLVAMKQLLALPQPPEAVFTSNDAMAVG VYQALHQAGLSIPQDMAVIGYDDI EIAQYMTPLTTHQPKDSLGLAIDTLIHLNS PEAEPQVLILTPELIERGSVATR" </pre>
gene	complement(14738..16162)	/locus-tag="YE0013"
CDS	complement(14738..16162)	<pre> /locus-tag="YE0013" /codon-start=1 /transl-table=11 /product="putative membrane transport protein" /protein-id="CAL10159.1" /db-xref="GI:122087378" /db-xref="GOA:A1JHS6" /db-xref="InterPro:IPR001411" /db-xref="InterPro:IPR007114" /db-xref="InterPro:IPR011701" /db-xref="UniProtKB/TrEMBL:A1JHS6" /translation="MIKSARSMAGLPWIAAMAFF MQALDATILNTALPSIAESLNRSP LTMQSAIISYTLTVAMLIPVSGWLADRFGTTRIF ILAVSLFTLGSLLCALSGSLPFLV ASRVIQGVGGAMMPVARLALIRAYPRSELLPVL NFVTIPGLIGPVMGPLLGLLVTY" </pre>

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PRDGDNLIQGRNVKKVTQPAKSEV"

sig-peptide    complement(16052..16162 /locus-tag="YE0013"
)

                /note="Signal peptide predicted
                for YE0013 by SignalP 2.0 HMM
                (Signal peptide probability 0.994)
                with cleavage site probability
                0.740 between residues 37 and 38"

misc-feature    complement(join(14816.. /locus-tag="YE0013"
14884,14927..14995,
15032..15100,
15128..15196,
15233..15301,
15344..15412,
15431..15499,
15527..15583,
15620..15679,
15689..15757,
15791..15859,
15869..15937,
15956..16015,
16058..16126))

                /inference="protein
                motif:TMHMM:2.0"
                /note="14 probable transmembrane
                helices predicted for YE0013 by
                TMHMM2.0 at aa 13-35, 50-69,
                76-98, 102-124,136-158, 162-181,
                194-212, 222-244, 251-273,
                288-310,323-345, 355-377, 390-412
                and 427-449"

misc-feature    complement(15830..16132 /locus-tag="YE0013"
)

                /inference="protein
                motif:PFAM:PF00083"
                /note="Pfam match to entry PF00083
                sugar-tr, Sugar (and other)
                transporter, score 20.7, E-value
                2.1e-06"

gene            complement(16237..16926 /locus-tag="YE0014"
)

CDS             complement(16237..16926 /locus-tag="YE0014"
)

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                /transl-table=11
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                transcriptional regulator"
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                /db-xref="GOA:A1JHS7"
                /db-xref="InterPro:IPR000524"
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misc-feature	complement(16696..16875)	/locus-tag="YE0014"  /inference="protein motif:PFAM:PF00392" /note="Pfam match to entry PF00392 gntR, Bacterial regulatory proteins, gntR family, score 79.0, E-value 6.6e-21"
misc-feature	complement(16744..16818)	/locus-tag="YE0014"  /inference="protein motif:Prosite:PS00043" /note="PS00043 Bacterial regulatory proteins, gntR family signature."
misc-feature	complement(16750..16815)	/locus-tag="YE0014"  /note="Predicted helix-turn-helix motif with score 1101.000, SD 2.94 at aa 38-59, sequence PGEIELGEQFGVSRTAVREAVK"
gene rRNA	17506..18994 17506..18994	/gene="16S rRNA" /gene="16S rRNA" /product="16S ribosomal RNA" /note="match to 16S-rRNA 1..1461 (Y.enterocolitica 16S)"
gene tRNA	19220..19295 19220..19295	/gene="tRNA-Glu (TTC)" /gene="tRNA-Glu (TTC)" /product="tRNA-Glu" /note="codon recognized: GAA"
gene rRNA	19674..22667 19674..22667	/gene="23S rRNA" /gene="23S rRNA" /product="23S ribosomal RNA" /note="match to 23S-rRNA 1..2994 (Y. enterocolitica 23S EMBL:U77925, Y.pestis KIM 98 38dentitity, Citrobacter freundii 23S EMBL:U77928 94 38dentitity)"
gene rRNA	22667..22908 22667..22908	/gene="5S rRNA" /gene="5S rRNA" /product="5S ribosomal RNA" /note="match to 5SrRNA 1..240 Y.enterocolitica"
gene	complement(23194..23721)	/gene="mobB"  /locus-tag="YE0016"
CDS	complement(23194..23721)	/gene="mobB"  /locus-tag="YE0016" /codon-start=1 /transl-table=11



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misc-feature	complement(23299..23703)	/locus-tag="YE0016" /inference="protein motif:PFAM:PF03205" /note="Pfam match to entry PF03205 MobB, Molybdopterin guanine dinucleotide synthesis protein B, score 184.3,E-value 1.3e-52" /gene="mobB"
misc-feature	complement(23662..23685)	/locus-tag="YE0016" /inference="protein motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)." /gene="mobA"
gene	complement(23718..24317)	/locus-tag="YE0017" /note="synonyms: chlB, mob, nar" /gene="mobA"
CDS	complement(23718..24317)	/locus-tag="YE0017" /codon-start=1 /transl-table=11 /product="molybdopterin-guanine dinucleotide biosynthesis protein A" /protein-id="CAL10162.1" /db-xref="GI:122087381" /db-xref="GOA:A1JHS9" /db-xref="InterPro:IPR013482" /db-xref="UniProtKB/TrEMBL:A1JHS9" /translation="MIEMQPNITGVILAGGRSSR MGGNDKGLTLLHDKPLFQYVIDRL KPQVNDLLINANRNQELYQASGVPVVSIIITGFV GPLAGMHAGLSYSPTIEWVVFAPCD VPALPSNLVSQLWQGGKQALAAVVDGERAHPTL ALMHVSLKSLLAEYLAKSDRKLM I FMDSVNAQPIIFRGQKDQFSNLNTPADCDLWEQS KRGEL" /locus-tag="YE0018" /locus-tag="YE0018" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein"
gene	24462..24731	
CDS	24462..24731	

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gene	24823..25809	/locus-tag="YE0019"
CDS	24823..25809	/locus-tag="YE0019" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10164.1" /db-xref="GI:122087383" /db-xref="InterPro:IPR002575" /db-xref="UniProtKB/TrEMBL:A1JHT1" /translation="MNSSAFNFQTLSPDLIMDAL EGVGLRVDSGLTALNSYENRVYQF MDEDRKRYVVKFYRPERWSSEQILEEHQFSLDLA ESEIPVIAPLQLDGRITLHTHGGFF FTVFPSVGGRRQYEIDNLDQLEWVGRYLGRIHQVG SDALFVARSTIGIEEYLTEPRQLL ASSELVPAKQRDKFLAATDLLISTIKQYWHTDWQ PLRLHGDCHPGNILWRDGPMPFVDL DDARNGPAVQDLWMLLHGERREQLIQLDILLEAY GEFADFDQRELALIEPLRAMRMVY YLAWVARRWQDPAPFKSFPWMAESDFWLQQTASF TEQVKLLQAPPLQLMPMY"
gene	25856..26479	/gene="dsbA"
CDS	25856..26479	/locus-tag="YE0020" /gene="dsbA" /locus-tag="YE0020" /codon-start=1 /transl-table=11 /product="secreted thiol:disulfide interchange protein DsbA" /protein-id="CAL10165.1" /db-xref="GI:122087384" /db-xref="GOA:A1JHT2" /db-xref="InterPro:IPR001853" /db-xref="InterPro:IPR006662" /db-xref="InterPro:IPR012335" /db-xref="UniProtKB/TrEMBL:A1JHT2" /translation="MKNVWLALVGMVMAFSASAA QFTDGTQYQTLNKPVTGEPQVLEF FSFYCPHCYQFEEVYHVPQAVKKALPEGTKMTRY HVEFLGPLGKQLTQAWAVAMALGV EEKITPLMFEGVQKTQTVQTPDDIRNVFIKAGVS GEEFDAALNSFVVKSLVVQQQKAA EDLELRGVPAMFVNGKYMINKNDGMDTSSMDTYVK QYADVVKFLLTQK"
sig-peptide	25856..25912	/gene="dsbA" /locus-tag="YE0020" /note="Signal peptide predicted for YE0020 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.992 between residues 19 and 20"
misc-feature	25856..26476	/gene="dsbA" /locus-tag="YE0020"

		/inference="protein motif:PFAM:PF01323" /note="Pfam match to entry PF01323 DSBA, DSBA oxidoreductase, score 486.2, E-value 1.7e-143" /gene="dsbA" /locus-tag="YE0020" /inference="protein motif:Prosites:PS00194" /note="PS00194 Thioredoxin family active site."
misc-feature	25976..26032	
gene	27070..29868	/gene="polA" /locus-tag="YE0021" /note="synonym: resA"
CDS	27070..29868	/gene="polA" /locus-tag="YE0021" /codon-start=1 /transl-table=11 /product="DNA polymerase I" /protein-id="CAL10166.1" /db-xref="GI:122087385" /db-xref="GOA:A1JHT3" /db-xref="InterPro:IPR001098" /db-xref="InterPro:IPR002298" /db-xref="InterPro:IPR002421" /db-xref="InterPro:IPR002562" /db-xref="InterPro:IPR003583" /db-xref="InterPro:IPR008918" /db-xref="UniProtKB/TrEMBL:A1JHT3" /translation="MAQIAENPLILVDGSSYLRY AYHAFPLTNSKGPTGAMYGVLN MLRSLLLQYRPSHVAVVFDAGKGTFRDELFAEYK SHRPPMPDDLRAQIEPLHQMVKAM GLPLLVSVEADDVIGTLAQEAKEAGHAVLIST GDKDMAQLVTPNITLINTMNNAIL GPQEVCEKYGVPELIIIDFLALMGDSSDNIPGVP GVGEKTAQALLQGLGGLDSLNLH DKIPTLTFRGAKTMSAKLEQNKDVAYLSYKLATI KTDVELDITCDELNVSA PDDEQLH QLFSRYEFKRWLADVEAGKWLDGKKDRPTAQASN KAFVAPESAPVAEVTAVLSQENYQ TILDEKSLSDWIERLKKAEVFAFD TETDGLDTLS SNLIGLSFAVAPGEAAYLPLAHDY LDAPAQLDRDWVLAQLKPLLEDDKALKVGQNLKF DQSM LARYGIDLRGIAFD TMLSY VLDSVAGRHDMDSLAERYLNHKTITFEEIAGKKG NQLTFNQIALEQAGPYAAEDADVT LQLHLVLWPKLQQSEGLKRVFQEIEMPLLPLSR IERTGVLIDQNILAAHSKELTIRL DELEKQAH ELAEEP FN LASPKQLQVILYEKQKLP ILKKT PGGAAS TNEEV LAELALDY PLPKVILEYRGLAKLKSTYTDKLPLMINPVSGRV HTSYHQAVTATGRLSSRDPNLQNI PVRNEEGRRIRQAFIAPEGYRIMAADYSQIELRI MAHLSQDKGLLAFAAGKDIHRAT AAEVFGLSLEKVTNEQRRSAKAINFGLIYGMSAF GLARQLNIPRGEAQRYMDLYFERY PGVLEYMERTRKQAAEQGYVTTL DGRRLYLPDIH SRNATRRKAAEREAINAPMQGTAA DIIKRAMIAVD AWLQQQPEPLVRVIMQVHDELVF EVHESVLES AEQKIRELMEQSMQL AVPLKVDVGVGYNWDQAH"

misc-feature	27088..27576	/gene="polA" /locus-tag="YE0021" /inference="protein motif:PFAM:PF02739" /note="Pfam match to entry PF02739 5-3-exonuc-N, 5'-3' exonuclease, N-terminal resolvase-like domain, score 316.3, E-value 2.4e-92"
misc-feature	27580..27900	/gene="polA" /locus-tag="YE0021" /inference="protein motif:PFAM:PF01367" /note="Pfam match to entry PF01367 5-3-exonuclease, 5'-3' exonuclease, C-terminal SAM fold, score 194.5, E-value 1.1e-55"
misc-feature	28048..28629	/gene="polA" /locus-tag="YE0021" /inference="protein motif:PFAM:PF01612" /note="Pfam match to entry PF01612 3-5-exonuclease, 3'-5' exonuclease, score 229.0, E-value 4.4e-66"
misc-feature	28717..29862	/gene="polA" /locus-tag="YE0021" /inference="protein motif:PFAM:PF00476" /note="Pfam match to entry PF00476 DNA-pol-A, DNA polymerase family A, score 698.2, E-value 2.6e-207"
misc-feature	29338..29397	/gene="polA" /locus-tag="YE0021" /inference="protein motif:Prosites:PS00447" /note="PS00447 DNA polymerase family A signature."
misc-RNA	30017..30134	/note="Spot 42 RNA (RF00021) as predicted by Rfam, score 91.54, positions 1 to 118"
gene	complement(30302..30955	/locus-tag="YE0022"
	)	
CDS	complement(30302..30955	/locus-tag="YE0022"
	)	

/codon-start=1  
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/product="conserved hypothetical  
protein"  
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/db-xref="InterPro:IPR002917"  
/db-xref="InterPro:IPR005289"  
/db-xref="UniProtKB/Swiss-Prot:A1J  
HT4"  
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EYLQKRNCCLKGLVVLMDIRHPLKDLDDQOMITWAV  
AVGTPVMLLLTKADKLASGARKAQ  
LNMVREAIIPFMGDIQVEAFSSLKKIGVDKLREK

misc-feature	complement(30830..30853)	LDTWFSEIPPEVMIDEYDDEEGK" /locus-tag="YE0022"  /inference="protein motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)." /note="CsrC family RNA (RF00084) as predicted by Rfam, score 35.38, positions 1 to 254" /locus-tag="YE0023" /locus-tag="YE0023" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10168.1" /db-xref="GI:122087387" /db-xref="InterPro:IPR007336" /db-xref="UniProtKB/Swiss-Prot:A1J HT5" /translation="MKQPNKAPRADRAAPKGTAT PKRHKKTRVELDIEARERKRQKRH SGNRSGARTNIEGSNKTGSTQAEKDPRIKSKVP VPLLVESKAKAKLTTKPVAKVEAK PRLTPEEELTKLENDERLDALLDRLDNDEVLSKE DQAYVDLTLDRIDALMEQLGIELG DDEDDEEREKPEDILKLLKSGNPKDTF"
misc-RNA	31382..31582	
gene	31718..32284	
CDS	31718..32284	
gene	32467..33840	/gene="hemN" /locus-tag="YE0024"
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misc-feature	32761..33522	/gene="hemN" /locus-tag="YE0024"

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                                score 555.2, E-value 2.8e-164"
gene      complement(33989..35401 /gene="ntrC"
)
                                /locus-tag="YE0025"
                                /note="synonyms: glnG, glnT"
CDS      complement(33989..35401 /gene="ntrC"
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                                E-value 2e-16"
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                                at aa 444-465, sequence
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misc-feature complement(34313..34342 /gene="ntrC"
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misc-feature	complement(34676..34723)	/locus-tag="YE0025" /inference="protein motif:Prosite:PS00676" /note="PS00676 Sigma-54 interaction domain ATP-binding region B signature." /gene="ntrC"
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gene	complement(35409..36458)	/locus-tag="YE0026" /note="synonyms: gln1, glnR" /gene="ntrB"
CDS	complement(35409..36458)	/locus-tag="YE0026" /codon-start=1 /transl-table=11 /product="Two component regulatory protein involved in nitrogen assimilation" /protein-id="CAL10171.1" /db-xref="GI:122087390" /db-xref="GOA:A1JHT8" /db-xref="InterPro:IPR000014" /db-xref="InterPro:IPR003594" /db-xref="InterPro:IPR003661" /db-xref="InterPro:IPR004358" /db-xref="InterPro:IPR005467" /db-xref="InterPro:IPR013767" /db-xref="UniProtKB/TrEMBL:A1JHT8" /translation="MATGTLPDAGQILNSLINSI"

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                score 104.0, E-value 1.9e-28"
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                /inference="protein
                motif:PFAM:PF00512"
                /note="Pfam match to entry PF00512
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                (phosphoacceptor) domain, score
                64.0, E-value 2.1e-16"
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CDS             complement(36607..38016 /gene="glnA"
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                RDPRSISKRAEEFLKSSGIADTVLFGPEPEFFLF
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                SSTKYEGGNKGRPAVKGGYFPVPPVDSSQDLRS
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                QNEVATRFNTMTKKADEIQIYKYVVHNVAHAFGK
                TATFMPKPMFGDNGSGMHCHMSLS
                KNGTNLFAGDKYAGLSEMALFYIGGIIKHAKAIN
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                /locus-tag="YE0027"
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                /note="PS00182 Glutamine
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                site."
misc-feature    complement(36868..37713 /gene="glnA"
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                /inference="protein
                motif:PFAM:PF00120"
                /note="Pfam match to entry PF00120
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                catalytic domain, score 563.6,
                E-value 8.6e-167"
misc-feature    complement(37195..37242 /gene="glnA"
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                /inference="protein
                motif:Prosite:PS00181"
                /note="PS00181 Glutamine
                synthetase putative ATP-binding
                region signature."
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                /locus-tag="YE0027"
                /inference="protein
                motif:PFAM:PF03951"
                /note="Pfam match to entry PF03951
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                beta-Grasp domain, score 169.3,
                E-value 4.1e-48"
misc-feature    complement(37813..37869 /gene="glnA"
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                /locus-tag="YE0027"
                /inference="protein
                motif:Prosite:PS00180"
                /note="PS00180 Glutamine
                synthetase signature 1."
gene            complement(38201..38311 /locus-tag="YE0028"
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CDS             complement(38201..38311 /locus-tag="YE0028"
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                /inference="similar to
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                /note="Poor database matches.
                Similar to the N-terminal region
                of Yersinia pestis possible
                membrane protein YPO0025
                SWALL:Q8ZJR4 (EMBL:AJ414141) (52
                aa) fasta scores: E(): 1.8e-12,
                80.55 38d in 36 aa. Doubtful CDS"
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CDS	38529..40352	/gene="bipA" /locus-tag="YE0029" /codon-start=1 /transl-table=11 /product="putative GTPase" /protein-id="CAL10174.1" /db-xref="GI:122087393" /db-xref="GOA:A1JHU1" /db-xref="InterPro:IPR000640" /db-xref="InterPro:IPR000795" /db-xref="InterPro:IPR004161" /db-xref="InterPro:IPR005225" /db-xref="InterPro:IPR006298" /db-xref="UniProtKB/TrEMBL:A1JHU1" /translation="MIENLRNIAIIAHVDHGKTT LVDKLLQQSGTFGERAEATERVMD SNDLEKERGITILAKNTAIKWKDYRINIVDTPGH ADFGGEVERVMSMVDSVLLVVDAM DGPMPQTRFVTKKAFANGLKPIVVINKVDRPGAR PDWVVDQVFDLFDVNLDATDEQLDF PIIYASALMGIAGNHDNDMAADMTPLYQAIVDHV SPPQVEPDAPFQMQLISQLDYNMYV GVIGIGRIKRGKVKPNQQVTIVDSEGKTRNGKVG KVLTHMGLERIEATEAEAGDIVAI TGLGELNISDTICDVNAVEALPALSVDDEPTVSMY FCVNTSPFCGKEGKYVTSRQILER LNKELIHNVALRVEETEDADAFRVSGRGELHLSV LIENMRREGFELAVSRPKVIVREI DGRKQEPFENVTLIDIEEQHQGSVMQAMGERKADL KNMDPDGKGRVRLDYLIIPARGLIG FRTEFMTMTSGTGLLYSTFSHYDDVRPGEIGQRQ NGVLISNGQGKAVAFALFKLQDRG KLFIGHGTEVYEGQIIIGIHSRNDLTVNCLTGKQ LTNMRASGTDEATTLPFLKKTLE QALEFIDDDDELVEVTPQSIRIRKRHLTENDRKRA GRGPKED"
misc-feature	38535..39122	/gene="bipA" /locus-tag="YE0029" /inference="protein" motif:PFAM:PF00009" /note="Pfam match to entry PF00009 GTP-EFTU, Elongation factor Tu GTP binding domain, score 258.2, E-value 7.1e-75"
misc-feature	38562..38585	/gene="bipA" /locus-tag="YE0029" /inference="protein" motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-feature	38658..38705	/gene="bipA" /locus-tag="YE0029" /inference="protein" motif:Prosite:PS00301" /note="PS00301 GTP-binding elongation factors signature."

misc-feature	39147..39395	/gene="bipA" /locus-tag="YE0029" /inference="protein motif:PFAM:PF03144" /note="Pfam match to entry PF03144 GTP-EFTU-D2, Elongation factor Tu domain 2, score 71.9, E-value 8.8e-19"
misc-feature	39711..39977	/gene="bipA" /locus-tag="YE0029" /inference="protein motif:PFAM:PF00679" /note="Pfam match to entry PF00679 EFG-C, Elongation factor G C-terminus, score 112.3, E-value 6e-31"
gene	40648..41235	/locus-tag="YE0030"
CDS	40648..41235	/locus-tag="YE0030" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10175.1" /db-xref="GI:122087394" /db-xref="GOA:A1JHU2" /db-xref="InterPro:IPR005834" /db-xref="InterPro:IPR006402" /db-xref="UniProtKB/TrEMBL:A1JHU2" /translation="MLYIFDLGNVIVDIDFKRVL GVWSKLSSVPLATLSERFTMGVEF QQHERGEISDEDFARQLSDEMGLSLSFEQFAEGW QAVFVALRPEVISIMQKLRAEGHR VVVLSNTNRLHCNYWPQHYPEVAAAADHMYLSQD LGMRKPEARIIYQHVLSAENIPAEQ AVFFDDVEANIVAARIEGITGIHVTDRKVIPAYF S"
misc-feature	40648..41208	/locus-tag="YE0030" /inference="protein motif:PFAM:PF00702" /note="Pfam match to entry PF00702 Hydrolase, haloacid dehalogenase-like hydrolase, score 61.6, E-value 1.1e-15"
gene	41328..42218	/gene="rbn"
CDS	41328..42218	/locus-tag="YE0031" /gene="rbn" /locus-tag="YE0031" /codon-start=1 /transl-table=11 /product="ribonuclease BN" /protein-id="CAL10176.1" /db-xref="GI:122087395" /db-xref="GOA:A1JHU3" /db-xref="InterPro:IPR004664" /db-xref="InterPro:IPR017039" /db-xref="UniProtKB/Swiss-Prot:A1J HU3" /translation="MASFLRFRLSASLKPYITFG RMLYTRIDKDGLTMLAGHLAYVSL LSLVPLVTIVIFALFAAFPMFADISIKLKAFIFTN FMPATGDIIQNYLEQFVANSNRMT VVGTCGLIVTALLLIYSVDSVLNIIWRSKVHRS

		VFSFAVYWMVLTILGPILVGASMTI SSYLLSLQWLANARVDSMIDETLRFLPLISWVS FWLLYSVVPTVRVPAQDALIGALV AALFFELGKKGFTMYITLFPSYQLIYGVLAVIPI LFLWVYWSWCIVLLGAEITVTLGE YRAQRHQAITEKSPSQSQEI"
misc-feature	41409..42161	/gene="rbn" /locus-tag="YE0031" /inference="protein" motif:PFAM:PF03631" /note="Pfam match to entry PF03631 Ribonuclease-BN, Ribonuclease BN-like family, score 289.2, E-value 3.5e-84"
misc-feature	join(41442..41510, 41628..41687, 41748..41816, 41874..41933, 41967..42035, 42063..42131)	/gene="rbn"
		/locus-tag="YE0031" /inference="protein" motif:TMHMM:2.0" /note="6 probable transmembrane helices predicted for YE0031 by TMHMM2.0 at aa 39-61, 101-120, 141-163, 183-202, 214-236 and 246-268"
gene	42225..42662	/locus-tag="YE0032"
CDS	42225..42662	/locus-tag="YE0032" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10177.1" /db-xref="GI:122087396" /db-xref="GOA:A1JHU4" /db-xref="InterPro:IPR003732" /db-xref="UniProtKB/Swiss-Prot:A1J HU4" /translation="MIALIQRALSANVVVDGEV GEIGPGLLILLGVEQQDTEQKAQR LCEKVLGYRIFGDENDKMNLNVKQAGGSVLVVSQ FTLVADTQKGMRPSFSRGASPAEA DRLYQYFVAQCRESHGVTETGLFAADMKVSLVND GPVTFWLQI"
misc-feature	42306..42659	/locus-tag="YE0032" /inference="protein" motif:PFAM:PF02580" /note="Pfam match to entry PF02580 DUF154, Uncharacterized ACR, COG1490, score 261.8, E-value 6e-76"
gene	42914..43837	/locus-tag="YE0033"
CDS	42914..43837	/locus-tag="YE0033" /codon-start=1 /transl-table=11 /product="conserved membrane protein" /protein-id="CAL10178.1" /db-xref="GI:122087397" /db-xref="GOA:A1JHU5"

		/db-xref="InterPro:IPR000182" /db-xref="InterPro:IPR012660" /db-xref="InterPro:IPR016181" /db-xref="UniProtKB/TrEMBL:A1JHU5" /translation="MYHLRVPTTEQELKDYYQFR WEMLRKPLHQPIGSEKDAYDAMAH HQMVVDEQGKPVVAIGRLYINADNEAAIRFLAVDP SVRSKGLGTLVAMTLESVARQEGV KRVVCSAREDAVDFFSKLGFVSQGEITAPQTTTPV RHFLMIKPVVTMDDILHRPDWCGQ LQQAWYDHIPLSEKMGVRISQYTGQRFVTTMPEA GNQNPHTLTFAGSLFSLATLTGWG LIWLLLRERHLGGTIILADAHIRYSAPVTGRPRA VAELSSLSGDLRLARGRRARVQL DVNLFGNEEAGAVFSGTYMVLVPVDAEGDGVN"
misc-feature	43052..43282	/locus-tag="YE0033" /inference="protein motif:PFAM:PF00583" /note="Pfam match to entry PF00583 Acetyltransf,Acetyltransferase (GNAT) family, score 63.3, E-value 3.3e-16"
misc-feature	43184..43249	/locus-tag="YE0033" /note="Predicted helix-turn-helix motif with score 1005.000, SD 2.61 at aa 91-112, sequence MTLESVARQEGVKRVVCSARED"
misc-feature	43517..43585	/locus-tag="YE0033" /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted for YE0033 by TMHMM2.0 at aa 202-224"
repeat-region	44408..45116	/note="repeat unit encoding a LuxR-family transcriptional regulator"
gene	44431..45117	/locus-tag="YE0035"
CDS	44431..45117	/locus-tag="YE0035" /inference="similar to sequence:INSDC:AE004433" /inference="similar to sequence:INSDC:AE004564" /note="Similar to Pseudomonas aeruginosa probable transcriptional regulator PA1347 SWALL:Q9I3Z7 (EMBL:AE004564) (230 aa) fasta scores: E(): 3e-09, 30.43 id in 207 aa, and to the C-terminal region of Vibrio cholerae LuxR family transcriptional regulator VCA1078 SWALL:Q9KKM5 (EMBL:AE004433) (319 aa) fasta scores: E(): 2.2e-10, 27.53 38d in 207 aa" /codon-start=1 /transl-table=11 /product="LuxR family transcription regulatory protein" /protein-id="CAL10179.1" /db-xref="GI:122087398" /db-xref="GOA:A1JHU6" /db-xref="InterPro:IPR000792"

		/db-xref="InterPro:IPR011991"
		/db-xref="InterPro:IPR013656"
		/db-xref="UniProtKB/TrEMBL:A1JHU6"
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misc-feature	44872..45069	/locus-tag="YE0035" /inference="protein motif:PFAM:PF00196" /note="Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 41.3, E-value 1.4e-09"
misc-feature	44926..44991	/locus-tag="YE0035" /note="Predicted helix-turn-helix motif with score 1060.000, SD 2.80 at aa 166-187, sequence FSSMEIATKLHLSSITVDNIIQ"
repeat-region	45117..45833	/note="repeat unit encoding a LuxR-family transcriptional regulator"
gene	45147..45833	/locus-tag="YE0036"
CDS	45147..45833	/locus-tag="YE0036" /inference="similar to sequence:INSDC:AE004433" /inference="similar to sequence:INSDC:AE004564" /note="Similar to Pseudomonas aeruginosa probable transcriptional regulator PA1347 SWALL:Q9I3Z7 (EMBL:AE004564) (230 aa) fasta scores: E(): 2.2e-09,30.37 38d in 214 aa, and to the C-terminal region of Vibrio cholerae LuxR family transcriptional regulator VCA1078 SWALL:Q9KKM5 (EMBL:AE004433) (319 aa) fasta scores: E(): 6.6e-13, 30.43 38d in 207 aa" /codon-start=1 /transl-table=11 /product="LuxR family transcription regulatory protein" /protein-id="CAL10180.1" /db-xref="GI:122087399" /db-xref="GOA:A1JHU7" /db-xref="InterPro:IPR000792" /db-xref="InterPro:IPR011991" /db-xref="UniProtKB/TrEMBL:A1JHU7" /translation="MDKPLKNQLEILIRFWERSS EPWGARDNQSRFIYSNDRHHKLLG LSDKYNLEGRLDSELPSTAAFQMEFQAHDRKVE LSQERITSVEIHEWDGLSYLKPNF CDKYPLIDESGVSQGIIFHVRPVEDIILSRLTKI KAPTSLTFTPPSKLFTKREWEVLF YILHSYSSKDIAKKLHISPRTVSNITQSVYRKVG"

		VSNKRQIVDYCYENKINNYVPQSF FEYSGSFPLM"
misc-feature	45588..45785	/locus-tag="YE0036" /inference="protein motif:PFAM:PF00196" /note="Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 49.3, E-value 5.5e-12"
misc-feature	45642..45707	/locus-tag="YE0036" /note="Predicted helix-turn-helix motif with score 2073.000, SD 6.25 at aa 166-187, sequence YSSKDIAKKLHISPRTVSNITQ"
repeat-region	45834..46549	/note="repeat unit encoding a LuxR-family transcriptional regulator"
gene	45863..46549	/locus-tag="YE0037"
CDS	45863..46549	/locus-tag="YE0037" /inference="similar to sequence:INSDC:AE004433" /inference="similar to sequence:INSDC:AE004564" /note="Similar to Pseudomonas aeruginosa probable transcriptional regulator PA347 SWALL:Q9I3Z7 (EMBL:AE004564) (230 aa) fasta scores: E(): 3.6e-10,30.47 38d in 210 aa, and to the C-terminal region of Vibrio cholerae LuxR family transcriptional regulator VCA1078 SWALL:Q9KKM5 (EMBL:AE004433) (319 aa) fasta scores: E(): 4.2e-10, 27.94 38d in 229 aa" /codon-start=1 /transl-table=11 /product="LuxR family transcription regulatory protein" /protein-id="CAL10181.1" /db-xref="GI:122087400" /db-xref="GOA:A1JHU8" /db-xref="InterPro:IPR000792" /db-xref="InterPro:IPR011991" /db-xref="InterPro:IPR013656" /db-xref="UniProtKB/TrEMBL:A1JHU8" /translation="MGETLKNQLEILIRFWEHSS EPWQIKDSQSRYIYANPRSHKLLS LPAKYNMEGRLDGELPSPISEFQAEFQRQDRQVE LLQDRITSAEIHIVDGKSYLTPFF CDKYPLIDENGISQGVICHARPVHNLMLTRLNKI KAPTSLTFTPPSKLFTKREWEVLF YILHSYSSKDIAKKLHLSARTVSNITQSVYRKVG VSNKRQIVDYCYENKINNYVPQSF FEYSGSFPLM"
misc-feature	46304..46501	/locus-tag="YE0037" /inference="protein motif:PFAM:PF00196" /note="Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 46.4, E-value 4.3e-11"

misc-feature	46358..46423	/locus-tag="YE0037" /note="Predicted helix-turn-helix motif with score 1813.000, SD 5.36 at aa 166-187, sequence YSSKDIAKKLHLSARTVSNITQ"
repeat-region	46550..47265	/note="repeat unit encoding a LuxR-family transcriptional regulator"
gene	46579..47265	/locus-tag="YE0038"
CDS	46579..47265	/locus-tag="YE0038" /inference="similar to sequence:INSDC:AE004433" /inference="similar to sequence:INSDC:AE004564" /note="Similar to Pseudomonas aeruginosa probable transcriptional regulator PA1347 SWALL:Q9I3Z7 (EMBL:AE004564) (230 aa) fasta scores: E(): 1e-09, 31.28 id in 211 aa, and to the C-terminal region of Vibrio cholerae LuxR family transcriptional regulator VCA1078 SWALL:Q9KKM5 (EMBL:AE004433) (319 aa) fasta scores: E(): 4.1e-10, 27.94 38d in 229 aa" /codon-start=1 /transl-table=11 /product="LuxR family transcription regulatory protein" /protein-id="CAL10182.1" /db-xref="GI:122087401" /db-xref="GOA:A1JHU9" /db-xref="InterPro:IPR000792" /db-xref="InterPro:IPR011991" /db-xref="InterPro:IPR013656" /db-xref="UniProtKB/TrEMBL:A1JHU9" /translation="MGETLKNQLEILIRFWEHSS EPWQIKDSQSRYYANPRT HKLLS LPAKYNMEGRLDGELPSPISEFQAEFQRQDRQVE LLQDRITSAEIHIVDGKSYLTLFF CDKYPLIDEYGISQGVICHDRPVHNLMLTRLNKI KAPTSLTFTPPSKLFTKREWEVLF YILHSYSSKDIAKKLHLSARTVSNITQSVYRKVG VSNKRQIVDYCYENKINNYVPQSF FEYSGSFPLM" /locus-tag="YE0038" /inference="protein motif:PFAM:PF00196" /note="Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 46.4, E-value 4.3e-11"
misc-feature	47020..47217	/locus-tag="YE0038" /inference="protein motif:PFAM:PF00196" /note="Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 46.4, E-value 4.3e-11"
misc-feature	47074..47139	/locus-tag="YE0038" /note="Predicted helix-turn-helix motif with score 1813.000, SD 5.36 at aa 166-187, sequence YSSKDIAKKLHLSARTVSNITQ"
repeat-region	47266..47965	/note="repeat unit encoding a LuxR-family transcriptional regulator"
gene	47294..47980	/locus-tag="YE0039"



CDS	47294..47980	/locus-tag="YE0039" /inference="similar to sequence:INSDC:AE004433" /inference="similar to sequence:INSDC:AE004564" /note="Similar to Pseudomonas aeruginosa probable transcriptional regulator PA1347 SWALL:Q9I3Z7 (EMBL:AE004564) (230 aa) fasta scores: E(): 3.8e-08,29.04 38d in 210 aa, and to Vibrio cholerae LuxR family transcriptional regulator VCA1078 SWALL:Q9KKM5 (EMBL:AE004433) (319 aa) fasta scores: E(): 2.9e-10, 28.5 id in 214 aa" /codon-start=1 /transl-table=11 /product="LuxR family transcription regulatory protein" /protein-id="CAL10183.1" /db-xref="GI:122087402" /db-xref="GOA:A1JHV0" /db-xref="InterPro:IPR000014" /db-xref="InterPro:IPR000792" /db-xref="InterPro:IPR011991" /db-xref="InterPro:IPR013656" /db-xref="UniProtKB/TrEMBL:A1JHV0" /translation="MDKPLKNQLEILIRFWERSS EPWAIKDNQSKFIYANRRVYKLFN LPNKYTLEGRLDGEIPTPSADFQDEFQQQDRQVE LSQDRVTSVDIQLYDGFSYFTPYF SDKYPLIDENGVSQGVICHARPVQDIMLTHLNKI KVPTSLIFTPPSKLFTKREWEVLF YILHSYSSKDLAEKLHLSPTVSNIIQSVYRKAG VSNKRQIVDYCYENKINNYVPQSF FEYSKSFPLM"
misc-feature	47735..47932	/locus-tag="YE0039" /inference="protein motif:PFAM:PF00196" /note="Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 43.2, E-value 3.9e-10"
misc-feature	47789..47854	/locus-tag="YE0039" /note="Predicted helix-turn-helix motif with score 2197.000, SD 6.67 at aa 166-187, sequence YSSKDLAEKLHLSPTVSNIIQ"
gene	complement(48077..49786	/locus-tag="YE0040"
	)	
CDS	complement(48077..49786	/locus-tag="YE0040"
	)	
		/codon-start=1 /transl-table=11 /product="possible exported protein" /protein-id="CAL10184.1" /db-xref="GI:122087403" /db-xref="InterPro:IPR007844" /db-xref="UniProtKB/TrEMBL:A1JHV1" /translation="MKFLGKVLLTLLLLLVLSIV

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IAQQAVLGLSWRQLTEPRHFRLN  
LQNGSLTLNNSTSPPLQADTLRLTNMALNTTIE  
PQNKAGQWKVTGQQVTGGLIPWQP  
LPGNSLGENAQFQFSAGSLTINGITAEKLYLQGS  
IQKNALTLSNFGADIAQGELTGNA  
SQSADGSWLVDRLRLSNIRLQTPATLEDVWNTFL  
QLPPITLKRFDLIDARVEGKNWAF  
NDLDLTLKNITFKQGDWQSDGELSLNAGDIK  
NIHLIDPIATFTLSPAGVAINQFS  
TRWQDGLLRAQGNWLRDSHRLQLDELTLVALVYT  
LPTDWKQQWQQTLPNWLSEVYISK  
LNANRNLLIDISPDPFQITSLDAAGTNLLLAKN  
HQWGVWSGSLMLNAGNATFNKNDV  
RRPSLALSANEQQITVSDLSTFTKEGLLEATATI  
DQTSGRALSLALTGRSVDLNLQN  
WGWPALPLQGLGNLKLRIISGNLTADKPLKPTING  
SLQATDNHGQQVNQTMQNGEVHGV AGQ"

sig-peptide complement (49694..49786 )

/note="Signal peptide predicted for YE0040 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.986 between residues 31 and 32"

misc-feature complement (49700..49768 )

/inference="protein motif:TMHMM:2.0"  
/note="1 probable transmembrane helix predicted for YE0040 by TMHMM2.0 at aa 7-29"

gene complement (49933..51318 )

/locus-tag="YE0041"

CDS complement (49933..51318 )

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/protein-id="CAL10185.1"  
/db-xref="GI:122087404"  
/db-xref="GOA:A1JHV2"  
/db-xref="InterPro:IPR006042"  
/db-xref="InterPro:IPR006043"  
/db-xref="InterPro:IPR017588"  
/db-xref="UniProtKB/TrEMBL:A1JHV2"  
/translation="MSTQSAELNTPQQATTHPSE  
LIYRLEDRPPLAQTLFAACQHLLA  
MFVAVITPGLLICQALGLPAEDTQRIISMSLFAS  
GLASLLQIKTWGPVGSGLLSIQGT  
SFNFVSPLIMGGLALKNGGADIPTMMAALFGTLM  
VASCTEIIILSRFLHLARRIITPLV  
SGIVVMIIGLSLIQVGLTSIGGGYGAMSDHTFGS  
PKNLMLAGAVLVVILLNRQNPY  
LRVASLVIAMAVGYLLAWTLGMLPESRPVVDAL  
ITIPTPLYYGLSFDWNLLVPLMLI  
FMVTSLETIGDITATSDVSEQPVHGPLYMKRLKG  
GVLANGLNSMLSAVFNTFPNSCFG  
QNNGVIQLTGVASRYVGFVVALMLIVLGLFPAVA  
GFVQHIPEPVLGGATLVMFGTIAA

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                                SGVRIVSRETLNRRRAIMIMALSLAVGMGVAQQPL
                                ILQFAPDWIKTLLSSGIAAGGITA
                                IVLNLIFPQEK"
misc-feature    complement(join(49948.. /locus-tag="YE0041"
                                50007,50035..50103,
                                50122..50190,
                                50203..50271,
                                50473..50541,
                                50599..50667,
                                50686..50745,
                                50788..50856,
                                50875..50943,
                                50971..51039,
                                51127..51195))

                                /inference="protein
                                motif:TMHMM:2.0"
                                /note="11 probable transmembrane
                                helices predicted for YE0041 by
                                TMHMM2.0 at aa 42-64, 94-116,
                                126-148, 155-177,192-211, 218-240,
                                260-282, 350-372, 377-399, 406-428
                                and 438-457"
misc-feature    complement(50038..51225 /locus-tag="YE0041"
                                )

                                /inference="protein
                                motif:PFAM:PF00860"
                                /note="Pfam match to entry PF00860
                                xan-ur-permease,Permease family,
                                score 528.7, E-value 2.8e-156"
misc-feature    complement(50137..50199 /locus-tag="YE0041"
                                )

                                /inference="protein
                                motif:Prosite:PS01116"
                                /note="PS01116 Xanthine/uracil
                                permeases family signature."
misc-feature    complement(50689..50736 /locus-tag="YE0041"
                                )

                                /inference="protein
                                motif:Prosite:PS00038"
                                /note="PS00038 Myc-type,
                                'helix-loop-helix' dimerization
                                domain signature."
misc-feature    complement(50899..50931 /locus-tag="YE0041"
                                )

                                /inference="protein
                                motif:Prosite:PS00013"
                                /note="PS00013 Prokaryotic
                                membrane lipoprotein lipid
                                attachment site."
misc-feature    complement(51202..51234 /locus-tag="YE0041"
                                )

                                /inference="protein
                                motif:Prosite:PS00013"
                                /note="PS00013 Prokaryotic
                                membrane lipoprotein lipid
                                attachment site."
gene            51557..52771          /gene="gltS"
                                /locus-tag="YE0042"
                                /note="synonym: gltC"
CDS             51557..52771          /gene="gltS"
                                /locus-tag="YE0042"
                                /codon-start=1

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		/transl-table=11 /product="sodium/glutamate symport carrier protein" /protein-id="CAL10186.1" /db-xref="GI:122087405" /db-xref="GOA:A1JHV3" /db-xref="InterPro:IPR004445" /db-xref="UniProtKB/TrEMBL:A1JHV3" /translation="MFHLDTYGTLVAACLVLALLG RKLVTQVTPFLKKYTIPEPVAGGLL VAFMMLLMQKTLGWEISFDMSLKDPLMLAFFATI GLNANLASLRAGGKALSVFVFVVV GLLLMQNAIGIALAKLMGLDPLMGLLAGSITLSG GHGTGAAWSKVVERYGFENATEV AMACATFGLVLGGLIGGPVARYLVKHSSTPDGTP EDSEIPSAFEKPSAGRMITSLVLT ETIAMIAICLMVGQVISAGLQGTMFELPTFVCVL FVGVILSNTLSAIGFYKVFDRVS VLGNVSLSLFLAMALMSLKLWELASLALPMLVIL SVQALAMALYAIFVTYRLMGKNYD AAVLAAGHCGFGLGATPTAIANMQAITDRFGPSH LAFLVVPVMGAFFIDIVNVIVIKL YLLLPIFPAVVG"
misc-feature	51560..52654	/gene="gltS" /locus-tag="YE0042" /inference="protein motif:PFAM:PF03616" /note="Pfam match to entry PF03616 Glt-symporter, Sodium/glutamate symporter, score 808.3, E-value 1.8e-240"
misc-feature	join(51566..51619, 51653..51706, 51764..51817, 51836..51904, 52025..52093, 52193..52261, 52289..52357, 52376..52432, 52460..52528, 52562..52630, 52658..52726)	/gene="gltS"
		/locus-tag="YE0042" /inference="protein motif:TMHMM:2.0" /note="11 probable transmembrane helices predicted for YE0042 by TMHMM2.0 at aa 4-21, 33-50, 70-87, 94-116, 157-179, 213-235, 245-267, 274-292, 302-324, 336-358 and 368-390"
gene	complement(52840..54921 )	/gene="recG"
		/locus-tag="YE0043"
CDS	complement(52840..54921 )	/gene="recG"
		/locus-tag="YE0043" /codon-start=1 /transl-table=11 /product="ATP-dependent DNA helicase" /protein-id="CAL10187.1"

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/db-xref="GOA:A1JHV4"
/db-xref="InterPro:IPR001650"
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/db-xref="InterPro:IPR004609"
/db-xref="InterPro:IPR011545"
/db-xref="InterPro:IPR014001"
/db-xref="InterPro:IPR014021"
/db-xref="UniProtKB/TrEMBL:A1JHV4"
/translation="MKGRLLDAVPLSTLSGVGAS
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EDRTRLYRIGDLLPGLSVTVEGEVLRSDISFGRR
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MKNSLSPGKHVIAYGEAKRGNTGPETIIHPEYRVH
GENIGVELQESLTPVYPTTEGIRQ
ATLRKLIDQALAMDSSVIAELLPIELSRSLISL
PEAIHILHRPPADIQLADLEQGKH
PAQRRLIMEELLAHNLSMLAVRAGAQSRYALPLL
PEEQLKRRFLAALPFTPTHAQQRV
VAEIEQDMTHSYPMMLRIQGDVSGSKTLVAALAA
LRAIAHGKQVALMAPTELLAEQHA
NTFRQWLEPLGLEVGWLAGKQKGKARLAQQEAVA
SGQVSMVVGTHAMFQEQVQFSGLA
LVIIDEQHRFGVHQRLALWEKGEEQGFHPHQLIM
TATPIPRTLAMTAYADLDTSVIDE
LPPGRTPVTTVAIPDTRSDVIQVRKNACLEEGR
QAYWVCTLIEESELLEAQAAEVC
EELKIALPEIKVGLVHGRMGPEKQAVMLAFKQG
ELQLLVATTVIEVGVDVPNASLMI
IDNPERLGLAQLHQLRGRVGRGAVASHCVLLYKT
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PEVQVRVARHLHQQYPEHAQALIER
WLPERTRYTNA"
sig-peptide      complement(54856..54921 /gene="recG"
)
/locus-tag="YE0043"
/note="Signal peptide predicted
for YE0043 by SignalP 2.0 HMM
(Signal peptide probability 0.878)
with cleavage site probability
0.798 between residues 22 and 23"
misc-feature      complement(53155..53373 /gene="recG"
)
/locus-tag="YE0043"
/inference="protein
motif:PFAM:PF00271"
/note="Pfam match to entry PF00271
helicase-C, Helicase conserved
C-terminal domain, score 79.9,
E-value 3.4e-21"
misc-feature      complement(53545..54147 /gene="recG"
)
/locus-tag="YE0043"
/inference="protein
motif:PFAM:PF00270"
/note="Pfam match to entry PF00270
DEAD, DEAD/DEAH box helicase,
score 123.2, E-value 3.1e-34"
misc-feature      complement(54013..54036 /gene="recG"
)
/locus-tag="YE0043"

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		/inference="protein motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)." /gene="recG"
misc-feature	complement(54514..54738)	/locus-tag="YE0043" /inference="protein motif:PFAM:PF01336" /note="Pfam match to entry PF01336 tRNA-anti, OB-fold nucleic acid binding domain, score 34.6, E-value 1.5e-07"
gene	complement(54922..55614)	/gene="trmH" /locus-tag="YE0044" /note="synonym: spoU"
CDS	complement(54922..55614)	/gene="trmH" /locus-tag="YE0044" /codon-start=1 /transl-table=11 /product="tRNA (guanosine-2'-O-)-methyltransferas e" /protein-id="CAL10188.1" /db-xref="GI:122087407" /db-xref="GOA:A1JHV5" /db-xref="InterPro:IPR001537" /db-xref="UniProtKB/TrEMBL:A1JHV5" /translation="MNPQRYARICEMLATRQPD LTVCLEEVHKPHNVSAIIRTADAVG IHQIHAIWPTPAMYTRLSSAAGSNSWVQVKTHSH ITDAITHLKSQGMQILATHLSDKA VDFREIDYTRPTCILMGQEKGTGISKEALAMADKD IIPMIGMVQSLNVSVASALILYE AQRQRQNAGMYQRTQSVLSEDEQQRLLFEGGYPV LAQVAKRKGLPQPYIDEQGQVIAD AQWWSAMQSTES"
misc-feature	complement(55138..55560)	/gene="trmH" /locus-tag="YE0044" /inference="protein motif:PFAM:PF00588" /note="Pfam match to entry PF00588 SpoU-methylase, SpoU rRNA Methylase family, score 188.6, E-value 6.6e-54"
gene	complement(55620..57722)	/gene="spoT" /locus-tag="YE0045"
CDS	complement(55620..57722)	/gene="spoT" /locus-tag="YE0045" /codon-start=1 /transl-table=11 /product="guanosine-3',5'-bisbis(d iphosphate) 3'-pyrophosphydrolase" /protein-id="CAL10189.1" /db-xref="GI:122087408" /db-xref="GOA:A1JHV6" /db-xref="InterPro:IPR003607"

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/db-xref="InterPro:IPR012675"
/db-xref="UniProtKB/TrEMBL:A1JHV6"
/translation="MYLFESLNLLIQRYLP EEQI
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LDKLNFRDKKEAQAENFRKMIMAMVQDIRVILIK
LADRTHNMRTLGLSLRPDKRRRIAR
ETLEIYSPLAHLRGLIHLKTELEELGFEALYPNR
YRVIKEVVKAARGNRKEMIQKILA
EIEGRLTEAGIPCRVSGREKHLYSIYCKMNLKEQ
RFHSIMDIYA FRVIVKEVDTCYRV
LGQAHSLYKPRPGRVKDYIAIPKANGYQSLHTSL
IGPHGVPVEVQIRTEDMDQMAEMG
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KHELD RMKLATLDDLLAEIGLGNAMSVVAKNLL
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TFAKCCRPIPGDPIIAHISPGKGLVIHHESCRNI
RGYQKEPEKFMAVEWDQETE QEFI
AEIKVDMFNQQGALANLTAAINA AESNIQSLNTE
EKDGRVYSAFIRLTTRDRVHLANI
MRKIRIMPDVVKVSRNRN"
misc-feature      complement(55629..55850 /gene="spoT"
)
/locus-tag="YE0045"
/inference="protein
motif:PFAM:PF01842"
/note="Pfam match to entry PF01842
ACT, ACT domain, score 15.3,
E-value 0.097"
misc-feature      complement(56382..56573 /gene="spoT"
)
/locus-tag="YE0045"
/inference="protein
motif:PFAM:PF02824"
/note="Pfam match to entry PF02824
TGS, TGS domain, score 110.2,
E-value 2.6e-30"
misc-feature      complement(57291..57590 /gene="spoT"
)
/locus-tag="YE0045"
/inference="protein
motif:PFAM:PF01966"
/note="Pfam match to entry PF01966
HD, HD domain, score 74.5, E-value
1.4e-19"
misc-feature      complement(57561..57593 /gene="spoT"
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/locus-tag="YE0045"
/inference="protein
motif:Prosites:PS00013"
/note="PS00013 Prokaryotic
membrane lipoprotein lipid

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gene      complement(57741..58016 attachment site."
)         /gene="rpoZ"

CDS       complement(57741..58016 /locus-tag="YE0046"
)         /gene="rpoZ"
          /locus-tag="YE0046"
          /codon-start=1
          /transl-table=11
          /product="DNA-directed RNA
polymerase, omega chain"
          /protein-id="CAL10190.1"
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          /db-xref="InterPro:IPR003716"
          /db-xref="InterPro:IPR006110"
          /db-xref="UniProtKB/Swiss-Prot:A1J
HV7"
          /translation="MARVTVQDAVEKIGNRFDLV
LVAARRARQIQSGKDALVPEEND
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EIQAVTAIAEGRR"

misc-feature complement(57822..57983 /gene="rpoZ"
)         /locus-tag="YE0046"
          /inference="protein
motif:PFAM:PF01192"
          /note="Pfam match to entry PF01192
RNA-pol-Rpb6, RNA polymerase Rpb6,
score 78.8, E-value 7.6e-21"

gene      complement(58071..58694 /gene="gmk"
)         /locus-tag="YE0047"
          /note="synonym: spoR"

CDS       complement(58071..58694 /gene="gmk"
)         /locus-tag="YE0047"
          /codon-start=1
          /transl-table=11
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          /protein-id="CAL10191.1"
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          /db-xref="UniProtKB/TrEMBL:A1JHV8"
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IQALLKTQPLYDTQVSI SHTTRAK
RPGENHGEHYFFVSKEEFCQMIDDDAFLEHAKVF
ENYYGTSRLAIEQVLATGVDVFLD
IDWQGAQQIRAKMPTARSIFILPPSKEELDRRLR
GRGQDSEEVIAKRMAQAVAEMTHY
AEYDYLIVNDDFNLALSDLKTIIRAERLRLGRQK
QRHDALITKLLAD"

misc-feature complement(58260..58574 /gene="gmk"
)         /locus-tag="YE0047"
          /inference="protein
motif:PFAM:PF00625"
          /note="Pfam match to entry PF00625
Guanylate-kin,Guanylate kinase,

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misc-feature	complement(58524..58577)	score 198.3, E-value 7.9e-57" /gene="gmk"  /locus-tag="YE0047" /inference="protein" motif:Prosite:PS00856" /note="PS00856 Guanylate kinase signature."
misc-feature	complement(58641..58664)	/gene="gmk"  /locus-tag="YE0047" /inference="protein" motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	58977..60674	/locus-tag="YE0048"
CDS	58977..60674	/locus-tag="YE0048" /codon-start=1 /transl-table=11 /product="putative DNA ligase" /protein-id="CAL10192.1" /db-xref="GI:122087411" /db-xref="GOA:A1JHV9" /db-xref="InterPro:IPR001679" /db-xref="InterPro:IPR003583" /db-xref="InterPro:IPR004150" /db-xref="InterPro:IPR012340" /db-xref="InterPro:IPR013839" /db-xref="InterPro:IPR013840" /db-xref="UniProtKB/Swiss-Prot:A1JHV9" /translation="MNVHKMKILSLLMVSFISWQ ARAESVCPEWSEERMSGEMHLEK QLDQWNIAYHQQGISPIADDIYDQLQDKLHRWRL CLGLPDKTDNRPIPGNGKMLHPVA HTGLKKLKDEAALISWMTGRKNLWVQPKIDGVAV TLVYQAGKLTQVLSRGNGLKGQNW ADKAPFISAIPQYIASAPLLTLQGEVFLQMEGH QQAQSGGANARASVAGALMRKSVS PLLAKLGIFIWAWPDGPKSMVEKSRLQLQEMGFPL TAHYSEPVISSSDVALWRDRWFKM PLPFVTDGVVIRQENVPAGRYWQATPGNWSVAWK YPPPPQQITEIKDIHFTVGRTGKIT AILQVIPVKIDDKWIRRVNIGSIARWKQWDIVPG DQVTISLAGQGIPRLDKVIWRVSQ RQEIVPPDADKFHQLTCFRRLPFCEPQFLSRLA WLSGTNGLDMQSVGNGLWRELIHH GFINGLLDWLSLSVEQIAAVPGIGQGRAEKIYQQ FQRARQQPFSQWLQALGFPQGIPL DTSWHSRLRQRSIAEWRLMPGIGQVRAKQINHFLH HPEVQMMADFLSQQGIAGFSPEE"
sig-peptide	58977..59045	/locus-tag="YE0048" /note="Signal peptide predicted for YE0048 by SignalP 2.0 HMM (Signal peptide probability 0.991) with cleavage site probability 0.950 between residues 23 and 24"
misc-feature	59073..59918	/locus-tag="YE0048" /inference="protein" motif:PFAM:PF01653" /note="Pfam match to entry PF01653 DNA-ligase-N,NAD-dependent DNA"



```

Similar to an internal region of
Halobacterium sp. hypothetical
protein VNG2239c SWALL:Q9HN60
(EMBL:AE005109) (308 aa) fasta
scores: E(): 2.7, 29.37 38d in 143
aa. Possible alternative
translational start sites"
/codon-start=1
/transl-table=11
/product="putative membrane
protein"
/protein-id="CAL10194.1"
/db-xref="GI:122087413"
/db-xref="UniProtKB/TrEMBL:A1JHW1"
/translation="MMIILPDCRVTHPMVAFISI
SSFISVGFFMSQCIQSFQYRAVLL
AGIAAVGVLLSGCVDRTGQANTATIKASPSTCIK
GEPMTQTTLYFGLNRPHPVISAT
EWQSFVDNDVTSRFKDGLTVIDAKGQWLGNMGTV
AKENSKALVLIHKADKETAETLR
ARYKQQFAQESVMRVDAAVCVDF"
misc-feature      join(61565..61624,
61634..61702)      /locus-tag="YE0050"

/inference="protein
motif:TMHMM:2.0"
/note="2 probable transmembrane
helices predicted for YE0050 by
TMHMM2.0 at aa 13-32 and 36-58"
gene              complement(62176..63360
)                  /gene="nupC"

/locus-tag="YE0051"
/note="synonym: cru"
CDS               complement(62176..63360
)                  /gene="nupC"

/locus-tag="YE0051"
/inference="similar to
sequence:INSDC:AL627274"
/inference="similar to
sequence:UniProtKB:P33031"
/note="Similar to Escherichia coli
nucleoside permease NupC or Cru
SWALL:NUPC-ECOLI (SWALL:P33031)
(400 aa) fasta scores: E():
4.2e-106, 71.75 38d in 400 aa, and
to Salmonella typhi nucleoside
permease STY2650 SWALL:Q8Z4X4
(EMBL:AL627274) (400 aa) fasta
scores: E(): 7.5e-106, 71.75 38d in
400 aa"
/codon-start=1
/transl-table=11
/product="nucleoside permease"
/protein-id="CAL10195.1"
/db-xref="GI:122087414"
/db-xref="GOA:A1JHW2"
/db-xref="InterPro:IPR002668"
/db-xref="InterPro:IPR008276"
/db-xref="InterPro:IPR011642"
/db-xref="InterPro:IPR011657"
/db-xref="UniProtKB/TrEMBL:A1JHW2"
/translation="MLQILHFLALIAIAVLALL
ASHDRKNIKLRYIFQLLIIEIALA

```

```

YFFLHSESGLGAIKYFAGLFESLMKFASIGTSFV
FGGMNEQGLAFIFLNVLCPIIFVS
ALIGILQHFRILPLIIRVIGTLLSKVNGMGKLES
FNAVSTLILGQSENFIA YKGIIAD
ISPRRMYTMAATAMSTVSMSIVSAYMTMLEPKFV
VTALILNMFSTFIVLSIINPYPVT
EEPELKLNNLHEDQSFFEMLG EYILAGFKIAMII
AAMLIGFIAIISAINALFSTLFHI
SFQGV LGYLFYPLALLIGIPTQDALHAGSIMATK
LVANEFVAMIELKKVAAEISPRGL
GILSVFLVSFANFASIGIVAGAIKGLNEQQGNV
SRFGLKLVYGSTLVSLLSATIAGL VL"

misc-feature    complement(62179..63357 /gene="nupC"
)
                /locus-tag="YE0051"
                /inference="protein"
                motif:PFAM:PF01773"
                /note="Pfam match to entry PF01773
                Nucleoside-tra2, Na+ dependent
                nucleoside transporter, score
                597.4, E-value 5.8e-177"

misc-feature    complement(join(62182.. /gene="nupC"
62250,62293..62361,
62476..62544,
62572..62640,
62716..62784,
62794..62862,
63037..63105,
63214..63273,
63292..63351))
                /locus-tag="YE0051"
                /inference="protein"
                motif:TMHMM:2.0"
                /note="9 probable transmembrane
                helices predicted for YE0051 by
                TMHMM2.0 at aa 4-23, 30-49,
                86-108, 167-189,193-215, 241-263,
                273-295, 334-356 and 371-393"

gene            63619..64512 /locus-tag="YE0052"
CDS             63619..64512 /locus-tag="YE0052"
                /inference="similar to
                sequence:INSDC:Y09701"
                /inference="similar to
                sequence:UniProtKB:P76082"
                /note="Similar to Escherichia coli
                probable enoyl-CoA hydratase PaaF
                SWALL:PAAF-ECOLI (SWALL:P76082)
                (255 aa) fasta scores: E():
                2.5e-06, 27.66 38d in 253 aa, and
                to Xanthomonas campestris RpfF
                protein, mutants of which are
                unable to produce a diffusible
                extracellular factor which
                regulates synthesis of
                extracellular enzymes and
                modulates virulence SWALL:O05175
                (EMBL:Y09701) (289 aa) fasta
                scores: E(): 1.2e-27, 34.02 38d in
                288 aa"
                /codon-start=1
                /transl-table=11
                /product="enoyl-CoA

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		hydratase/isomerase family protein" /protein-id="CAL10196.1" /db-xref="GI:122087415" /db-xref="GOA:A1JHW3" /db-xref="InterPro:IPR001753" /db-xref="UniProtKB/TrEMBL:A1JHW3" /translation="MFNSLIGWNMMINLPSCRS FTEAGHLSQISAYYEEGRNTLWML LRAHPRPCFNLELIENIMTLAQAAKESKLPIDFW VTGSVVPNMFNVGGDLNFFAQMIK NRKREALMAYARACVDCVHAASRGFDTGAISIAM IEGSALGGGFEEAALAHHFVLAQTT ARMGFPEIAFNLFPGMGGYSLVARKAGMRVAEQL IWTGESHAAEWYESRGLVDKLFQP GDAYIATRTRFIDTIRPKLNGMRAMVRVRQRLQL TRSELMEDITEDWVDSAFSIEPKDI AYIERLVMLQDRHTSGMPKAI"
misc-feature	63745..64269	/locus-tag="YE0052" /inference="protein motif:PFAM:PF00378" /note="Pfam match to entry PF00378 ECH, Enoyl-CoA hydratase/isomerase family, score 25.7, E-value 2.7e-10"
gene	complement(64538..66532 )	/locus-tag="YE0053"
CDS	complement(64538..66532 )	/locus-tag="YE0053"  /inference="similar to sequence:INSDC:AL627270" /inference="similar to sequence:UniProtKB:P77334" /note="Similar to Escherichia coli hypothetical protein YciR SWALL:YCIR-ECOLI (SWALL:P77334) (661 aa) fasta scores: E(): 3.9e-156, 60.61 38d in 650 aa, and to Salmonella typhi hypothetical protein STY1349 SWALL:Q8Z7D0 (EMBL:AL627270) (660 aa) fasta scores: E(): 1.3e-152, 60.24 38d in 654 aa" /codon-start=1 /transl-table=11 /product="putative signalling protein" /protein-id="CAL10197.1" /db-xref="GI:122087416" /db-xref="GOA:A1JHW4" /db-xref="InterPro:IPR000014" /db-xref="InterPro:IPR000160" /db-xref="InterPro:IPR001633" /db-xref="InterPro:IPR013767" /db-xref="UniProtKB/TrEMBL:A1JHW4" /translation="MFQDQDTSILNTYFGTHRPF WRLAFDSQALELSAIKEIANIAIP LNSVQTMKIRSLTGITASLDIEIEIYGHPLHLHL VGRKINDKEWGGTASAYADTESVA RDLVMGLSFAEQVVSEANSVIVILDKDGCVQRFN HLSEEYTGKKEQDVIGKNVYDLFM TAKEGASSRKNIEGFFQRGASYEAERWVNTVKGK

```

RLFLFRNKFVHSGSGKNERYLICS
GTDITKERRAQERLRILANTDMITGLPNRHAIHE
RINSAIQTRGDSSVGIIYLDLDFNF
KKVNDHYGHMFGDRLLKDVSLAILSCLGDNEMLA
RLGGDEFIVLVENATLDLLEITTQ
RILNRMKLPFRIGLIEVYTGC SIGIALCPEHGDT
LENIIRSADTAMYTAKEHGKQTYS
IFSQQMNKKVSEYVWLDTNLRKAIEQHQLQIFYQ
PKISTKTGKVLGVEALVRWLSPER
GLIAPQEFISYAEESGLIRPLGKWVLQTSMQQAV
DWKKRGINLRIAVNV SARQLIDEA
IVTSFIESLEACELESSLVDVELTESCLIDNEDA
AINIMKQLRHLGAQVHLDDFGTGY
SSLSQLARIPIDAIKLDQSFVRHIDTNPISQSLV
RAIIVVAEALKMQVIAEGVETKEE
EEFLDSIGVDEKQGFLYAKPMPADKLEHWLVTQH
PHLLLD"

misc-feature      complement(64586..65323 /locus-tag="YE0053"
)
                  /inference="protein
                  motif:PFAM:PF00563"
                  /note="Pfam match to entry PF00563
                  EAL, EAL domain, score 401.0,
                  E-value 7.4e-118"

misc-feature      complement(65363..65839 /locus-tag="YE0053"
)
                  /inference="protein
                  motif:PFAM:PF00990"
                  /note="Pfam match to entry PF00990
                  GGDEF, GGDEF domain ,score 195.5,
                  E-value 5.2e-56"

misc-feature      complement(66056..66205 /locus-tag="YE0053"
)
                  /inference="protein
                  motif:PFAM:PF00989"
                  /note="Pfam match to entry PF00989
                  PAS, PAS domain, score 22.5,
                  E-value 8.3e-06"

gene              complement(67055..67885 /locus-tag="YE0055"
)

CDS               complement(67055..67885 /locus-tag="YE0055"
)
                  /inference="similar to
                  sequence:INSDC:AE007569"
                  /inference="similar to
                  sequence:INSDC:AE010879"
                  /note="Similar to Methanosarcina
                  acetivorans metallo-beta-lactamase
                  superfamily protein MA1962
                  SWALL:AAM05365 (EMBL:AE010879)
                  (280 aa) fasta scores: E(): 3e-44,
                  44.84 38d in 281 aa, and to
                  Clostridium acetobutylicum
                  metal-dependent hydrolase of the
                  beta-lactamase superfamily II
                  CAC0535 SWALL:Q97LM2
                  (EMBL:AE007569) (268 aa) fasta
                  scores: E(): 2.8e-41,41.66 38d in
                  276 aa"
                  /codon-start=1
                  /transl-table=11
                  /product="metallo-beta-lactamase

```

```

superfamily protein"
/protein-id="CAL10198.1"
/db-xref="GI:122087417"
/db-xref="GOA:A1JHW5"
/db-xref="InterPro:IPR001279"
/db-xref="UniProtKB/TrEMBL:A1JHW5"
/translation="MQLTVLVDNNTLIDKYLTAE
PGVCYHLKIDGKTYLFDTGYSDFV
LRNAAILGIDISDIDSVIIISHGHNDHSWGLIHLA
QYLDRTNYPVSKKIKLVAHPNAFV
PKYHEDKSIGANLPADSYPSFFERINQTVYYLT
DNLLFLGEIVRSNDFEGLHPIGKT
INCCGHEVDDFVIDDSAIVYTSPEGIVIITGCSH
SGICNIIDYAIKVTGDKRIRAVIG
GFHLLNAETSTLTRTSDYFKQLNAQALYPCHCTD
LKAKIALAGAVDIEEVGVGMVLNF"
misc-feature    complement(67139..67837 /locus-tag="YE0055"
)
                /inference="protein
motif:PFAM:PF00753"
/note="Pfam match to entry PF00753
lactamase-B,Metallo-beta-lactamase
superfamily, score 11.7, E-value
0.00023"
misc-feature    complement(67406..67429 /locus-tag="YE0055"
)
                /inference="protein
motif:Prosite:PS00017"
/note="PS00017 ATP/GTP-binding
site motif A (P-loop)."
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gene complement(68287..69150 /locus-tag="YE0057"

CDS complement(68287..69150 /locus-tag="YE0057"

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)
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                /transl-table=11
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protein"
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                /db-xref="GI:122087418"
                /db-xref="InterPro:IPR005229"
                /db-xref="InterPro:IPR013527"
                /db-xref="InterPro:IPR013551"
                /db-xref="UniProtKB/TrEMBL:A1JHW6"
                /translation="MIRSMTAYARRDIKGEWGSA
AWELRSVNQRYLETYIRLPEQFRS
LEPVIRERIRGRLTRGKIECNLRFELDANAQSSL
ILNEKLAKQLVEAGNWVKMQSDEG
EINPVDILRWPGVMAAEEQDLDAISTELMQALDI
VLDDFIISRETEGAALKALIEQRL
DGVSAEIVKVRAHMPNQLQWRERLLNKLEEAQV
QLENTRELEQLVLMAQRVDVAEEL
DRLEAHVKETHNILKKKEAVGRRLDFMMQEFNRE
SNTLASKSINAEVTNSAIELKVLII
EQMREQIQNIE"
misc-feature    complement(68686..69147 /locus-tag="YE0057"
)
                /inference="protein
motif:PFAM:PF03755"
/note="Pfam match to entry PF03755
YicC-N-term, YicC-like family,
N-terminal region, score 272.9,
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gene	69277..69993	E-value 2.8e-79" /gene="rph" /locus-tag="YE0058"
CDS	69277..69993	/gene="rph" /locus-tag="YE0058" /codon-start=1 /transl-table=11 /product="ribonuclease PH" /protein-id="CAL10200.1" /db-xref="GI:122087419" /db-xref="GOA:A1JHW7" /db-xref="InterPro:IPR001247" /db-xref="InterPro:IPR002381" /db-xref="InterPro:IPR015847" /db-xref="UniProtKB/Swiss-Prot:A1JHW7" /translation="MRPADRAAQQVRPLTLTRNY TKHAEGSVLVEFGDTKVLCTATVE EGVPRFLKGQGQGWITA EYGM LPRSTHSRNAREA AKGKQGGRTLEIQRLIARSLRAAV DLKKLG EFTITLDCDVLQADGGTRTASISGACVA LADALNKLVASGK LKANPMKGLVA AVSVGIVKGEALCDLEYVEDSAAETDMNVMMED GRMIEVQGTAE GEPFSHEELLTLL ALARGGIETIFQAQKAAL EQ"
misc-feature	69304..69705	/gene="rph" /locus-tag="YE0058" /inference="protein" motif:PFAM:PF01138" /note="Pfam match to entry PF01138 RNase-PH, 3' exoribonuclease family, domain 1, score 196.1, E-value 3.5e-56"
misc-feature	69622..69660	/gene="rph" /locus-tag="YE0058" /inference="protein" motif:Prosite:PS01277" /note="PS01277 Ribonuclease PH signature."
misc-feature	69745..69948	/gene="rph" /locus-tag="YE0058" /inference="protein" motif:PFAM:PF03725" /note="Pfam match to entry PF03725 RNase-PH-C, 3' exoribonuclease family, domain 2, score 73.9, E-value 2.2e-19"
gene	70145..70786	/gene="pyrE" /locus-tag="YE0059"
CDS	70145..70786	/gene="pyrE" /locus-tag="YE0059" /codon-start=1 /transl-table=11 /product="orotate phosphoribosyltransferase" /protein-id="CAL10201.1" /db-xref="GI:122087420" /db-xref="GOA:A1JHW8" /db-xref="InterPro:IPR000836" /db-xref="InterPro:IPR002375" /db-xref="InterPro:IPR004467" /db-xref="UniProtKB/Swiss-Prot:A1J



		HW8"
		/translation="MKAYQREFIEFALNKQVLKF GEFTLKSGRISPYFFNAGLFNTGL ELAKLGRFYAAALMDCGVEFDLLFGPAYKGIPIA TTTAVALAEEHNRDLPYCFNRKEA KDHGEGGSLVGSPLEGRVMLVDDVITAGTAIRES MEIINAQGATLAGVMISLDRQERG RGEISAIQEVERDYHCKVIAIVTLNDVISYLEEK PEMADHLAAVRHYREQYGV"
misc-feature	70238..70699	/gene="pyrE" /locus-tag="YE0059" /inference="protein motif:PFAM:PF00156" /note="Pfam match to entry PF00156 Pribosyltran,Phosphoribosyl transferase domain, score 103.2, E-value 3.2e-28"
misc-feature	70502..70540	/gene="pyrE" /locus-tag="YE0059" /inference="protein motif:Prosite:PS00103" /note="PS00103 Purine/pyrimidine phosphoribosyl transferases signature."
gene	complement(70864..71460 )	/gene="ttk"
CDS	complement(70864..71460 )	/locus-tag="YE0060" /gene="ttk"  /locus-tag="YE0060" /codon-start=1 /transl-table=11 /product="TetR-family regulatory protein" /protein-id="CAL10202.1" /db-xref="GI:122087421" /db-xref="GOA:A1JHW9" /db-xref="InterPro:IPR001647" /db-xref="InterPro:IPR012287" /db-xref="UniProtKB/Swiss-Prot:A1J HW9" /translation="MAEKENTKRNREEILQALA QMLESSDGSQRITTAKLAANVGVS EAALYRHFPSKTRMFDSLIEFIEDSLMSRINLIL QDEKETFNRLRLILLVLGFAERN PGLTRIMTGHALMFEQDRLQGRINQLFERIEVQL RQVLREKKLRDQGQFIHDEALLAT QLLAFCEGMLSRFVRSEFRYRPTQEFDARWPLIV AQLQ"
misc-feature	complement(71275..71418 )	/gene="ttk"  /locus-tag="YE0060" /inference="protein motif:PFAM:PF00440" /note="Pfam match to entry PF00440 tetR, Bacterial regulatory proteins, tetR family, score 41.0, E-value 1.7e-09"
misc-feature	complement(71287..71379 )	/gene="ttk"  /locus-tag="YE0060" /inference="protein"

		motif:Prosist:PS01081"
		/note="PS01081 Bacterial regulatory proteins, tetR family signature."
misc-feature	complement(71302..71367)	/gene="ttk"
		/locus-tag="YE0060"
		/note="Predicted helix-turn-helix motif with score 1905.000, SD 5.68 at aa 32-53, sequence ITTAKLAANVGVSSEALYRHFP"
gene	complement(71581..72036)	/gene="dut"
		/locus-tag="YE0061"
		/note="synonyms: dnaS, sof"
CDS	complement(71581..72036)	/gene="dut"
		/locus-tag="YE0061"
		/codon-start=1
		/transl-table=11
		/product="deoxyuridine 5'-triphosphate nucleotidohydrolase"
		/protein-id="CAL10203.1"
		/db-xref="GI:122087422"
		/db-xref="GOA:A1JHX0"
		/db-xref="InterPro:IPR008180"
		/db-xref="InterPro:IPR008181"
		/db-xref="UniProtKB/Swiss-Prot:A1JHX0"
		/translation="MKKIDIKILDPRVGNEFPLP TYATEGSAGLDLRACLSEAVDLLP GQTLLPTGLAIHIGDSSLAAILPRSGLGHKHG VVLGNLVGLIDSDYQQQLMVSVMN RGQQPFTIEPGERIAQMVFVPVIQAEFNLVEDFD LSEKGTGGFGHSGRQ"
misc-feature	complement(71590..71994)	/gene="dut"
		/locus-tag="YE0061"
		/inference="protein motif:PFAM:PF00692"
		/note="Pfam match to entry PF00692 dUTPase, dUTPase ,score 180.9, E-value 1.3e-51"
gene	complement(72017..73204)	/gene="dfp"
		/locus-tag="YE0062"
CDS	complement(72017..73204)	/gene="dfp"
		/locus-tag="YE0062"
		/codon-start=1
		/transl-table=11
		/product="DNA/pantothenate metabolism flavoprotein"
		/protein-id="CAL10204.1"
		/db-xref="GI:122087423"
		/db-xref="GOA:A1JHX1"
		/db-xref="InterPro:IPR003382"
		/db-xref="InterPro:IPR005252"
		/db-xref="InterPro:IPR007085"
		/db-xref="UniProtKB/TrEMBL:A1JHX1"
		/translation="MLGISGGIAAYKSPQLVRRR"

		RDRGAEVRVVMTHAAKAFITPLTL QAVSGYPVSDDLDPAAEAAMGHIELGKWADLVI MAPATADLLARVATGMANDLLTTV CLATAAPIAAVPAMNQMYRAAATQANLQTLASR GMLLWGPDSGSQACGDVGPGRMLD PLDIVALAHDFSVKQDLQHLVSMITAGPTREAL DPVRFISNQSSGKMGFAIAQAAAA RGAKVTLVAGPVMLPTPAGVNRIDVVSALQMOT VQNLAQQNIFISCAAVADYRAEQ VSDEKIKKQGDEITLKLKVPDIVAGVASMTKKR PFVVGFAAETQNVVEYARQKLARK NLDLICANDVSLAEHGFNSDTNALHLFWPTGEKR LPLSDKHLLSQHLIDEIVSRYDEK NRH"
misc-feature	complement(72407..72439)	/gene="dfp"  /locus-tag="YE0062" /inference="protein" motif:Prosite:PS00013" /note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site."
misc-feature	complement(72860..73201)	/gene="dfp"  /locus-tag="YE0062" /inference="protein" motif:PFAM:PF02441" /note="Pfam match to entry PF02441 Flavoprotein, Flavoprotein, score 147.6, E-value 1.5e-41"
gene	73442..74110	/gene="radC"
CDS	73442..74110	/locus-tag="YE0063" /gene="radC" /locus-tag="YE0063" /codon-start=1 /transl-table=11 /product="putative DNA repair protein" /protein-id="CAL10205.1" /db-xref="GI:122087424" /db-xref="GOA:A1JHX2" /db-xref="InterPro:IPR001405" /db-xref="UniProtKB/Swiss-Prot:A1J HX2" /translation="MEEWYGQVAPREKLLKYGAA VLTDALLAIFLRTGIPGMHVMQM AEYLIEEFGSLYGLISADYQALCAQKGIGVSKYS QIQAI AELAGRCFSSHLMQESVLQ NPEITQKFLQNILSHREREIFLVMFLDNQHRVIR HEEMFTGTISSVEIHPREIVREAL KVNAALILAHNHPSGKAEPSQADRLMTTQVIKA CSLLDIRVLDHLVVGRGECVSFAE RGWL"
misc-feature	73733..74107	/gene="radC" /locus-tag="YE0063" /inference="protein" motif:PFAM:PF04002" /note="Pfam match to entry PF04002 RadC, RadC, DNA repair protein, score 263.4, E-value 2e-76"
misc-feature	73952..73969	/gene="radC" /locus-tag="YE0063" /inference="protein" motif:Prosite:PS01302"

		/note="PS01302 DNA repair protein radC family signature."
gene	74374..74610	/gene="rpmB"
		/locus-tag="YE0064"
CDS	74374..74610	/gene="rpmB"
		/locus-tag="YE0064"
		/codon-start=1
		/transl-table=11
		/product="50S ribosomal protein L28"
		/protein-id="CAL10206.1"
		/db-xref="GI:122087425"
		/db-xref="GOA:A1JHR2"
		/db-xref="InterPro:IPR001383"
		/db-xref="UniProtKB/Swiss-Prot:A1J HR2"
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misc-feature	74380..74562	/gene="rpmB"
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		/inference="protein"
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		/note="Pfam match to entry PF00830 Ribosomal-L28,Ribosomal L28 family, score 133.2, E-value 3.1e-37"
gene	74622..74789	/gene="rpmG"
		/locus-tag="YE0065"
CDS	74622..74789	/gene="rpmG"
		/locus-tag="YE0065"
		/codon-start=1
		/transl-table=11
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		/protein-id="CAL10207.1"
		/db-xref="GI:122087426"
		/db-xref="GOA:A1JHR4"
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		/db-xref="UniProtKB/Swiss-Prot:A1J HR4"
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misc-feature	74637..74780	/gene="rpmG"
		/locus-tag="YE0065"
		/inference="protein"
		motif:PFAM:PF00471"
		/note="Pfam match to entry PF00471 Ribosomal-L33,Ribosomal protein L33, score 94.5, E-value 1.3e-25"
misc-feature	74682..74741	/gene="rpmG"
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		/inference="protein"
		motif:Prosite:PS00582"
		/note="PS00582 Ribosomal protein L33 signature."
gene	74876..75685	/gene="mutM"
		/locus-tag="YE0066"
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CDS	74876..75685	/gene="mutM"

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/transl-table=11
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/db-xref="GOA:A1JHR7"
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HR7"
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LRYTDPRRFGAWLWAKDLETNSVLAHLGPEPLSD
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NKVVVGVGNIYASESLFTAGILPERAAGSLTETE
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misc-feature    74876..75679    /gene="mutM"
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                                     /inference="protein
motif:PFAM:PF01149"
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Fapy-DNA-glyco,Formamidopyrimidine
-DNA glycosylase, score 483.1,
E-value 1.4e-142"
gene            complement(75792..76271    /gene="coaD"
)
                                     /locus-tag="YE0067"
                                     /note="synonym: kdtB"
CDS             complement(75792..76271    /gene="coaD"
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                                     /db-xref="UniProtKB/Swiss-Prot:A1J
HR9"
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misc-feature    complement(75870..76268    /gene="coaD"
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		/locus-tag="YE0067" /inference="protein" motif:PFAM:PF01467" /note="Pfam match to entry PF01467 CTP-transf-2,Cytidyltransferase, score 151.3, E-value 1.1e-42"
gene	complement(76268..77050)	/gene="kdtX"
		/locus-tag="YE0068" /note="synonym: waaE"
CDS	complement(76268..77050)	/gene="kdtX"
		/locus-tag="YE0068" /codon-start=1 /transl-table=11 /product="lipopolysaccharide core biosynthesis glycosyl transferase" /protein-id="CAL10210.1" /db-xref="GI:122087429" /db-xref="GOA:A1JHS0" /db-xref="InterPro:IPR001173" /db-xref="UniProtKB/TrEMBL:A1JHS0" /translation="MSAKKRLSVVMIVKNEASLL ADCLASVTWADEIVVLDSGSEDET VALAEQYGAKVYSNTEWPGYGKQRQLAQQYATGD YILMLDADERVTPELKSAIETVLL APEEGAVYSCARRNLFGRFMRHSGWYPDRVTRL YPREQYRYNDDLHVHESLDSGSAKV ILLAGDLLHLTCRDFFAFQRKQLNYAQAWANQRH QQGKSCRYFAIISHTLGAFCKTWL LLAGFLDGKQGLLLAVVNAQYTFNKYAALWALSH QYQKSENS"
sig-peptide	complement(76961..77050)	/gene="kdtX"
		/locus-tag="YE0068" /note="Signal peptide predicted for YE0068 by SignalP 2.0 HMM (Signal peptide probability 0.844) with cleavage site probability 0.843 between residues 30 and 31"
misc-feature	complement(76565..77029)	/gene="kdtX"
		/locus-tag="YE0068" /inference="protein" motif:PFAM:PF00535" /note="Pfam match to entry PF00535 Glycos-transf-2,Glycosyl transferase, score 88.5, E-value 8.8e-24"
gene	complement(77051..78328)	/gene="kdtA"
		/locus-tag="YE0069" /note="synonym: waaA"
CDS	complement(77051..78328)	/gene="kdtA"
		/locus-tag="YE0069" /codon-start=1 /transl-table=11 /product="3-deoxy-D-manno-octuloso nic-acid transferase" /protein-id="CAL10211.1" /db-xref="GI:122087430"

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misc-feature    complement(77126..77638 /gene="kdtA"
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motif:PFAM:PF00534"
/note="Pfam match to entry PF00534
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E-value 1.6e-06"

gene            complement(78869..79834 /gene="rfaC"
)

/locus-tag="YE0070"
/note="synonyms: rfa-2, waaC"

CDS            complement(78869..79834 /gene="rfaC"
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misc-feature    complement(78884..79612 /gene="rfaC"
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/locus-tag="YE0070"
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motif:PFAM:PF01075"

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                                /note="Pfam match to entry PF01075
                                Glyco-transf-9,Glycosyltransferase
                                family 9 (heptosyltransferase),
                                score 316.4, E-value 2.1e-92"
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)
                                /locus-tag="YE0071"
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CDS      complement(79834..80898 /gene="rfaF"
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                                /transl-table=11
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                                LGSAKDNEAGEEIRQALDESAREYCLNLAGQTSL
                                DQAVVMIAACNAVVSND SGLMHVA
                                AALNKPLVALYGPSSPDFTPPLSDKATVIRLITG
                                YHKVRKGD SAQGYHQSLIDIQPEQ
                                VMAALEKQLSAQTSSVKEGD"
misc-feature complement(79927..80694 /gene="rfaF"
)
                                /locus-tag="YE0071"
                                /inference="protein
                                motif:PFAM:PF01075"
                                /note="Pfam match to entry PF01075
                                Glyco-transf-9,Glycosyltransferase
                                family 9 (heptosyltransferase),
                                score 372.2, E-value 3.5e-109"
gene      complement(80929..81861 /gene="rfaD"
)
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CDS      complement(80929..81861 /gene="rfaD"
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                                /protein-id="CAL10214.1"
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                                /db-xref="InterPro:IPR011912"
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                                /db-xref="UniProtKB/Swiss-Prot:A1J
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misc-feature	complement(80932..81858)	/gene="rfaD"  /locus-tag="YE0072" /inference="protein motif:PFAM:PF01370" /note="Pfam match to entry PF01370 Epimerase, NAD dependent epimerase/dehydratase family, score -1.0, E-value 2.2e-13"
gene	82105..83316	/gene="kbl"
CDS	82105..83316	/locus-tag="YE0073" /gene="kbl" /locus-tag="YE0073" /codon-start=1 /transl-table=11 /product="2-amino-3-ketobutyrate coenzyme A ligase" /protein-id="CAL10215.1" /db-xref="GI:122087434" /db-xref="GOA:A1JHX7" /db-xref="InterPro:IPR001917" /db-xref="InterPro:IPR004839" /db-xref="InterPro:IPR011282" /db-xref="InterPro:IPR015421" /db-xref="UniProtKB/TrEMBL:A1JHX7" /translation="MSLPFDRNAFYQQLEQQLK TRAEGLYKNERIITSQQADIABA DGRHVINFCAANNYLGLANHPRLIAAAKKGMDTHG FGMAVRFICGTQDTHKELEQKLA SFLGMEDAILYSSCFDANGGLFETLLGPEDAIIS DALNHASIIDGVRLCKAKRYRYAN NDMSELKAQLEQAKADGARHIMIATDGVFSMDGV IANLKGVCDLADEYQALVMVDDSH AVGFVGANGRGTHEYCEVMDRVDIITGTLGKALG GASGGYTAGRKEVVEWLRQSRPY LFSNSLAPAIVAASIEVLSLLEDGAELRDRLWSN ARLFREKMSAAGFTLAGADHAIIP VMLGDATLAQEFANALLKEGIYVTGFFYPVVPKG QARIRTQMSADHTPEQVERAVEAF IRIGKQLNVIA"
misc-feature	82339..83283	/gene="kbl" /locus-tag="YE0073" /inference="protein motif:PFAM:PF00155" /note="Pfam match to entry PF00155 aminotran-1-2, Aminotransferase class I and II, score 260.1, E-value 1.9e-75"
misc-feature	82840..82869	/gene="kbl" /locus-tag="YE0073"

		/inference="protein motif:Prosite:PS00599" /note="PS00599 Aminotransferases class-II pyridoxal-phosphate attachment site." /gene="tdh" /locus-tag="YE0074" /gene="tdh" /locus-tag="YE0074" /codon-start=1 /transl-table=11 /product="threonine 3-dehydrogenase" /protein-id="CAL10216.1" /db-xref="GI:122087435" /db-xref="GOA:A1JHX8" /db-xref="InterPro:IPR002085" /db-xref="InterPro:IPR002328" /db-xref="InterPro:IPR004627" /db-xref="InterPro:IPR013149" /db-xref="InterPro:IPR013154" /db-xref="UniProtKB/Swiss-Prot:A1J HX8" /translation="MKALAKLKAEEGIWMTNVPQ PELGHNDIMIKIRKTAICGTDVHI YNWDEWSQKTIPVPMVVGHEYVGEVVAIGQEVKG FNIGDRVSGEGHITCGHCRNCRGG RTHLCRNTVGVGVNRPGSFAEYLVIPAFNAFKIP DNISDELAEIFDPFGNAVHTALSF DLVGEDVLVSGAGPIGIMAAVCKHVGARHVVIT DVNEYRLDLARKMGVTRAVNVNKE NLNDVMAELGMTEGFDVGLEMSGAPPAFRALLNS MNHGGRIAMLGIPPSDMSIDWNQV IFKGLFIKGIYGREMFEWYKMAALIQSGLDLTP IITHRFSIDFQQGFDAMRSGKSG KVILNWD"
gene	83341..84366	
CDS	83341..84366	
misc-feature	83359..84360	/gene="tdh" /locus-tag="YE0074" /inference="protein motif:PFAM:PF00107" /note="Pfam match to entry PF00107 adh-zinc, Zinc-binding dehydrogenase, score 375.2, E-value 4.2e-110"
misc-feature	83524..83568	/gene="tdh" /locus-tag="YE0074" /inference="protein motif:Prosite:PS00059" /note="PS00059 Zinc-containing alcohol dehydrogenases signature."
gene	complement(84557..85582	/locus-tag="YE0075"
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CDS	complement(84557..85582	/locus-tag="YE0075"
	)	
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		Salmonella typhi putative exported protein STY4089 SWALL:Q8Z2F2 (EMBL:AL627280) (320 aa) fasta scores: E(): 1.3e-64,62.46 38d in 325 aa"
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		/transl-table=11
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		/protein-id="CAL10217.1"
		/db-xref="GI:122087436"
		/db-xref="InterPro:IPR006837"
		/db-xref="UniProtKB/TrEMBL:A1JHX9"
		/translation="MRYFNTHRLIIVSTLLIANT SLAGKLSIVIDDFGYRPQENKVL QMPLPISVAILPNAPYAKEMAIKAHNQGREILIH LPMAPLSKQPLERDTLQPLMSSEE IQRIIRQAVNNVPYATGMNNHMGSA MTSSLPGMQ KVMQVLEHYQLYFLDSVTIGNSQA SRAAEGTGKVIKRVFLDDSQNEAAIRQQFNRA VELARRNGSAIAIGHPHPATIKVL QQMLPQLPADIVLVKASALLNEPVH NITGHNNSG SGTVSPGKSKPRDPAKGQRLKA IK QCNAKASYAPEKIYADKMFII LGESLMQSPAVTF VQKHWQQYFPPAVPVPVEKSTIE KPKAENP"
sig-peptide	complement(85514..85582 )	/locus-tag="YE0075"
		/note="Signal peptide predicted for YE0075 by SignalP 2.0 HMM (Signal peptide probability 0.995) with cleavage site probability 0.979 between residues 23 and 24"
misc-feature	complement(84800..84823 )	/locus-tag="YE0075"
		/inference="protein motif:Prosite:PS00017"
		/note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	complement(85606..86760 )	/locus-tag="YE0076"
CDS	complement(85606..86760 )	/locus-tag="YE0076"
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		/transl-table=11
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		/db-xref="InterPro:IPR002886"
		/db-xref="InterPro:IPR016047"
		/db-xref="UniProtKB/TrEMBL:A1JHY0"
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                6.8e-33"
gene            complement(86983..88530 /locus-tag="YE0077"
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CDS             complement(86983..88530 /locus-tag="YE0077"
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                YDLQPEMSSAELTEKLVGAIASGK
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                /note="Pfam match to entry PF01676
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                superfamily, score 186.2, E-value
                3.5e-53"
gene            88772..89206 /locus-tag="YE0078"
CDS             88772..89206 /locus-tag="YE0078"
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misc-feature	88808..88864	/locus-tag="YE0078" /inference="protein" motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted for YE0078 by TMHMM2.0 at aa 13-31"
misc-feature	88895..89179	/locus-tag="YE0078" /inference="protein" motif:PFAM:PF00581" /note="Pfam match to entry PF00581 Rhodanese, Rhodanese-like domain, score 76.3, E-value 4.1e-20"
gene	89256..89504	/gene="grxC"
CDS	89256..89504	/locus-tag="YE0079" /gene="grxC" /locus-tag="YE0079" /codon-start=1 /transl-table=11 /product="glutaredoxin" /protein-id="CAL10221.1" /db-xref="GI:122087440" /db-xref="GOA:A1JHY3" /db-xref="InterPro:IPR002109" /db-xref="InterPro:IPR011767" /db-xref="InterPro:IPR011900" /db-xref="InterPro:IPR012335" /db-xref="InterPro:IPR014025" /db-xref="UniProtKB/TrEMBL:A1JHY3" /translation="MAKIEIYTKATCPFCHRAKA LLNSKGAAFHEIAIDNDPAKREEM IARSGRTTVPQVFIDGQHIGGCDDLHALDARGGL DPLL"
misc-feature	89262..89435	/gene="grxC" /locus-tag="YE0079" /inference="protein" motif:PFAM:PF00462" /note="Pfam match to entry PF00462 glutaredoxin, Glutaredoxin, score 85.5, E-value 7.3e-23"
misc-feature	89271..89321	/gene="grxC" /locus-tag="YE0079" /inference="protein" motif:Prosite:PS00195" /note="PS00195 Glutaredoxin active site."
gene	89596..90066	/gene="secB"
CDS	89596..90066	/locus-tag="YE0080" /gene="secB" /locus-tag="YE0080" /codon-start=1 /transl-table=11 /product="protein-export protein"

		/protein-id="CAL10222.1" /db-xref="GI:122087441" /db-xref="GOA:A1JHY4" /db-xref="InterPro:IPR003708" /db-xref="UniProtKB/Swiss-Prot:A1JHY4" /translation="MSEQNNTEMAFQIQRIYTKD ISFEAPNAPQVFQQDWQPEVKLDL DTASSQLAEDVYEVVLRVTVTASLGEETAFLCEV QQGGIFSIAGIDGTQLAHCLGAYC PNILFPYARECITSLVSRGTFPQLNLAPVNFDA LFMNYLQQQAEGEGAEQRQDA"
misc-feature	89596..90033	/gene="secB" /locus-tag="YE0080" /inference="protein" motif:PFAM:PF02556" /note="Pfam match to entry PF02556 SecB, Preprotein translocase subunit SecB, score 338.5, E-value 4.8e-99"
gene	90066..91085	/gene="gpsA"
CDS	90066..91085	/locus-tag="YE0081" /gene="gpsA" /locus-tag="YE0081" /codon-start=1 /transl-table=11 /product="glycerol-3-phosphate dehydrogenase" /protein-id="CAL10223.1" /db-xref="GI:122087442" /db-xref="GOA:A1JHY5" /db-xref="InterPro:IPR006109" /db-xref="InterPro:IPR006168" /db-xref="InterPro:IPR011128" /db-xref="InterPro:IPR013328" /db-xref="InterPro:IPR016040" /db-xref="UniProtKB/Swiss-Prot:A1JHY5" /translation="MNTTHASMTVIGAGSYGTAL AITLARNGHQVVWLWGHDPKHIQTL QQDRCNQAFLPDVPFPDTLLLETDLARALAASRD VLVVVP SHVFGAVLNQLKPHLRPD ARIVWATKGLEAETGRLLADVAREVLGESIPLAV VSGPTFAKELAAGLP TAIALASTD VQFSEDLQQLLHCGKSFRVYSNPDFIGVQLGGAV KNVIAIGAGMSDGIGFGANARTAL ITRGLAEMTRLGSALGADPSTFMGMAGLGDVLVT CTDNQSRNRRFGIMLGQGLGVQEA QDKIGQVVEGYRNTKEVLALAQNRNGVEMPITEQI YQVLYSHKNAREEAALTLLGRTKKD EKSGI"
sig-peptide	90066..90128	/gene="gpsA" /locus-tag="YE0081" /note="Signal peptide predicted for YE0081 by SignalP 2.0 HMM (Signal peptide probability 0.931) with cleavage site probability 0.910 between residues 21 and 22"
misc-feature	90078..91046	/gene="gpsA" /locus-tag="YE0081" /inference="protein" motif:PFAM:PF01210" /note="Pfam match to entry PF01210"

		NAD-Gly3P-dh, NAD-dependent glycerol-3-phosphate dehydrogenase, score 543.4, E-value 1e-160"
misc-feature	90639..90704	/gene="gpsA" /locus-tag="YE0081" /inference="protein motif:Prosite:PS00957" /note="PS00957 NAD-dependent glycerol-3-phosphate dehydrogenase signature."
gene	91211..92032	/gene="cysE" /locus-tag="YE0082"
CDS	91211..92032	/gene="cysE" /locus-tag="YE0082" /codon-start=1 /transl-table=11 /product="serine acetyltransferase" /protein-id="CAL10224.1" /db-xref="GI:122087443" /db-xref="GOA:A1JHY6" /db-xref="InterPro:IPR001451" /db-xref="InterPro:IPR005881" /db-xref="InterPro:IPR010493" /db-xref="UniProtKB/TrEMBL:A1JHY6" /translation="MSSEELVWSSIKSEARAL AECEPMLASFFHATLLKHENLGSA LSYILANKLANPIMPAAIAIREVVEDAYRADAQMI VSAARDILAVRLRDPVAVDKYSTPL LYLKGFHALQAYRIGHWLWAQDRKALAIYLNQV SVAFGVDIHPAATIGCGIMLDHAT GIVIGETAVVENDVSILQSVTLGGTGKTSGDRHP KIREGVMIGAGAKILGNIEVGRGA KIGAGSVVLQAVPPHTTAAGVPARIVGKPESDKP SLDMDQHFNGVSHGFEYGDGI"
misc-feature	91613..91666	/gene="cysE" /locus-tag="YE0082" /inference="protein motif:PFAM:PF00132" /note="Pfam match to entry PF00132 hexapep, Bacterial transferase hexapeptide (four repeats), score 4.6, E-value 12"
misc-feature	91709..91762	/gene="cysE" /locus-tag="YE0082" /inference="protein motif:PFAM:PF00132" /note="Pfam match to entry PF00132 hexapep, Bacterial transferase hexapeptide (four repeats), score 10.4, E-value 2.2"
misc-feature	91787..91840	/gene="cysE" /locus-tag="YE0082" /inference="protein motif:PFAM:PF00132" /note="Pfam match to entry PF00132 hexapep, Bacterial transferase hexapeptide (four repeats), score 9.3, E-value 3"
misc-feature	91814..91900	/gene="cysE" /locus-tag="YE0082"

		/inference="protein motif:Prosite:PS00101" /note="PS00101 Hexapeptide-repeat containing-transferases signature." /gene="cysE" /locus-tag="YE0082" /inference="protein motif:PFAM:PF00132" /note="Pfam match to entry PF00132 hexapep, Bacterial transferase hexapeptide (four repeats), score 11.9, E-value 1"
misc-feature	91841..91894	
gene	complement(92213..92716	/locus-tag="YE0083"
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CDS	complement(92213..92716	/locus-tag="YE0083"
	)	
		/codon-start=1 /transl-table=11 /product="putative methyltransferase" /protein-id="CAL10225.1" /db-xref="GI:122087444" /db-xref="GOA:A1JHY7" /db-xref="InterPro:IPR001537" /db-xref="InterPro:IPR004440" /db-xref="InterPro:IPR016914" /db-xref="UniProtKB/TrEMBL:A1JHY7" /translation="MLNIVLFEPEIIPPNTGNIIR LCANTGCQLHLIKPLGFTWDDKRL RRAGLDYHEFANIKHHHDYQAFLDSENLDGAQSA GTNPARLFALTTKGTPAHSAVNYQ VNDYLLFGPETRGLPSNVLDALPAQQKIRIPMLA ASRSMNLSNAVSVVVEAWRQLGY PGALLKE"
misc-feature	complement(92261..92716	/locus-tag="YE0083"
	)	
		/inference="protein motif:PFAM:PF00588" /note="Pfam match to entry PF00588 SpoU-methylase, SpoU rRNA Methylase family, score 180.0, E-value 2.6e-51"
gene	92988..93986	/locus-tag="YE0084"
CDS	92988..93986	/locus-tag="YE0084"
		/codon-start=1 /transl-table=11 /product="bifunctional regulatory protein/DNA repair protein" /protein-id="CAL10226.1" /db-xref="GI:122087445" /db-xref="GOA:A1JHY8" /db-xref="InterPro:IPR000005" /db-xref="InterPro:IPR001497" /db-xref="InterPro:IPR004026" /db-xref="InterPro:IPR008332" /db-xref="InterPro:IPR011991" /db-xref="InterPro:IPR014048" /db-xref="InterPro:IPR016221" /db-xref="UniProtKB/TrEMBL:A1JHY8" /translation="MKTTGVYCRPSCSSRQAKVE NIEFYADNDAAELAGYRCKRCRP TQLSQAQQHAEKISQACRLIEQAETPFTLDALAA



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misc-feature      92991..93122    /locus-tag="YE0084"
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                               /note="Pfam match to entry PF02805
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                               domain of Ada, score 56.3, E-value
                               4.3e-14"
misc-feature      93153..93284    /locus-tag="YE0084"
                               /inference="protein
                               motif:Prosite:PS00041"
                               /note="PS00041 Bacterial
                               regulatory proteins, araC family
                               signature."
misc-feature      93165..93299    /locus-tag="YE0084"
                               /inference="protein
                               motif:PFAM:PF00165"
                               /note="Pfam match to entry PF00165
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                               helix-turn-helix proteins, araC
                               family, score 47.7, E-value
                               1.7e-11"
misc-feature      93198..93263    /locus-tag="YE0084"
                               /note="Predicted helix-turn-helix
                               motif with score 1245.000, SD 3.43
                               at aa 71-92, sequence
                               FTLDALAAELNLSTFHFHRLFK"
misc-feature      93309..93446    /locus-tag="YE0084"
                               /inference="protein
                               motif:PFAM:PF00165"
                               /note="Pfam match to entry PF00165
                               HTH-AraC, Bacterial regulatory
                               helix-turn-helix proteins, araC
                               family, score 15.0, E-value 0.062"
misc-feature      93462..93698    /locus-tag="YE0084"
                               /inference="protein
                               motif:PFAM:PF02870"
                               /note="Pfam match to entry PF02870
                               Methyltransf-1N,6-O-methylguanine
                               DNA methyltransferase,
                               ribonuclease-like domain, score
                               25.9, E-value 6.2e-05"
misc-feature      93702..93968    /locus-tag="YE0084"
                               /inference="protein
                               motif:PFAM:PF01035"
                               /note="Pfam match to entry PF01035
                               Methyltransf-1,6-O-methylguanine
                               DNA methyltransferase, DNA binding
                               domain, score 172.2, E-value
                               5.7e-49"
misc-feature      93855..93875    /locus-tag="YE0084"
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Methylated-DNA--protein-cysteine
methyltransferase active site."
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/locus-tag="YE0085"
CDS       complement(94056..95432 /gene="cpxA"
)
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/codon-start=1
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kinase"
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/db-xref="GOA:A1JHY9"
/db-xref="InterPro:IPR003594"
/db-xref="InterPro:IPR003660"
/db-xref="InterPro:IPR003661"
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PLTRLQLATALMRRRHGEGKELER
IEMEAQRLDSMINDLLVLSRSQHKNELHREPIKA
NELWSEVLENAQFEADQMCKTLEV
TAPPGPWTLFGNPAALDSALENIVRNALRYSHHH
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PEDREQIFRPFYRTDEARDRESSGGTGLGLAIVET
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sig-peptide complement(95355..95432 /gene="cpxA"
)
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/locus-tag="YE0085"
/note="Signal peptide predicted
for YE0085 by SignalP 2.0 HMM
(Signal peptide probability 0.757)
with cleavage site probability
0.304 between residues 26 and 27"
misc-feature complement(94071..94400 /gene="cpxA"
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/locus-tag="YE0085"
/inference="protein
motif:PFAM:PF02518"
/note="Pfam match to entry PF02518
HATPase-c, Histidine kinase-, DNA
gyrase B-, and HSP90-like ATPase,
score 133.2, E-value 3.1e-37"
misc-feature complement(94533..94721 /gene="cpxA"
)
)
/locus-tag="YE0085"
/inference="protein
motif:PFAM:PF00512"
/note="Pfam match to entry PF00512
HisKA, His Kinase A
(phosphoacceptor) domain, score

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misc-feature	complement(94731..94943)	65.3, E-value 8.7e-17" /gene="cpxA"  /locus-tag="YE0085" /inference="protein" motif:PFAM:PF00672" /note="Pfam match to entry PF00672 HAMP, HAMP domain ,score 52.4, E-value 6.6e-13"
misc-feature	complement(join(94872..94940,95352..95420))	/gene="cpxA"  /locus-tag="YE0085" /inference="protein" motif:TMHMM:2.0" /note="2 probable transmembrane helices predicted for YE0085 by TMHMM2.0 at aa 5-27 and 165-187"
gene	complement(95429..96127)	/gene="cpxR"
CDS	complement(95429..96127)	/locus-tag="YE0086" /gene="cpxR"  /locus-tag="YE0086" /codon-start=1 /transl-table=11 /product="two component system response regulatory protein" /protein-id="CAL10228.1" /db-xref="GI:122087447" /db-xref="GOA:A1JHZ0" /db-xref="InterPro:IPR001789" /db-xref="InterPro:IPR001867" /db-xref="UniProtKB/TrEMBL:A1JHZ0" /translation="MHKILLVDDRELTSLLKEL LEMEGFNVVVAHDGEQALNLLDSS IDLLLLDIMMPRKNGIETLKELRQHHQTPVIMLT ARGSDLDRVLGLELGADDYLAKPF NDRELVARIRAILRRSNWSEQQNVDQGAPTLEV DCLQLNPGRQEASFEGQSLELTGT EFTLLYLLAQHLGQVVSREHLSQEVLGKRLTPFD RAIDMHISNLRRKLPDRKDGLPWF KTLRGRGYLMVSET"
misc-feature	complement(95453..95671)	/gene="cpxR"  /locus-tag="YE0086" /inference="protein" motif:PFAM:PF00486" /note="Pfam match to entry PF00486 trans-reg-C,Transcriptional regulatory protein, C terminal, score 110.2, E-value 2.5e-30"
misc-feature	complement(95771..96124)	/gene="cpxR"  /locus-tag="YE0086" /inference="protein" motif:PFAM:PF00072" /note="Pfam match to entry PF00072 response-reg, Response regulator receiver domain, score 152.2, E-value 5.9e-43"
gene	96348..96812	/gene="cpxP" /locus-tag="YE0087"

CDS	96348..96812	/gene="cpxP" /locus-tag="YE0087" /codon-start=1 /transl-table=11 /product="putative exported protein" /protein-id="CAL10229.1" /db-xref="GI:122087448" /db-xref="GOA:A1JHZ1" /db-xref="InterPro:IPR012899" /db-xref="UniProtKB/TrEMBL:A1JHZ1" /translation="MASMLVIGSQAAFAADKTGATDGWCHGDGAMMNKKDGRGHHNMF DGLNLTEQQRQQMRDLMRQSRQDQPRVDLADREAMHKLITADKFDEAAVRAQAEKMSK DQIDRQVEMAKVRNQMFNLLTPEQKAALNQKHQQRIEKMQQAPAAQPSSAQK"
sig-peptide	96348..96389	/gene="cpxP" /locus-tag="YE0087" /note="Signal peptide predicted for YE0087 by SignalP 2.0 HMM (Signal peptide probability 0.647) with cleavage site probability 0.643 between residues 14 and 15"
gene	96944..97846	/locus-tag="YE0088"
CDS	96944..97846	/locus-tag="YE0088" /codon-start=1 /transl-table=11 /product="putative integral membrane protein" /protein-id="CAL10230.1" /db-xref="GI:122087449" /db-xref="GOA:A1JHZ2" /db-xref="InterPro:IPR002524" /db-xref="UniProtKB/Swiss-Prot:A1JHZ2" /translation="MDPQYARLVKAAALSATVLA SILLIIKIFAWWHTGVSLLAALV DSLVDLAASLTNLFVVRYSLQPADEEHTFGHGKA ESLAALQSMFISGSALFLFLTGF QHLASPEPLQDPGLGIWVTLIALFSTLILVTFQR WVVRKTQSQAIRADMLHYQSDVMM NGAILIALALSWYGFHRADALFALGIGAYILYSA LRMGYEAVQALLDRALPDDERQEI INIVTSWPGVIGAHDLRTRQSGPTRFIQLHLEME DMLPLMEAHILADQVERALLHRFP GADILIHQDPTAVVPKERHAHWEL"
sig-peptide	96944..97066	/locus-tag="YE0088" /note="Signal peptide predicted for YE0088 by SignalP 2.0 HMM (Signal peptide probability 0.831) with cleavage site probability 0.693 between residues 41 and 42"
misc-feature	join(96977..97045, 97055..97123, 97181..97249, 97292..97360, 97415..97468, 97481..97540)	/locus-tag="YE0088"  /inference="protein motif:TMHMM:2.0" /note="6 probable transmembrane

		helices predicted for YE0088 by TMHMM2.0 at aa 12-34, 38-60, 80-102, 117-139, 158-175 and 180-199"
misc-feature	96980..97816	/locus-tag="YE0088" /inference="protein motif:PFAM:PF01545" /note="Pfam match to entry PF01545 Cation-efflux, Cation efflux family, score 354.0, E-value 1e-103"
gene	98096..99091	/gene="pfkA"
CDS	98096..99091	/locus-tag="YE0089" /gene="pfkA" /locus-tag="YE0089" /codon-start=1 /transl-table=11 /product="6-phosphofructokinase" /protein-id="CAL10231.1" /db-xref="GI:122087450" /db-xref="GOA:A1JHZ3" /db-xref="InterPro:IPR000023" /db-xref="InterPro:IPR012003" /db-xref="InterPro:IPR012828" /db-xref="InterPro:IPR015912" /db-xref="UniProtKB/Swiss-Prot:A1J HZ3" /translation="MVKKIGVLTSGGDAPGMNAA IRGVVRAALSEGLEYGIEDGYLG LYHNRMKQLDRYSVSDMINRGGTFLGSARFPFPR DPEIRKIALQNMKERGIDGLVVIG GDGSYAGADLLTKEGGIHCVGLPGTIDNDVAGTD YTIGFFTALETVVEAIDRLRDTSS SHQRISIVEVMGRFCGDLTLAAAIAGGCEFIAIP EVEFKREDLVKEIKAGIAKGKKHA IVAITEKLDNIDELAKYIEKETDRETRGTVLGH IQRGGAPVAYDRILASRMGAYAVDL LVNKISPPLNFFSSGGFCVGIQNEKMHVHELISVCI APENKKSFKEDWYDTAKKLF"
misc-feature	98102..98932	/gene="pfkA" /locus-tag="YE0089" /inference="protein motif:PFAM:PF00365" /note="Pfam match to entry PF00365 PFK, Phosphofructokinase, score 607.0, E-value 7.1e-180"
misc-feature	98627..98659	/gene="pfkA" /locus-tag="YE0089" /inference="protein motif:Prosite:PS00013" /note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site."
misc-feature	98828..98884	/gene="pfkA" /locus-tag="YE0089" /inference="protein motif:Prosite:PS00433" /note="PS00433 Phosphofructokinase signature."
repeat-region	complement(99130..10055 6)	/note="label:IS1660; IS4-like insertion sequence element IS1660"
repeat-region	99130..99145	/note="Inverted repeat for

		IS4-like element IS1660" /rpt-type=INVERTED
stem-loop	complement(99131..99162 )	
gene	complement(99139..10047 3)	/locus-tag="YE0090"
CDS	complement(99139..10047 3)	/locus-tag="YE0090"
		/inference="similar to sequence:INSDC:X81894" /inference="similar to sequence:UniProtKB:P03835" /note="Highly similar to many transposases from the IS element IS4 including: Escherichia coli transposase InsG for insertion sequence element IS4 SWALL:INSG-ECOLI (SWALL:P03835) (442 aa) fasta scores: E(): 9.8e-166, 89.54 38d in 440 aa and to Pantoea agglomerans insertion element protein SWALL:P71168 (EMBL:X81894) (440 aa) fasta scores: E(): 1.7e-86, 52.42 38d in 433 aa" /codon-start=1 /transl-table=11 /product="transposase for insertion sequence element IS1660" /protein-id="CAL10232.1" /db-xref="GI:122087451" /db-xref="GOA:A1JHZ4" /db-xref="InterPro:IPR002559" /db-xref="UniProtKB/TrEMBL:A1JHZ4" /translation="MHIGQALDLVSRYSRLNPL TTLGDYLDLPQLISRCLAESGTVTL RKRRLPLEMMVWCIVGMALERKEPLHQIVNRLDI MLPGDRPFVAPSAVIQARQRLGSE AVRRVFSQTAQLWHGSVTHPHWCGLTLLAVDGVV WRTPDTPENDTAFPRQTYAGQPGL YPQVKMVCQMELTSHLLTAAAFGTMKESEYTLAE QLIDQTADNTLTLMDKGYISLGLL NAWSQAGEHRHWMIPKKGAYEEIRKLGKGDHL VKLKTSPQARKKWPELGAEMTARL LTITRKGKVYHLLTSMTDTMRYPGGEMADLYGHR WEIELGYREIKQTMQLSRLTLRSK KPELVEQELWGVLLAYNLVRYQMIKMAGALKGYW PNQLSFSESCGMVMRMLMTLQGAS PGRIPELMRDMESMAQMVKLPIRRERAFPRVKE RPYKYGKARNKNASQLLN"
misc-feature	complement(99418..10009 5)	/locus-tag="YE0090"
		/inference="protein motif:PFAM:PF01609" /note="Pfam match to entry PF01609 Transposase-11, Transposase DDE domain, score 160.8, E-value 1.5e-45"
repeat-region	complement(100541..1005 56)	/note="Inverted repeat for IS4-like element IS1660" /rpt-type=INVERTED
gene	100712..101701	/gene="sbp1"

CDS	100712..101701	/locus-tag="YE0091" /gene="sbp1" /locus-tag="YE0091" /codon-start=1 /transl-table=11 /product="exported sulfate-binding protein" /protein-id="CAL10233.1" /db-xref="GI:122087452" /db-xref="GOA:A1JHZ5" /db-xref="InterPro:IPR000957" /db-xref="InterPro:IPR005669" /db-xref="InterPro:IPR006059" /db-xref="UniProtKB/TrEMBL:A1JHZ5" /translation="MRKWGVGLSLLLLASGAMAK DIQLLNVSYPDTREFYQEYNQAFS KHWQEQTGDKVTVRQSHGGSGKQATSVINGIEAD VVTLLALAYDVDAIAERGRIDKDWI KRLPDNSAPYTSTIVFLVRKGNPKQIHDWSDLVK PGTSVITPNPKTSGGARWNYLAAW AYALEHNNNDQAKAQEFVKQLYKNVEVLDSGARG ATNTFVERGIGDVLIAWENEALLA VNEVGKDQFDIITPSISILAEPTVSVDKVVDKR GTREVADAYLKLYLSPEGQTIAAK NYRPRDPAAVAAKFAKEFPQLKLITIDVFGGWT KAQQVHFATGGVFDEISKR"
sig-peptide	100712..100768	/gene="sbp1" /locus-tag="YE0091" /note="Signal peptide predicted for YE0091 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 1.000 between residues 19 and 20"
misc-feature	100712..101698	/gene="sbp1" /locus-tag="YE0091" /inference="protein motif:PFAM:PF01100" /note="Pfam match to entry PF01100 Sulphate-bind, Prokaryotic sulphate- and thiosulphate-binding protein ,score 761.1, E-value 2.9e-226"
misc-feature	101144..101170	/gene="sbp1" /locus-tag="YE0091" /inference="protein motif:Prosite:PS00757" /note="PS00757 Prokaryotic sulfate-binding proteins signature 2."
gene	101902..102093	/locus-tag="YE0092"
CDS	101902..102093	/locus-tag="YE0092" /inference="similar to sequence:INSDC:U59485" /note="Poor database matches. Weakly similar to the N-terminal region of Agrobacterium tumefaciens hypothetical protein AttU SWALL:Q9WWC8 (EMBL:U59485) (78 aa) fasta scores: E(): 9.2, 32.55 38d in 43 aa. Doubtful CDS" /codon-start=1 /transl-table=11

		/product="hypothetical protein" /protein-id="CAL10234.1" /db-xref="GI:122087453" /db-xref="UniProtKB/TrEMBL:A1JHZ6" /translation="MANYAEKIIDIHGVSSAILI DNPGLDSPSPSLSGLARSGSIESL HSNSSICEPIWHCHIKGGG"
gene	complement(102318..103085)	/gene="tpiA"
CDS	complement(102318..103085)	/locus-tag="YE0093" /note="synonym: tpi" /gene="tpiA" /locus-tag="YE0093" /codon-start=1 /transl-table=11 /product="triosephosphate isomerase" /protein-id="CAL10235.1" /db-xref="GI:122087454" /db-xref="GOA:A1JHZ7" /db-xref="InterPro:IPR000652" /db-xref="InterPro:IPR013785" /db-xref="UniProtKB/Swiss-Prot:A1JHZ7" /translation="MRHPLVMGNWKLNGSTHMVN ELIANLRKELSTVEGCGVAIAPPA IYLNQAKHELSGSRIALGAQNVVDVNLGAFTGET SAEMLKDIGAQYIIIGHSERRTYH KESDEFIAKKFGVLKEVGLTPVLCIGETEAENEA GQTEAVCAKQLDAVLNTLGAKAFE GAVIAYEPIWAIGTGKSATPAQAQAVHKFIRDHI AKQDAAIAAQVIIQYGGSVNDKNA AELFTQPDIDGALVGGASLKADAFVIVKAAAAA KKA"
misc-feature	complement(102330..103082)	/gene="tpiA" /locus-tag="YE0093" /inference="protein motif:PFAM:PF00121" /note="Pfam match to entry PF00121 TIM, Triosephosphate isomerase, score 523.6, E-value 9.4e-155"
misc-feature	complement(102561..102593)	/gene="tpiA" /locus-tag="YE0093" /inference="protein motif:Prosite:PS00171" /note="PS00171 Triosephosphate isomerase active site."
gene	complement(103214..103798)	/locus-tag="YE0094"
CDS	complement(103214..103798)	/locus-tag="YE0094" /codon-start=1 /transl-table=11 /product="putative exported protein" /protein-id="CAL10236.1" /db-xref="GI:122087455" /db-xref="InterPro:IPR009918" /db-xref="UniProtKB/TrEMBL:A1JHZ8"



		/translation="MLTILLIATVSRHADPD GSYQQAEEETQPTAPYLLSGAPTFD LTLVKFRERYNHANPTLPISEFHAITVKDDAPPL TRAASKINENLYASTALERTGKI KTIQITYLPIKGSEEKAARLVAVNYMAALMRQFE PTLTLEQSIISNVQQLLTQGKGSFP FAHPVGAIRYVVADNGEKGLTFAVEPIKLSLSEA "
sig-peptide	complement(103751..103798)	/locus-tag="YE0094"  /note="Signal peptide predicted for YE0094 by SignalP 2.0 HMM (Signal peptide probability 0.988) with cleavage site probability 0.985 between residues 16 and 17"
gene	104103..104537	/locus-tag="YE0095"
CDS	104103..104537	/locus-tag="YE0095" /codon-start=1 /transl-table=11 /product="conserved membrane protein" /protein-id="CAL10237.1" /db-xref="GI:122087456" /db-xref="GOA:A1JHZ9" /db-xref="InterPro:IPR008523" /db-xref="UniProtKB/TrEMBL:A1JHZ9" /translation="MTIQQWCFSLKGRIGRRDFW IWIGLWLLAMLIIFTLAGQNWLS QTAAFAIVFLLWPTAAVMVKRLHNRNKAAGWWALL VVLAWMLMAGNWQMLAPIWQWGVG RFIPTLIMVMMLIDCGAFLGTEGENRFGPEAVPV KFLAEKSQ"
sig-peptide	104103..104252	/locus-tag="YE0095" /note="Signal peptide predicted for YE0095 by SignalP 2.0 HMM (Signal peptide probability 0.698) with cleavage site probability 0.268 between residues 50 and 51"
misc-feature	join(104160..104213, 104223..104291, 104316..104384, 104397..104465)	/locus-tag="YE0095"  /inference="protein motif:TMHMM:2.0" /note="4 probable transmembrane helices predicted for YE0095 by TMHMM2.0 at aa 20-37, 41-63, 72-94 and 99-121"
gene	complement(104780..105526)	/gene="fpr"
		/locus-tag="YE0096"
		/note="synonym: mvrA"
CDS	complement(104780..105526)	/gene="fpr"  /locus-tag="YE0096" /codon-start=1 /transl-table=11 /product="ferredoxin--NADP reductase" /protein-id="CAL10238.1" /db-xref="GI:122087457" /db-xref="GOA:A1JI00"

		/db-xref="InterPro:IPR001433" /db-xref="InterPro:IPR008333" /db-xref="UniProtKB/TrEMBL:A1JI00" /translation="MAEWVSGKITHIEHWTDTLF SIRVNAPIDPFTAGQFAKLALDID GERVQRAYSIVNAPSDNNLEFYLVTVPEGKLSR LDQLAVGGEVMVTKQAAGFFVLEE IPDCDTLWMLATGTAIGPYLSILQEGRDLERFKN LVLVHAARFARDLSYLPLMQQLEQ RYNGKLRIQTVVSREQSPGSLTGRVPALIENGSL EAAVGLKIDAEDSHVMLCGNPQMV RDTQQMLKEQGRMKHLRRKPGHMTSEQYW"
misc-feature	complement(104855..105211)	/gene="fpr"  /locus-tag="YE0096" /inference="protein" motif:PFAM:PF00175" /note="Pfam match to entry PF00175 NAD-binding-1,Oxidoreductase NAD-binding domain, score 82.4, E-value 6.1e-22"
misc-feature	complement(105227..105511)	/gene="fpr"  /locus-tag="YE0096" /inference="protein" motif:PFAM:PF00970" /note="Pfam match to entry PF00970 FAD-binding-6,Oxidoreductase FAD-binding domain, score 25.6, E-value 3.3e-06"
gene	105845..107029	/gene="emrD"
CDS	105845..107029	/locus-tag="YE0097" /gene="emrD" /locus-tag="YE0097" /inference="similar to sequence:INSDC:AL627280" /inference="similar to sequence:UniProtKB:P31442" /note="Similar to Escherichia coli multidrug resistance protein D EmrD SWALL:EMRD-ECOLI (SWALL:P31442) (394 aa) fasta scores: E(): 6.1e-104, 71.28 38d in 390 aa, and to Salmonella typhi multidrug resistance protein D STY3981 SWALL:Q8Z2L0 (EMBL:AL627280) (394 aa) fasta scores: E(): 2.3e-106, 72.33 38d in 394 aa" /codon-start=1 /transl-table=11 /product="multidrug resistance protein D" /protein-id="CAL10239.1" /db-xref="GI:122087458" /db-xref="GOA:A1JI01" /db-xref="InterPro:IPR004812" /db-xref="InterPro:IPR007114" /db-xref="InterPro:IPR011701" /db-xref="UniProtKB/TrEMBL:A1JI01" /translation="MRKIENFHLLVMLILLVAVG QMAQTIYVPVADIARDLSVRSQT

		VQRVMAAYLLTYGFSQLIYGPLSDRVGRRPVILA GMMIFMLGALGAWLANSLSLLVAA SALQGMGTGVAGVMARTMPRDLYAGTALRYANS LNMGILVSPLMAPVIGGVLASLFG WRACYAFLLFLCGGVAFCFRFLPETRPQQTEKR RMLASFRLLLSDRAFSCYLVMFIG ALAGIAVFEASAGVLMGGVGLSGVTVSILFILP IPAAFFGAWYAGRDGKTFHNLMMWH SVISCLLAGLMMWIPGWFVGMNIWTLVIPAAFF FGAGMLFPLATTGAMEPPPYLAGA AGALVGGLQNVGSGLATWLSAMLPQTGQFSLGLL MFAMAVLILLCWVPLSHRMQPQEH RV"
sig-peptide	105845..105913	/gene="emrD" /locus-tag="YE0097" /note="Signal peptide predicted for YE0097 by SignalP 2.0 HMM (Signal peptide probability 0.998) with cleavage site probability 0.934 between residues 23 and 24"
misc-feature	105881..107017	/gene="emrD" /locus-tag="YE0097" /inference="protein motif:PFAM:PF00083" /note="Pfam match to entry PF00083 sugar-tr, Sugar (and other) transporter, score -92.8, E-value 0.00014"
misc-feature	join(105986..106045, 106064..106123, 106136..106195, 106253..106321, 106334..106393, 106451..106519, 106562..106630, 106667..106735, 106745..106813, 106832..106900, 106928..106996)	/gene="emrD"
		/locus-tag="YE0097" /inference="protein motif:TMHMM:2.0" /note="12 probable transmembrane helices predicted for YE0097 by TMHMM2.0 at aa 7-28, 48-67, 74-93, 98-117,137-159, 164-183, 203-225, 240-262, 275-297, 301-323,330-352 and 362-384"
gene	complement(107115..1081 25)	/gene="glpX"
CDS	complement(107115..1081 25)	/locus-tag="YE0098" /gene="glpX"
		/locus-tag="YE0098" /inference="similar to sequence:UniProtKB:P28860" /inference="similar to sequence:UniProtKB:P28900" /note="Similar to Escherichia coli putative fructose 1,6-bisphosphatase GlpX SWALL:GLPX-ECOLI (SWALL:P28860) (336 aa) fasta scores: E():

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6.2e-107, 86.01 38d in 336 aa, and
to Shigella flexneri putative
fructose 1, 6-bisphosphatase GlpX
SWALL:GLPX-SHIFL (SWALL:P28900)
(336 aa) fasta scores: E():
2.2e-106, 85.71 38d in 336 aa"
/codon-start=1
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/product="putative fructose 1,
6-bisphosphatase"
/protein-id="CAL10240.1"
/db-xref="GI:122087459"
/db-xref="GOA:A1JI02"
/db-xref="InterPro:IPR004464"
/db-xref="UniProtKB/TrEMBL:A1JI02"
/translation="MKRELAIEFSRVTEAAALAG
YKWLGRGDKNAADGAAVKAMRIML
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AVDIAVDPIEGTRMTAMQANALA
VLAVGDKGTFLHAPDMYMEKLVVGPAGAKGAIDLN
LPLELNLRNVAIKLNKPLTDLTVI
TLAKPRHDGIIAEMQQLGVKVFAIPDGDVAASIL
TCMPESEVDVMYCIGGAPEGVISA
AVIRALDGDMMQGRLLPRHQVKGDNEDNRRIGEEE
LVRCKSMGIEAGKVLLLGDMARND
NVIFSATGITKGDLLEGIYRKGNMATTETLLIRG
KSRTIRRI RSTHFLDRKDPALHEF LL"
misc-feature    complement(107160..1081 /gene="glpX"
22)

/locus-tag="YE0098"
/inference="protein
motif:PFAM:PF03320"
/note="Pfam match to entry PF03320
FBPase-glpX, Bacterial
fructose-1,6-bisphosphatase,
glpX-encoded, score 788.7,E-value
1.4e-234"
gene            complement(108307..1098 /gene="glpK"
30)

/locus-tag="YE0099"
CDS             complement(108307..1098 /gene="glpK"
30)

/locus-tag="YE0099"
/EC-number="2.7.1.30"
/inference="similar to
sequence:INSDC:AL627279"
/inference="similar to
sequence:UniProtKB:P08859"
/note="Similar to Escherichia coli
glycerol kinase GlpK
SWALL:GLPK-ECOLI (SWALL:P08859)
(501 aa) fasta scores: E():
2e-178, 85.23 38d in 501 aa, and
to Salmonella typhi glycerol
kinase STY3784 SWALL:Q8Z2Y6
(EMBL:AL627279) (501 aa) fasta
scores: E(): 1.6e-177, 85.17 38d
in 499 aa"
/codon-start=1
/transl-table=11
/product="glycerol kinase"
/protein-id="CAL10241.1"

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misc-feature	complement(108373..109050)	/gene="glpK"  /locus-tag="YE0099" /inference="protein" motif:PFAM:PF02782" /note="Pfam match to entry PF02782 FGGY-C, FGGY family of carbohydrate kinases, C-terminal domain, score 353.3,E-value 1.7e-103"
misc-feature	complement(108667..108729)	/gene="glpK"  /locus-tag="YE0099" /inference="protein" motif:Prosites:PS00445" /note="PS00445 FGGY family of carbohydrate kinases signature 2."
misc-feature	complement(109057..109800)	/gene="glpK"  /locus-tag="YE0099" /inference="protein" motif:PFAM:PF00370" /note="Pfam match to entry PF00370 FGGY, FGGY family of carbohydrate kinases, N-terminal domain, score 452.8,E-value 1.9e-133"
misc-feature	complement(109372..109410)	/gene="glpK"  /locus-tag="YE0099" /inference="protein" motif:Prosites:PS00933" /note="PS00933 FGGY family of carbohydrate kinases signature 1."
gene	complement(109907..110755)	/gene="glpF"
CDS	complement(109907..110755)	/locus-tag="YE0100" /gene="glpF"  /locus-tag="YE0100"

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/transl-table=11
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facilitator protein"
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/db-xref="InterPro:IPR000425"
/db-xref="InterPro:IPR012269"
/db-xref="UniProtKB/TrEMBL:A1JI04"
/translation="MSQTASSTLKGQCIAEFLGT
ALLIFFGVGCVAALKLAGASFGQW
EISIIWGLGVAMAIYLTAAISGAHLNPAVTIALW
LFACFDRRKVLPYIVAQVAGAFCA
AALVFGLYYNLFIDFEQTHQIARGSVESLNLGI
FSTYPNPHisVFQAFLVETVITAI
LMCLILALTDGNGIPRGPLAPLLIGILIAVIGG
SMGPLTGFALNPARDFGPKLFAYF
AGWGEVAFTGGRDIPYFLVPIFGPIVGALVGAFG
YRALIGRHLPCDVCVADDEETTVT TTERKA"
misc-feature      complement(join(109985. /gene="glpF"
.110053,110150..110218,
110255..110323,
110423..110491,
110549..110617,
110660..110719))

/locus-tag="YE0100"
/inference="protein
motif:TMHMM:2.0"
/note="6 probable transmembrane
helices predicted for YE0100 by
TMHMM2.0 at aa 13-32, 47-69,
89-111, 145-167,180-202 and
235-257"
misc-feature      complement(109997..1107 /gene="glpF"
55)

/locus-tag="YE0100"
/inference="protein
motif:PFAM:PF00230"
/note="Pfam match to entry PF00230
MIP, Major intrinsic protein,
score 420.9, E-value 7.8e-124"
misc-feature      complement(110510..1105 /gene="glpF"
42)

/locus-tag="YE0100"
/inference="protein
motif:Prosites:PS00013"
/note="PS00013 Prokaryotic
membrane lipoprotein lipid
attachment site."
misc-feature      complement(110528..1105 /gene="glpF"
54)

/locus-tag="YE0100"
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motif:Prosites:PS00221"
/note="PS00221 MIP family
signature."
misc-feature      complement(110666..1106 /gene="glpF"
98)

/locus-tag="YE0100"
/inference="protein
motif:Prosites:PS00013"

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		/note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site."
gene	111350..111589	/locus-tag="YE0101"
CDS	111350..111589	/locus-tag="YE0101" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10243.1" /db-xref="GI:122087462" /db-xref="InterPro:IPR009252" /db-xref="UniProtKB/Swiss-Prot:A1J I05" /translation="MSFEVFEEKLEVKVQQAIDTI TLLQMEIEELKEKNNTLSQEVQEA AGGREALVRENEQLKQEQHVWQDRLRALLGKMEE V"
gene	complement(111726..1122 11)	/gene="menG"  /locus-tag="YE0102"
CDS	complement(111726..1122 11)	/gene="menG"  /locus-tag="YE0102" /codon-start=1 /transl-table=11 /product="S-adenosylmethionine:2-d emethylmenaquinone methyltransferase" /protein-id="CAL10244.1" /db-xref="GI:122087463" /db-xref="GOA:A1JI06" /db-xref="InterPro:IPR005493" /db-xref="InterPro:IPR010203" /db-xref="InterPro:IPR014339" /db-xref="UniProtKB/Swiss-Prot:A1J I06" /translation="MKYDTS DLCDIYHEEVNVVE PLFSNFGGRTSFGGKITTVKCFED NGLLFDLLEENGLGRVLVVDGGGSVRRALINAEL ADLALKNEWEGIVVYGAVRQVDEL AELDIGIQAMAAIPVGADEGIGESDIRVNFGGV TFFSGDHLIYADNTGIILSEEPLDI E"
misc-feature	complement(111753..1122 11)	/gene="menG"  /locus-tag="YE0102" /inference="protein" motif:PFAM:PF03737" /note="Pfam match to entry PF03737 Methyltransf-6,Dimethylmenaquinone methyltransferase, score 262.7,E-value 3.2e-76"
gene	complement(112342..1131 96)	/gene="menA"
CDS	complement(112342..1131 96)	/locus-tag="YE0103" /gene="menA"  /locus-tag="YE0103" /codon-start=1 /transl-table=11 /product="1,4-dihydroxy-2-naphthoa te octaprenyltransferase"

		/protein-id="CAL10245.1" /db-xref="GI:122087464" /db-xref="GOA:A1JI07" /db-xref="InterPro:IPR000537" /db-xref="InterPro:IPR004657" /db-xref="UniProtKB/TrEMBL:A1JI07" /translation="MPLAFASIVTGSALAVWLDS FKPAVALLALLTAGLLQILSNLAN DYGDAIKGSDTEERIGPLRGMQKGIITRHQMKVA LIITVSLTVISGIALIAVACEKPS DVLGFLLLGLMAIVAAITYTVGSKPYGYMGLGDI SVLVFFGWLSVAGTYYLQAGHFDS IVMLPATACGLLATAVLNINNLRDIENDKANGKN TLAVRLGPAVARYYHALLIVAAIF CLTLFNILYLHSWAGWIFVLAIPLLARHALFVLR EPTAAGMRPMLHEHMKAAALLTNIL FAIGLVLS"
sig-peptide	complement(113152..113196)	/gene="menA"  /locus-tag="YE0103" /note="Signal peptide predicted for YE0103 by SignalP 2.0 HMM (Signal peptide probability 0.814) with cleavage site probability 0.628 between residues 15 and 16"
misc-feature	complement(112345..113196)	/gene="menA"  /locus-tag="YE0103" /inference="protein" motif:PFAM:PF01040" /note="Pfam match to entry PF01040 UbiA, UbiA prenyltransferase family, score 121.0, E-value 1.5e-33"
misc-feature	complement(join(112348..112416,112450..112509,112522..112590,112651..112719,112732..112791,112828..112887,112900..112968,113068..113127))	/gene="menA"  /locus-tag="YE0103" /inference="protein" motif:TMHMM:2.0" /note="8 probable transmembrane helices predicted for YE0103 by TMHMM2.0 at aa 24-43, 77-99, 104-123, 136-155,160-182, 203-225, 230-249 and 261-283"
misc-feature	complement(112903..112935)	/gene="menA"  /locus-tag="YE0103" /inference="protein" motif:Prosite:PS00013" /note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site."
gene	complement(113424..114755)	/gene="hslU"
CDS	complement(113424..114755)	/locus-tag="YE0104" /gene="hslU"



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/transl-table=11
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/db-xref="GI:122087465"
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/db-xref="InterPro:IPR013093"
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I08"
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LTDAVKMVRHQSIKMRYRAEELAEERILDVLI
PPAKNNWGQPEETQEPSPTRQAFR
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KEAFKLLIEEEAAKLVNPEELKQQAIDAVEQHGI
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VQRDLLPLVEGCTVSTKHGMVKTDHILFIASGAF
QVSSPSDLIPELQGRLPPIRVELQA
LTDDFERILTEPSASLTEQYKALMATEGVTVEF
TREGIRKIAEAAWQVNERTENIGA
RRLHTVLERLMEDISYDASESNGQSITIDAAYVG
KHLDELVADEDLRFIL"
misc-feature    complement(113607..1146
02)              /gene="hslU"

/locus-tag="YE0104"
/inference="protein
motif:PFAM:PF00004"
/note="Pfam match to entry PF00004
AAA, ATPase family associated with
various cellular activities (AAA),
score 27.3, E-value 5.6e-07"
misc-feature    complement(114564..1145
87)              /gene="hslU"

/locus-tag="YE0104"
/inference="protein
motif:Prosite:PS00017"
/note="PS00017 ATP/GTP-binding
site motif A (P-loop)."
gene            complement(114810..1153
34)              /gene="hslV"

/locus-tag="YE0105"
/gene="hslV"
CDS             complement(114810..1153
34)

/locus-tag="YE0105"
/codon-start=1
/transl-table=11
/product="heat shock protein"
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/db-xref="GI:122087466"
/db-xref="GOA:A1JI09"
/db-xref="InterPro:IPR001353"
/db-xref="UniProtKB/Swiss-Prot:A1J
I09"
/translation="MTTIVSVRRNGHVIVGGDQ
VTLGNTVMKGNNAKKVRRLYNNKVI

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IYTNRFTQIEELTY"
misc-feature    complement(115164..1152 /gene="hslV"
23)
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                /inference="protein
                motif:TMHMM:2.0"
                /note="1 probable transmembrane
                helix predicted for YE0105 by
                TMHMM2.0 at aa 38-57"
gene            complement(115434..1162 /gene="ftsN"
97)
                /locus-tag="YE0106"
                /note="synonym: msgA"
CDS             complement(115434..1162 /gene="ftsN"
97)
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                /codon-start=1
                /transl-table=11
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                VGGLYFITHNKPGEPLLP SHDPRTGNGLPPKPE
                ERWRYIKELENRQIGVPTPTPEPSA
                GGEVNSKTQLTNEQRQLLEQM QADM RQQPTQLSE
                VPYNEGMPVPRSAVTIKPPVTNMQ
                QPLTPPRQTVPAPVPAQTQVQPPVTTPRTQQPT
                APVTQAATPPKPEKEKEKAQRWMV
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                RVVLGPYSTKAAADKALQRLKGAG
                QSGCIPLAVGG"
sig-peptide     complement(116136..1162 /gene="ftsN"
97)
                /locus-tag="YE0106"
                /note="Signal peptide predicted
                for YE0106 by SignalP 2.0 HMM
                (Signal peptide probabiltiy 0.661)
                with cleavage site probability
                0.196 between residues 54 and 55"
misc-feature    complement(116145..1162 /gene="ftsN"
13)
                /locus-tag="YE0106"
                /inference="protein
                motif:TMHMM:2.0"
                /note="1 probable transmembrane
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                TMHMM2.0 at aa 29-51"
gene            complement(116363..1173 /gene="cytR"
91)
                /locus-tag="YE0107"
CDS             complement(116363..1173 /gene="cytR"
91)
                /locus-tag="YE0107"

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misc-feature	complement(116387..117193)	/gene="cytR"  /locus-tag="YE0107" /inference="protein motif:PFAM:PF00532" /note="Pfam match to entry PF00532 Peripla-BP-like, Periplasmic binding proteins and sugar binding domain of the LacI family, score 116.6, E-value 3.1e-32"
misc-feature	complement(117287..117370)	/gene="cytR"  /locus-tag="YE0107" /inference="protein motif:PFAM:PF00356" /note="Pfam match to entry PF00356 lacI, Bacterial regulatory proteins, lacI family, score 53.4, E-value 3.2e-13"
misc-feature	complement(117299..117364)	/gene="cytR"  /locus-tag="YE0107" /note="Predicted helix-turn-helix motif with score 1874.000, SD 5.57 at aa 10-31, sequence ATMKDVAEMAGVSTATVSRALM"
misc-feature	complement(117302..117358)	/gene="cytR"  /locus-tag="YE0107" /inference="protein motif:Prosite:PS00356" /note="PS00356 Bacterial regulatory proteins, lacI family signature."
gene	complement(117622..119820)	/gene="priA"
CDS	complement(117622..119820)	/locus-tag="YE0108" /gene="priA"
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TESALQTLRSKGLIDLRAQEVAATDWRNGFSVLG
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PEIGLTPQTIARFRERFNAPVEVL
HSGLNDSERLSVWLRARNGEAAIVIGTRSALFTP
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YHARDLAVFRAREEGIPVIMGTATPALETLHNVQ
MGKYRQLTLSKRAGNAKPAVQHLL
DLKGLPLKVGLSQPLLKRMKAHLQADNQVILFLN
RRGYAPALLCHECGWIAECQRCDH
YYTLHQNHRLRCHHCDSQRPVPQQCPKCGSTHM
VSVGVGTEQLENELAPLFPDTPIT
RIDRDTTSRKGSLEQHLADVHQGGARILIGTQML
AKGHHFPDVTLLVALLDVDGALFSA
DFRSAERFAQLYTQVSGRAGRAGKQGEVILQTHH
PEHPLLQILLQQGYDAFAKQALAE
RKS VFLPPYTSHIIVRSEDHDNQQSALFLQQLRN
LLEASPLKDEALWIMGPVPALQAK
RGGFRFWQLLLQHPSRQLLQRLIKTSQPLINTLP
QARKVKWTLDVDPIDS"

misc-feature    complement(118054..1183
11)

/locus-tag="YE0108"
/inference="protein
motif:PFAM:PF00271"
/note="Pfam match to entry PF00271
helicase-C, Helicase conserved
C-terminal domain, score 27.9,
E-value 1.6e-05"

misc-feature    complement(119128..1191
51)

/locus-tag="YE0108"
/inference="protein
motif:Prosite:PS00017"
/note="PS00017 ATP/GTP-binding
site motif A (P-loop)."
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CDS 120213..120431 /locus-tag="YE0109"

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/locus-tag="YE0109"

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misc-feature	120213..120413	/gene="rpmE" /locus-tag="YE0109" /inference="protein" motif:PFAM:PF01197" /note="Pfam match to entry PF01197 Ribosomal-L31,Ribosomal protein L31, score 144.6, E-value 1.1e-40"
misc-feature	120321..120338	/gene="rpmE" /locus-tag="YE0109" /inference="protein" motif:Prosites:PS00190" /note="PS00190 Cytochrome c family heme-binding site signature."
misc-feature	120333..120389	/gene="rpmE" /locus-tag="YE0109" /inference="protein" motif:Prosites:PS01143" /note="PS01143 Ribosomal protein L31 signature."
gene	complement(120521..120838)	/gene="metJ"
CDS	complement(120521..120838)	/locus-tag="YE0110" /gene="metJ" /locus-tag="YE0110" /codon-start=1 /transl-table=11 /product="transcriptional repressor protein" /protein-id="CAL10252.1" /db-xref="GI:122087471" /db-xref="GOA:A1JI14" /db-xref="InterPro:IPR002084" /db-xref="UniProtKB/Swiss-Prot:A1J I14" /translation="MAEWNGEYVSPYAEHGKKSE QVKKITVSIPLKVLKILTDERTTR QVNNLRHATNSELLCEAFHLAFTGQPLPNDEDLR KERSDEIPEAAKILMRELGVDPDT WEY"
misc-feature	complement(120524..120835)	/gene="metJ" /locus-tag="YE0110" /inference="protein" motif:PFAM:PF01340" /note="Pfam match to entry PF01340 MetJ, Met Apo-repressor, MetJ, score 292.2, E-value 4.2e-85"
gene	121214..122371	/gene="metB"
CDS	121214..122371	/locus-tag="YE0111" /gene="metB" /locus-tag="YE0111" /codon-start=1 /transl-table=11 /product="cystathionine"

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		/db-xref="InterPro:IPR000277"
		/db-xref="InterPro:IPR011821"
		/db-xref="InterPro:IPR015421"
		/db-xref="InterPro:IPR015422"
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		AIHLVCTTFLKPDDLLVAPHDCYG
		GSYRLFDLSKRGAYRVLFVDQGDEVALSQALAK
		KPKLVLIETPSNPLL RVVDIAAIC
		KDAHAVGALTVC DNTFLSPALQQPLALGADLVVH
		SCTKYLNGHSDVVAGAVIAKDPEL
		AVELAWWANNIGVTGAAFDSYLLLRGLRTLSPRM
		AQQQRNADDIVRYLQQQPLVKKLY
		HPSLLQHPGHEIACRQQSGFGAMLSFELDGDEQV
		LRRFLSALELFTLAESLGGVESLI
		SHAATMTHAGMAPEARTAAGITDSSLRISVGIED
		SEDLIADLDNAFRLARD"
misc-feature	121229..122356	/gene="metB"
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		/inference="protein"
		motif:PFAM:PF01053"
		/note="Pfam match to entry PF01053
		Cys-Met-Meta-PP,Cys/Met metabolism
		PLP-dependent enzyme, score
		708.0,E-value 2.9e-210"
misc-feature	121781..121825	/gene="metB"
		/locus-tag="YE0111"
		/inference="protein"
		motif:Prosite:PS00868"
		/note="PS00868 Cys/Met metabolism
		enzymes pyridoxal-phosphate
		attachment site."
gene	122379..124814	/gene="metL"
		/locus-tag="YE0112"
		/note="synonym: metM"
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		FIHDLERLAGLLDNKVDDAIYAEVVGHGEIWSAR LMSAVLNKLDMAADWLDARSFLRA ERAAQPQIDEGRSYPLLQQLMAQHPHQRLVVTGF ISRNNAGETVLLGRNGSDYSATLV GALAGVERVTIWSDVAGVYSADPRKVKDACLLPL LRLDEASELARLAAPVLHTRTLQP VSGSDIDLQLRCSYQPEQGSTRIERVLASGSGAK IVTSHDDVCLIELQIAGHHDFSLA QKEIDLLLKRAQIKPLATGIHPDRNLLQLCYTSE VVNSALRVLEDATLPGKLSLREGL ALVALVGAGVSKNPLHSHRFYQQLKDQPVEFIWQ AEDGISLVAVLRLGPTTEHLIQGLH QSLFRAEKRIGLMLFGKGNIGARWLELFAREQKN ISARSGFEFVLAVVDSRRSLLSY DGLDASRTLAFYDDEAKEQDEESLFLWMRAHPFD DLVVLDVTASESLAEQYLDFAASYG FHVISANKLAGASSSNNYRQIRDAFAKTGRHWLY NATVGAGLPVNHTVRDLRDSGDSI LAISGIFSGTLSWLFLQFDGTVPFTELVDQAWQQ GLTEPDPRVDLSGQDVMRKLVLILA REAGYDIEPNQVRVESLVPAGADIGSVDQFFENG EALNQQMIQRLEAANEMGLVLRVY ARFDANGKARVGVEAVRADHPLASLLPCDNVFAI ESRWYRDNPLVIRGPGAGRDTVAG AIQSDLNRLAQLL"
misc-feature	122412..123242	/gene="metL" /locus-tag="YE0112" /inference="protein" motif:PFAM:PF00696" /note="Pfam match to entry PF00696 aakinase, Amino acid kinase family, score 162.5, E-value 4.7e-46"
misc-feature	122421..122447	/gene="metL" /locus-tag="YE0112" /inference="protein" motif:Prosite:PS00324" /note="PS00324 Aspartokinase signature."
misc-feature	123795..124199	/gene="metL" /locus-tag="YE0112" /inference="protein" motif:PFAM:PF03447" /note="Pfam match to entry PF03447 NAD-binding-3, Homoserine dehydrogenase, NAD binding domain, score 167.0, E-value 2.1e-47"
misc-feature	124203..124793	/gene="metL" /locus-tag="YE0112" /inference="protein" motif:PFAM:PF00742" /note="Pfam match to entry PF00742 Homoserine-dh, Homoserine dehydrogenase, score 344.9, E-value 5.8e-101"
misc-feature	124341..124409	/gene="metL" /locus-tag="YE0112" /inference="protein" motif:Prosite:PS01042" /note="PS01042 Homoserine dehydrogenase signature."
gene	complement(124892..1270	/locus-tag="YE0113"

	00)		
CDS	complement(124892..1270	/locus-tag="YE0113"	
	00)		
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		/inference="similar to	
		sequence:UniProtKB:P57414"	
		/note="Similar to several	
		including: Clostridium	
		acetobutylicum predicted permease	
		Cac2003 SWALL:Q97HK8	
		(EMBL:AE007704) (832 aa) fasta	
		scores: E(): 0.072, 24.67 id in	
		535 aa and Buchnera aphidicola	
		OmpA-like protein precursor or	
		bu332 SWALL:OMPA-BUCAI	
		(SWALL:P57414) (349 aa) fasta	
		scores: E(): 6.6, 24.17 38d in 273	
		aa. Note that this CDS lies within	
		a localised low G+C region."	
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		TFTSAYITNDLKDKIYNNGFRLSNENIVNYLKS	
		ADEYALLLTIIATTTTSKVLRDNI	
		INSVDSDISTDGSSSAGMSYSENDELTTWINKH	
		VKPEHKSKVDLLLAPDRHAELKD	
		KVYLSMMLFSGKKTIPFKLKEIILNNTVVVKFN	
		NTSLRLSHSRIDKINNASDKKTAL	
		QMGFLKKIQYICMNGKRLSDLYDFTHDHKNGEK	
		LFIQSNGRIQEKLTSVINKKMPRL	
		KTVEIDNSETVAKELQKILKEKAINLQDNIFTKI	
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		EKFSTKNNFHDLDKGLNSIKTGLVV	
		APDLMISHNAGICLIDHLNNNAPLPQSVFKIAVN	
		ELKKLHEIQGYLRDIKPANMAYDG	
		KQVNFIDVDDRIKAHEITKISAPVFKIYGKEVIY	
		TPKYITQGLVNNIYESNPGNPGKK	
		TLKQTDITHDLQIADEYAFLMTMITATTKDNALK	
		SSIKNAKVDIIGVRIINRIKNEID	
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misc-feature	127404..128246	
gene	128578..129780	/locus-tag="YE0115" /inference="similar to sequence:INSDC:AL139076" /inference="similar to sequence:UniProtKB:Q9Z9E3" /note="Similar in parts to Campylobacter jejuni hypothetical protein Cj0849C SWALL:Q9PP74 (EMBL:AL139076) (719 aa) fasta scores: E(): 0.19, 22.86 38d in 258 aa and to Chlamydia pneumoniae phosphoenolpyruvate-protein phosphotransferase PtsI or Cpn0038 SWALL:PT1-CHLPN (SWALL:Q9Z9E3) (571 aa) fasta scores: E(): 3.5, 19.57 38d in 332 aa" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAL10257.1" /db-xref="GI:122087476" /db-xref="UniProtKB/TrEMBL:A1JI19" /translation="MSRISQSSSPVTTAKLAGKN TLHQEKNTLCANIQKVENVLTNVN REIKAKTNDLNKNNALLTSLTSIASKHGDDANIR LKNDHFKLGQGSNFLKNL INGGRY KLEQQAATSKLVVKGSEVSARTGIAKLTQQIKTI QDSDLSSNKELKNNKTEYDSL NFK LGAVDQQIETFNKA KIAADKADNNNNKALC NNF SM IYQSNAGCKAINAEARHQFGNANQ SAKLNGNQVIAEYVKTHGDNVFSGGNAPVKSAIQ SHCSNLPTLVKDVAKAWYSPTD TT TTSHRGQGMTQD GIDKLMSQFKSDRAGSVYKLGQ FFSTSKEVNVAKAFADRTGDSVKI MFEVKGNSGRGIVVSGGLKFDNNEREVLYSPLAK FAVTDIKGSNAKG YTIKLNEVEQD TKAKLLPY"
CDS	128578..129780	
gene	complement(129861..132500)	/gene="ppc" /locus-tag="YE0116"

CDS	complement(129861..132500)	/note="synonym: glu" /gene="ppc"  /locus-tag="YE0116" /codon-start=1 /transl-table=11 /product="phosphoenolpyruvate carboxylase" /protein-id="CAL10258.1" /db-xref="GI:122087477" /db-xref="GOA:A1JI20" /db-xref="InterPro:IPR001449" /db-xref="InterPro:IPR015813" /db-xref="UniProtKB/Swiss-Prot:A1J I20" /translation="MNEQYSAMRSNVSM LGTLLG DTIKEALGEHILEKVETIRKLSKS SRAGNEASRQELLTTLQNLNDELLPVARAFSQF LNLNTAEQYHSISPHGEAASNPE ALAQLFTRLKDKKLSEQDMRSAVDELSIELVLTA HPTEITRRTLIHKLVEVNTCLS QL DHNDLADYERNKIMRRLRQLVAQSWHTDEIRKIR PSPVDEAKWGFVAVVENS LWEGVPA FLREFNEQLQNSLDYRLPVEAVPIRFTSWMG GDR DGNPNVTAEITRHVLLL SRWKATD LFLRDIQVLVSELSMSECTPELRELAGEEVLEP YRELMKRVRTQLTNTQAYLEARLK GERVLPTDLLVSNDQLWDPLYACYQSLKACGME I IANGQLLDTLRRVRCFGVPLVRI DVRQESTRHTDAIAELTRYLGLGDYESWSEADKQ AFLIRELNSKRPLVPLKWEPSADT QEVLETCRVIAEAPQGSIAAYVISMAKVPSDVL A VHLLLKEAGCPFTLPVAPLFETLD DLNNADDVMTQLLNIDWYRGLIQGKQVMVIGYSD SAKDAGVMAASWAQYRAQDALIKT CEKAGISLTLFHGRGGSIGRGGAPAHAAALLSQPP GSLKGGRLRVTEQGEMIRFKFGLPE VTISLALYASAVLEANLLPPPEPKKEWNEVMDI LSDASCEMYRGYVREN PQFVPYFR AATPELELGKLP LGS RPAKRRPNGGVESLRAIPW IFAWTQNRLMLPAWL GAGAGLQKA IDAGKKEVLATMCRDWPFFSTRIGMLEMVFAKAD LWLAEYYDQRLVDKSLWPLGQQLR DQLEADIKVVLAIANDDHLMADLPWIAESIALRN VYTDPLNVLQAELLHRSRQQENAA DACVEQALMVTIAGVAAGMRNTG"
misc-feature	complement(129864..132500)	/gene="ppc"  /locus-tag="YE0116" /inference="protein motif:PFAM:PF00311" /note="Pfam match to entry PF00311 PEPcase, Phosphoenolpyruvate carboxylase, score 763.6, E-value 5.3e-227"
misc-feature	complement(130857..130895)	/gene="ppc"  /locus-tag="YE0116" /inference="protein motif:Prosites:PS00393" /note="PS00393 Phosphoenolpyruvate carboxylase active site 2."

misc-feature complement(132069..1321 /gene="ppc"  
04)  
/locus-tag="YE0116"  
/inference="protein  
motif:Prosite:PS00781"  
/note="PS00781 Phosphoenolpyruvate  
carboxylase active site 1."

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32)  
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CDS complement(132848..1340 /gene="argE"  
32)  
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RDPFTLTEHDNKLYGLGTADMKGFFAFILDAVRD  
IDASTLSKPLYILATADEETTMAG  
ARYFAASTQLRPDFAIIGEPTSLQPVRAHKGHIS  
NAIRITGQSGHSSDPARGVNAIDL  
MHESITELMKLRITTLQERYNNPAFAIPYPTMNF  
HINGGDAANRICACCELHMDIRPL  
PGLTSLSDLDELMTEALAPVSARWPGRLSIDQLHP  
PIPGYECPTDHMMVGVEELLGER  
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EFIDMAFIEPTRELIGQLVDHFCQ QK"

misc-feature complement(133004..1339 /gene="argE"  
99)  
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/inference="protein  
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/note="Pfam match to entry PF01546  
Peptidase-M20,Peptidase family  
M20/M25/M40, score 236.5, E-value  
2.5e-68"

misc-feature complement(133562..1336 /gene="argE"  
75)  
/locus-tag="YE0117"  
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motif:Prosite:PS00759"  
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/ CPG2 / yscS family signature 2."

misc-feature complement(133751..1337 /gene="argE"  
80)  
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/inference="protein  
motif:Prosite:PS00758"  
/note="PS00758 ArgE / dapE / ACY1  
/ CPG2 / yscS family signature 1."

gene	134395..135399	/gene="argC"
		/locus-tag="YE0119"
CDS	134395..135399	/gene="argC"
		/locus-tag="YE0119"
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		/transl-table=11
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		/db-xref="GI:122087479"
		/db-xref="GOA:A1JI22"
		/db-xref="InterPro:IPR000534"
		/db-xref="InterPro:IPR000706"
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		/db-xref="UniProtKB/TrEMBL:A1JI22"
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misc-feature	134395..134844	/gene="argC"
		/locus-tag="YE0119"
		/inference="protein"
		motif:PFAM:PF01118"
		/note="Pfam match to entry PF01118 Semialdehyde-dh, Semialdehyde dehydrogenase, NAD binding domain, score 174.7, E-value 1e-49"
misc-feature	134629..134658	/gene="argC"
		/locus-tag="YE0119"
		/inference="protein"
		motif:Prosite:PS00142"
		/note="PS00142 Neutral zinc metallopeptidases, zinc-binding region signature."
misc-feature	134839..134889	/gene="argC"
		/locus-tag="YE0119"
		/inference="protein"
		motif:Prosite:PS01224"
		/note="PS01224 N-acetyl-gamma-glutamyl-phosphate reductase active site."
misc-feature	134869..135327	/gene="argC"
		/locus-tag="YE0119"
		/inference="protein"
		motif:PFAM:PF02774"
		/note="Pfam match to entry PF02774 Semialdehyde-dhC, Semialdehyde dehydrogenase, dimerisation domain, score 103.9, E-value 2e-28"
gene	135487..136251	/gene="argB"
		/locus-tag="YE0120"
CDS	135487..136251	/gene="argB"

		/locus-tag="YE0120" /codon-start=1 /transl-table=11 /product="acetylglutamate kinase" /protein-id="CAL10261.1" /db-xref="GI:122087480" /db-xref="GOA:A1JI23" /db-xref="InterPro:IPR001048" /db-xref="InterPro:IPR004662" /db-xref="InterPro:IPR011148" /db-xref="UniProtKB/Swiss-Prot:A1JI23" /translation="MVIKLGGVLLDSEEALERLF TALVTYREKHERPLVIMHGGGCLV DDLMKKLALPVVKKNGLRVTPADQIDIITGALAG TANKTLLAWAVKHDINAVGLCLGD GNTVSVTPLDAALGHVGKAEAGSPALVQTLLAAN YMPIISSIGITKDGSLMNVNADQA ATALAATLGADLILLSDVSGILDGKGQRIEMTA QKAEQLIAQGIITDGMVVKVNAAL DAARSLGRPVDIASWRHADQLPALFNGVPIGTRI LA"
misc-feature	135487..136182	/gene="argB" /locus-tag="YE0120" /inference="protein motif:PFAM:PF00696" /note="Pfam match to entry PF00696 aakinase, Amino acid kinase family, score 120.0, E-value 2.8e-33"
gene	136489..137862	/gene="argH"
CDS	136489..137862	/locus-tag="YE0121" /gene="argH" /locus-tag="YE0121" /codon-start=1 /transl-table=11 /product="putative argininosuccinate lyase" /protein-id="CAL10262.1" /db-xref="GI:122087481" /db-xref="GOA:A1JI24" /db-xref="InterPro:IPR000362" /db-xref="InterPro:IPR003031" /db-xref="InterPro:IPR009049" /db-xref="UniProtKB/Swiss-Prot:A1JI24" /translation="MALWGGRFSQAADQRFKQFN DSLRFDYRLAEQDIIGSVAWSKAL VTVGVLTAEQQQLEQALSVLLEEVQADPQAILA SDAEDIHSWVETKLIDKVGDLGKK LHTGRSRNDQVATDLKLWCKFQITELKTAVQQLO QALVITAEANQDAVMPGYTHLQRA QPVTFAHWCLAYAEMLARDESRLQDTLKRLDVSP LGSGALAGTAYAIIDREQLAGWLGF ASATRNSLDSVSDRDHVLELLSDASIGMVHLSRF AEDLIFFNSGEAAFVDLSDRVTS SSLMPQKKNPDALELIRGKCGRVQGALTGMMMTL KGLPLAYNKDMQEDKEGLFDALDT WLDCLHMAALVLDGIQVKRPRCKEAAEQGYANAT ELADYLVAKGVFPFREAHHIVGEAV VEAIRQGKALEALSLSDLQKFSAVIGDDVYPILA LQSCLDKRVAKGGVSPQQVASAIA EAKARLF"

misc-feature	136504..137784	/gene="argH" /locus-tag="YE0121" /inference="protein motif:PFAM:PF00206" /note="Pfam match to entry PF00206 lyase-1, Lyase, score 606.8, E-value 8.1e-180"
misc-feature	137314..137343	/gene="argH" /locus-tag="YE0121" /inference="protein motif:Prosite:PS00163" /note="PS00163 Fumarate lyases signature."
gene	138584..140911	/locus-tag="YE0122"
CDS	138584..140911	/locus-tag="YE0122" /codon-start=1 /transl-table=11 /product="putative TonB dependent receptor protein" /protein-id="CAL10263.1" /db-xref="GI:122087482" /db-xref="GOA:A1JI25" /db-xref="InterPro:IPR000531" /db-xref="InterPro:IPR010949" /db-xref="InterPro:IPR011276" /db-xref="InterPro:IPR012910" /db-xref="UniProtKB/TrEMBL:A1JI25" /translation="MEGTSNAHEGDWVYDELHSV SEISREQLDSRPARHAADILEQTS GVYSSVSQQDPALSVNIRGMQDYGRVNMNIDGMR QNFMSKSGHGQRNGVMYIDPEILNN VVIEKGVTSIGGAGVIGGIATFNTINASNFLEP GKEIGGQIRVLTGDNGTNFIGSAA LALGNEYGDILIAASERNLSDYWPGNKGNMGDIR FGTAAERFNFDLKNKVEYTRYKM RSQTLKLGWNLPAQRLMLSYLQTQINSPNASML TQIVDKADPYRIIKMGWKNSSVSD VLNRNIGLDYSLKPEHIAWLDVAVKVYYVDTDD TNTLCSDAIYCKKFWTQTRLTTRG LQLQNTSFFTYADHHQFHINYGLEWFSRDRSGNS THETILGLTPPGKRTITSTFAQLN YDYDNWLRLEGGLRYDQFRLQGNTWMHSKNFRGN YTRENPCNQKTHEQYIINEGRRC FNWPSKMTWEVDREQQLSPTLAIGIKPGVQWLE FFGNYGKSWRPPAITEVLATGSAH GHSWTLPNPILAAEHKAWGAGMNIQHSNLFIAE DRLVAKLAYFDTRVTDYINLELSK TKPLHSGSGFTNATYINNLLATHFRGLEYQLSYD AGVFYTNLNYTRMIGVNTICSKRA WLGGVNGIASNKNYEIYSIDRDDINNIVDCFAAN NLFSSAYLPGDRGSLTLGGRIFD KKLDLGTVIRYNKGRQDKSVLNNKGHVNTAYVAD WPKYTIFDLIASYKMTNNLTLRSS IENITNRAYLISYGDSLSPAPNRGRTIQGGFEYK F"
misc-feature	140567..140908	/locus-tag="YE0122" /inference="protein motif:PFAM:PF00593" /note="Pfam match to entry PF00593 TonB-boxC, TonB dependent receptor C-terminal region, score 31.5, E-value 1.3e-06"

gene	141014..141649	/locus-tag="YE0123"
CDS	141014..141649	/locus-tag="YE0123"
		/codon-start=1
		/transl-table=11
		/product="hemophore HasA"
		/protein-id="CAL10264.1"
		/db-xref="GI:122087483"
		/db-xref="InterPro:IPR010495"
		/db-xref="UniProtKB/TrEMBL:A1JI26"
		/translation="MLLTIRKFIMTVTIKYQGQF SNDTLTSYTKQWATTHGDIKDTEA EGYSKDFGQFAGGGWFDGTQYSIGSSSHSGSSTGM IIEGDLTYNFAQHTLHGKVDSLEL GKNLSINSNGIGKQLDQLQLKMSDLDTGEFDPG KTMAENHQGDMHKSIYGLMRGNAD PLLEVLTAKGIDVNTPLKDMAIASQFEAMVSDMP MIDTVGVVESDMLLAA"
misc-feature	141404..141427	/locus-tag="YE0123"
		/inference="protein"
		motif:Prosite:PS00017"
		/note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	141797..142450	/locus-tag="YE0124"
CDS	141797..142450	/locus-tag="YE0124"
		/inference="similar to sequence:INSDC:AJ414159"
		/note="Similar to Yersinia pestis hemophore HasA or Ypo3922 SWALL:Q8ZA90 (EMBL:AJ414159) (205 aa) fasta scores: E(): 1.5e-05, 28.05 38d in 221 aa. Note the product of this CDS is also significantly similar to the CDS directly upstream and downstream, YE0123, YE0125 and YE0126."
		/codon-start=1
		/transl-table=11
		/product="probable hemophore"
		/protein-id="CAL10265.1"
		/db-xref="GI:122087484"
		/db-xref="InterPro:IPR010495"
		/db-xref="UniProtKB/TrEMBL:A1JI27"
		/translation="MTITIKYHEKIANETITSYS QQWATNFGNMLWTMGVDYTLNASG YPIPPADSIKYVAASTHNSQESNAIIVIALKKV AGIENDQSITDLRVSLEFGEALVP IANDGTSKHPHQLLLQQVQLDISGLDIRADVESS MPTLDYALWQDIYYQGGQNLGIYN LLKGNANPLLDILKAQGIDVNTVPKDMTIASQFE VPTDELLIETVGITDGGNTLLAA"
gene	142509..143150	/locus-tag="YE0125"
CDS	142509..143150	/locus-tag="YE0125"
		/inference="similar to sequence:INSDC:AJ414159"
		/inference="similar to sequence:UniProtKB:Q54450"
		/note="Similar to Yersinia pestis hemophore HasA or Ypo3922 SWALL:Q8ZA90 (EMBL:AJ414159) (205 aa) fasta scores: E(): 1.8e-08, 33.48 38d in 218 aa and Serratia marcescens hemophore HasA"

		SWALL:HASA-SERMA (SWALL:Q54450)
		(188 aa) fasta scores: E(): 0.051,
		23.38 38d in 201 aa. Note the
		product of this CDS is also
		significantly similar to the CDS
		directly upstream and downstream,
		YE0123, YE0124 and YE0126."
		/codon-start=1
		/transl-table=11
		/product="probable hemophore"
		/protein-id="CAL10266.1"
		/db-xref="GI:122087485"
		/db-xref="InterPro:IPR010495"
		/db-xref="UniProtKB/TrEMBL:A1JI28"
		/translation="MTITIKYHSQFAEYSVSSYI
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		NRIDANNNESVQAEFQSFYESNVAMIVGGSRL
		EQGSTSFIMKKQIQTLFEGESLIS
		NADNTGKQLQQLQLKLDGLNIEDDFYPSLCSISQ
		ALDAEPGKPYQGGIDHGTYNLLRG
		KAAPMLEILKAQGINLDSPLKDIAIASQFGVVD
		TPIIDTVGAADNSGILLAA"
gene	143211..143819	/locus-tag="YE0126"
CDS	143211..143819	/locus-tag="YE0126"
		/inference="similar to
		sequence:INSDC:AJ414159"
		/note="Similar to Yersinia pestis
		hemophore HasA or Ypo3922
		SWALL:Q8ZA90 (EMBL:AJ414159) (205
		aa) fasta scores: E(): 2.1e-13,
		28.23 38d in 209 aa. Note the
		product of this CDS is also
		significantly similar to the CDS
		directly upstream, YE0123, YE0124
		and YE0125."
		/codon-start=1
		/transl-table=11
		/product="probable hemophore"
		/protein-id="CAL10267.1"
		/db-xref="GI:122087486"
		/db-xref="InterPro:IPR010495"
		/db-xref="UniProtKB/TrEMBL:A1JI29"
		/translation="MTVTIIFNGNIKDETIYSY
		HKWIADFNIPTVDGYNFTEFHSIK
		DTISRQYEQFSVTNTSGDKATIIMSGEISFKMCH
		RTIHGKVESLELGKEGVIQNEKNN
		IILEKHLVEPQLIFNGLSIIGDYDNLKITGENQR
		NDVHQMGFNLKAGNADVLLLEILIS
		QGIDVNTPLKDMPIASQFEVVANMPIIEVVGEAN
		GGGILLAA"
gene	144005..145786	/locus-tag="YE0127"
CDS	144005..145786	/locus-tag="YE0127"
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		/transl-table=11
		/product="ABC transporter protein"
		/protein-id="CAL10268.1"
		/db-xref="GI:122087487"
		/db-xref="GOA:A1JI30"
		/db-xref="InterPro:IPR003439"
		/db-xref="InterPro:IPR003593"
		/db-xref="InterPro:IPR010128"
		/db-xref="InterPro:IPR011527"



		/db-xref="UniProtKB/TrEMBL:A1JI30" /translation="MESSQNASASLVSP TLISTL GRHKKILWGIGLFTAVINLLMLAP AIYMLQVYDRVLASANTMTLLMLTVLVLAIFAFI GLEWVRS AIVIRLGTRIDMQLNQ QVFNAAFASNLNGQKVQAAQALNDLTTLRQFATG NALFAFFDAPWFPFYLLVIFILHP WLGALAALGAVFLIFLAWLNHWICRKLKEASHI TSQATQQANANLRNADAIQAMGML KALRDRWLKQHSFLYQQNIASDKSSRV TALS KS SRQALQSMMLGLGALLVIDGAITA GVM IAGSILVGRVLGPIDQLIAVWKQWSHTRLAY QRLSSLLAQHSQPTTGMVLP PPKG KLSVTQLTVCKPGTHIPVLQSINFELQPGGVLGV LGPSGSGKSTLAKLLVASQPAFSG SVRLDSADLARWDKSHLGEFIGYLPQDIQLFRGS IAENIARFGLIDHAKVIAAAQLAD VHD LILHLPQGYDTSLGDEGEGLSGGQRQRIALA RAMYGVPRLIVLDEPNASLDKVGE QALLASISQLKQQGCTIVMVTHKPELLSGSDYLL FLQNGQIELFDRTQTILQDGQGN KATTGRNSWGSMSYGVAPIRTASQKS" /locus-tag="YE0127"
misc-feature	join(144080..144148, 144191..144259, 144410..144478, 144488..144556, 144794..144862)	/inference="protein motif:TMHMM:2.0" /note="5 probable transmembrane helices predicted for YE0127 by TMHMM2.0 at aa 26-48, 63-85, 136-158, 162-184 and 264-286" /locus-tag="YE0127"
misc-feature	144083..144883	/inference="protein motif:PFAM:PF00664" /note="Pfam match to entry PF00664 ABC-membrane, ABC transporter transmembrane region, score 19.6, E-value 4.6e-05" /locus-tag="YE0127"
misc-feature	145091..145645	/inference="protein motif:PFAM:PF00005" /note="Pfam match to entry PF00005 ABC-tran, ABC transporter, score 204.6, E-value 1e-58" /locus-tag="YE0127"
misc-feature	145112..145135	/inference="protein motif:Prosites:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)." /locus-tag="YE0127"
misc-feature	145421..145465	/inference="protein motif:Prosites:PS00211" /note="PS00211 ABC transporters family signature." /locus-tag="YE0128"
gene	145917..147149	/locus-tag="YE0128"
CDS	145917..147149	/locus-tag="YE0128" /codon-start=1 /transl-table=11 /product="HlyD family secretion protein"

		/protein-id="CAL10269.1" /db-xref="GI:122087488" /db-xref="GOA:A1JI31" /db-xref="InterPro:IPR003997" /db-xref="InterPro:IPR006143" /db-xref="InterPro:IPR010129" /db-xref="UniProtKB/TrEMBL:A1JI31" /translation="MVCGGFIGSLLWAGLAPLDK GIAVMGHIVVAENRKLVPLOQGR IQQLHVAEGDDVTQGQLLITLDDTALLSHRDNLQ NQYLSALAQESRLTAEQHELPTIT FPPALLQHPAQALVERN TVLQQQLFLHRRQAQLS DIARLSAQITRHE SRLDGLQVARG HNQRQFDLFQRQLQGVQLLAKNGHVAQSQLEME RQAISLRANIEKNTSEILELHKQI GETEQHILQRREQYKSENREQLAKAQQSTQELEQ RLGIAEYELDNTRIYAPVSGTVIA LTQHTVGGVVSTGQTLMELVPNGQPLLAEALPVP SLIDKVMVGLPVDLNFSAFNQSST PRLQGSVLHVGADRIQNSHTLEPYPLTVAIDIT QTELEIRPGMSVDIFIRTGERSLL NYL FKPLTDRLHVAF AEE" /locus-tag="YE0128" /inference="protein motif:PFAM:PF00529" /note="Pfam match to entry PF00529 HlyD, HlyD family secretion protein, score 152.6, E-value 4.5e-43"
misc-feature	146013..146948	
gene	147226..148026	/locus-tag="YE0129"
CDS	147226..148026	/locus-tag="YE0129" /codon-start=1 /transl-table=11 /product="putative membrane protein" /protein-id="CAL10270.1" /db-xref="GI:122087489" /db-xref="GOA:A1JI32" /db-xref="InterPro:IPR006260" /db-xref="UniProtKB/TrEMBL:A1JI32" /translation="MIFFWVSALLTSGVHIYLIW LLSNTPIPPAYTEVSPVAIMLAVS TEPEFTQHMEQDSVVGITQ NINEPVTELSEHQPE EVSHILTAP EHSNAALIVEREVNE PPKELNKAKRPQQKVMTPRQPINERTPENHSNPS TPAVVTSTPLSGESH RVAAAANSH SLHNQQSKMNWKSRLQGHLAGFKRYPPHARKQRQ QGTVIIRFVVNKEGDV LSTKL VKS SGVIALDQEALAVVKRAQPLPQPPVGLLSNEQVS LTMPVDFDLKNIRR" /note="label:IS1330; IS1330"
repeat-region	complement(148088..1493 91)	
gene	complement(148114..1493 07)	/gene="tpn1330"
CDS	complement(148114..1493 07)	/locus-tag="YE0130" /gene="tpn1330" /locus-tag="YE0130" /inference="similar to sequence:INSDC:AJ344215" /inference="similar to sequence:INSDC:S67119"

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/feature "misc-feature" complement(148318..149037)
    /note="Previously sequenced as Yersinia enterocolitica IS10-like
transposase for IS1330 element SWALL:Q8RSF5 (EMBL:AJ344215) (397
aa) fasta scores: E(): 2.6e-162,99.24 38d in 397 aa. Also
similar to Escherichia coli, and Salmonella typhi IS 10 transposase
SWALL:Q53371 (EMBL:S67119) (402 aa) fasta scores: E(): 2e-43,
35.27 38d in 394 aa"
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    /db-xref="GOA:A1JI33"
    /db-xref="InterPro:IPR002559"
    /db-xref="UniProtKB/TrEMBL:A1JI33"
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YRQSALMDATVALINGASLTLTSTI
GRFLPGQAQVKNKIKRVDRLLGNESLHRDIPLIF
NNIIAMLTRKLSLCVVAVDWSGYH
SHEYHILRASLICDGRSIPLLSQIVPSAEQQSEQ
IHKTFNLNALARAVNP DARV IIVTD
AGFQNAWFKHIKSLGWDFVGRIRGYTRLRLHREG
DIWYKPQELQARSQPEYLGPGTSL
RTQYARCEGHFYLYKKAPKGRKNRRSRGRIKRYK
QERDGRSSAKTPWLLFTSSDDFRP
REVIKIYSRRMQIEQNFRDEKSERFGFGLRASRS
RTTERMQVLSLLATLSTIVMWLMG
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    /gene="tpn1330"

/feature "gene" complement(149422..150870)
    /locus-tag="YE0130"
    /inference="protein"
    motif:PFAM:PF01609"
    /note="Pfam match to entry PF01609
Transposase-11,Transposase DDE
domain, score 52.8, E-value
4.8e-13"

/feature "CDS" complement(149422..150870)
    /locus-tag="YE0131"
    /codon-start=1
    /transl-table=11
    /product="putative pyridine
nucleotide-disulphide
oxidoreductase"
    /protein-id="CAL10272.1"
    /db-xref="GI:122087491"
    /db-xref="GOA:A1JI34"
    /db-xref="InterPro:IPR000815"
    /db-xref="InterPro:IPR001100"
    /db-xref="InterPro:IPR001327"
    /db-xref="InterPro:IPR004099"
    /db-xref="InterPro:IPR013027"
    /db-xref="UniProtKB/TrEMBL:A1JI34"
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YRAAKLATPNVVMIEGGEYGTTC"

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misc-feature	complement(149494..149826)	/locus-tag="YE0131"  /inference="protein motif:PFAM:PF02852" /note="Pfam match to entry PF02852 pyr-redox-dim, Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain, score 48.8, E-value 7.9e-12"
misc-feature	complement(149908..150852)	/locus-tag="YE0131"  /inference="protein motif:PFAM:PF00070" /note="Pfam match to entry PF00070 pyr-redox, Pyridine nucleotide-disulphide oxidoreductase, score 150.3, E-value 2.2e-42"
gene	complement(151070..151801)	/locus-tag="YE0132"
CDS	complement(151070..151801)	/locus-tag="YE0132"  /codon-start=1 /transl-table=11 /product="putative peroxiredoxin/glutaredoxin family protein" /protein-id="CAL10273.1" /db-xref="GI:122087492" /db-xref="GOA:A1JI35" /db-xref="InterPro:IPR002109" /db-xref="InterPro:IPR011767" /db-xref="InterPro:IPR011906" /db-xref="InterPro:IPR012335" /db-xref="InterPro:IPR013740" /db-xref="InterPro:IPR014025" /db-xref="UniProtKB/TrEMBL:A1JI35" /translation="MFTSQEGKKVPQVTFHTRQG DQWVDVTTDELFNKTKVIVFSLPG AFTPTCSSSHLPRYNELAGVFKQHGVDLSILCVSV NDTFVMNAWKADQHAENITFIPDG NGEFTKGMDMLVEKADLGFGPRSWRYSMLVRNGV VEKMFVEPNKPGDPFEVSDADTML KYLAPDFKVVQESVSVFTKPGCPFCAKAKQMLQDR GIQYEEIVLGKDATTVSLRAVTGR GTVPQVFIGGRHIGGSDDLENYLSA"

misc-feature	complement(151118..151288)	/locus-tag="YE0132" /inference="protein motif:PFAM:PF00462" /note="Pfam match to entry PF00462 glutaredoxin,Glutaredoxin, score 42.7, E-value 5.5e-10"
misc-feature	complement(151229..151279)	/locus-tag="YE0132" /inference="protein motif:Prosite:PS00195" /note="PS00195 Glutaredoxin active site."
misc-feature	complement(151319..151786)	/locus-tag="YE0132" /inference="protein motif:PFAM:PF00578" /note="Pfam match to entry PF00578 AhpC-TSA, AhpC/TSA family, score 159.1, E-value 4.8e-45"
gene	151949..152881	/gene="oxyR"
CDS	151949..152881	/locus-tag="YE0133" /gene="oxyR" /locus-tag="YE0133" /codon-start=1 /transl-table=11 /product="oxidative stress transcriptional regulatory protein" /protein-id="CAL10274.1" /db-xref="GI:122087493" /db-xref="GOA:A1JI36" /db-xref="InterPro:IPR000847" /db-xref="InterPro:IPR005119" /db-xref="InterPro:IPR011991" /db-xref="UniProtKB/TrEMBL:A1JI36" /translation="MNIRDLEYLVALAEFRHFRR AADSCHVSQPTLSGQIRKLEDELG VMLLERTSRKVLFTQAGLLLVEQARTVLRVVKVL KEMASLQGESMSGPLHIGLIPTVG PYLLPQIIIPMLHQTFPKLEMYLHEAQTQNLLAQL DSGKLDCAILALVKETEAFIEVPL FDEPMQLAIYADHPWADRDKVQMHELAGEKLLML EDGHCLRDQAMGFCFQAGADEDTH FRATSLETLRNMVAAGSGITLLPSLAVPNERKRD GVCYLECYKPVPKRTIALVYRPGS PLRGRYEQLAEAIREHMQPRMNSDVINQKLEQAV "
misc-feature	151955..152134	/gene="oxyR" /locus-tag="YE0133" /inference="protein motif:PFAM:PF00126" /note="Pfam match to entry PF00126 HTH-1, Bacterial regulatory helix-turn-helix protein, lysR family, score 97.2, E-value 2.1e-26"
misc-feature	151994..152059	/gene="oxyR" /locus-tag="YE0133" /note="Predicted helix-turn-helix motif with score 1674.000, SD 4.89 at aa 16-37, sequence"

misc-feature	151997..152089	RHFERRAADSCHVSQPTLSGQIR" /gene="oxyR" /locus-tag="YE0133" /inference="protein motif:Prosite:PS00044" /note="PS00044 Bacterial regulatory proteins, lysR family signature."
misc-feature	152204..152830	/gene="oxyR" /locus-tag="YE0133" /inference="protein motif:PFAM:PF03466" /note="Pfam match to entry PF03466 LysR-substrate, LysR substrate binding domain, score 202.6, E-value 3.9e-58"
gene	complement(152864..154264)	/gene="sthA"  /locus-tag="YE0134" /note="synonyms: sth, udhA"
CDS	complement(152864..154264)	/gene="sthA"  /locus-tag="YE0134" /codon-start=1 /transl-table=11 /product="soluble pyridine nucleotide transhydrogenase" /protein-id="CAL10275.1" /db-xref="GI:122087494" /db-xref="GOA:A1JI37" /db-xref="InterPro:IPR000815" /db-xref="InterPro:IPR001100" /db-xref="InterPro:IPR001327" /db-xref="InterPro:IPR004099" /db-xref="InterPro:IPR013027" /db-xref="UniProtKB/Swiss-Prot:A1J I37" /translation="MQQHFHFDAIVIGSGPGGEG AAMGLVKQGARVAVIERYNVGGG CTHWGTIPSKALRHAVSRIIEFNQNPLYSDNART ISSSFSDILNHADRVINQQTRMRQ GFYDRNHCQMFSGDASFIDANTINVRADGTNDT LRADNIVIATGSRPYRPANVDFTH ERIYDSDTILQLSHEPQHVI IYGAGVIGCEYASI FRGLSVKVDLINTRDLLAFLDQE MSDALSYHFWNNGVVIRHNEEFEQIEGTVDGVIV HLKSGKKVKADCLLYANGRTGNTS GLGLEKIGLEADSRGLLKVNSMYQTALSHVYAVG DVIGYPSLASAAYDQGRIAAQAMI KGEANTHLIEDIPTGIYTIPEISSVGKTEQDLTA MKVPYEVGRAQFKHLARAQIVGMD TGSLKILFHRETKQILGIHCFGERAAEIIHIGQA IMEQKGEGNTIEYFVNTTFNYPTM AEAYRVAALNGLNRLF"
misc-feature	complement(152891..153229)	/gene="sthA"  /locus-tag="YE0134" /inference="protein motif:PFAM:PF02852" /note="Pfam match to entry PF02852 pyr-redox-dim, Pyridine nucleotide-disulphide

		oxidoreductase, dimerisation domain, score 134.6, E-value 1.2e-37"
misc-feature	complement(153302..154243)	/gene="sthA"  /locus-tag="YE0134" /inference="protein motif:PFAM:PF00070" /note="Pfam match to entry PF00070 pyr-redox, Pyridine nucleotide-disulphide oxidoreductase, score 251.7, E-value 6.7e-73"
misc-feature	complement(153698..153730)	/gene="sthA"  /locus-tag="YE0134" /inference="protein motif:Prosite:PS00013" /note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site."
gene	154470..155114	/locus-tag="YE0135"
CDS	154470..155114	/locus-tag="YE0135" /codon-start=1 /transl-table=11 /product="TetR-family transcriptional regulatory protein" /protein-id="CAL10276.1" /db-xref="GI:122087495" /db-xref="GOA:A1JI38" /db-xref="InterPro:IPR001647" /db-xref="InterPro:IPR012287" /db-xref="UniProtKB/Swiss-Prot:A1J I38" /translation="MGTIMGVRAQQKERTRRSLI EAAFSQLSAERSFASLSLREVSRE AGIAPTSFYRHFRDDELGLTMVDESGLMLRQLM RQARQRIAKGGSVIRTSVSTFMEF IGNNPNAFRLLLLRERSGTSAAAFRAAVAREIQHFI AELADYLELENHMPRSFTQAQAEA MVTIVFSAGAEVLDVDAEQRRQLEERLVLQLRMI SKGAYYWYRREQEKLAVSRA"
misc-feature	154524..154667	/locus-tag="YE0135" /inference="protein motif:PFAM:PF00440" /note="Pfam match to entry PF00440 tetR, Bacterial regulatory proteins, tetR family, score 46.6, E-value 3.7e-11"
misc-feature	154575..154640	/locus-tag="YE0135" /note="Predicted helix-turn-helix motif with score 1615.000, SD 4.69 at aa 36-57, sequence LSLREVSREAGIAPTSFYRHFR"
gene	155245..155607	/gene="yijD"
CDS	155245..155607	/locus-tag="YE0136" /gene="yijD" /locus-tag="YE0136" /codon-start=1 /transl-table=11 /product="putative membrane

		protein"
		/protein-id="CAL10277.1"
		/db-xref="GI:122087496"
		/db-xref="InterPro:IPR009867"
		/db-xref="UniProtKB/TrEMBL:A1JI39"
		/translation="MITGLAINGSFNALFSGFVP
		FSVFPLLTLLAVYCLHQRYLNFA
		MPQGLPVLGACFLLGILLYSAIVRVEHPAIGSN
		FVPSILSVVLVFWILFKLKARKSA
		QTDINADTDTDIDNQPPQ"
misc-feature	join(155287..155355, 155389..155448, 155458..155526)	/gene="yijD"
		/locus-tag="YE0136"
		/inference="protein"
		motif:TMHMM:2.0"
		/note="3 probable transmembrane helices predicted for YE0136 by TMHMM2.0 at aa 15-37, 49-68 and 72-94"
misc-feature	155380..155412	/gene="yijD"
		/locus-tag="YE0136"
		/inference="protein"
		motif:Prosite:PS00013"
		/note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site."
gene	complement(155840..1569 43)	/gene="trmA"
CDS	complement(155840..1569 43)	/locus-tag="YE0138"
		/gene="trmA"
		/locus-tag="YE0138"
		/codon-start=1
		/transl-table=11
		/product="tRNA
		(uracil-5)-methyltransferase"
		/protein-id="CAL10278.1"
		/db-xref="GI:122087497"
		/db-xref="GOA:A1JI40"
		/db-xref="InterPro:IPR010280"
		/db-xref="InterPro:IPR011869"
		/db-xref="UniProtKB/TrEMBL:A1JI40"
		/translation="MTPDILPTDGYEHLAEKSA
		RLQAMMSPFQAPAAEIFRSPAHEY
		RMRAEFRVWHEDDLYHIMFDQQTKLRIRVEQFP
		VASLLINRLMSALMTAIRAEPILR
		HKLFQIDYLSLSTLGGKLLATLLYHRPLDEEWQQKA
		RELRLQLREQGFDLQLIGRASKTK
		IMLDHDYIDEVLPVAGRDMIYRQVENSFTQPNA
		VNIHMLEWAIDVTQHASGDLLLEY
		CGNGNFSALARNFDRVLATEIAKPSVAAAQYNI
		AANHIDNVQIIRMSAEFTQAMQG
		VREFNRLKGIDLTSYNCETIFVDPPRSGLDDET
		KLQYAYPRILYISCNPETLCANLE
		QLQYTHKISRLALFDQFPYTHHMECGVLLEKRD"
misc-feature	complement(155870..1559 02)	/gene="trmA"
		/locus-tag="YE0138"
		/inference="protein"
		motif:Prosite:PS01231"
		/note="PS01231 RNA



		methyltransferase trmA family signature 2." /gene="trmA" /locus-tag="YE0138" /inference="protein" motif:Prosite:PS01230" /note="PS01230 RNA methyltransferase trmA family signature 1."
misc-feature	complement(155960..156049)	
misc-RNA	157085..157301	/note="Cobalamin riboswitch (RF00174) as predicted by Rfam, score 104.18, positions 1 to 190"
gene	157369..159267	/gene="btuB" /locus-tag="YE0139"
CDS	157369..159267	/gene="btuB" /locus-tag="YE0139" /inference="similar to sequence:INSDC:AJ414159" /inference="similar to sequence:UniProtKB:P06129" /note="Similar to Escherichia coli vitamin B12 receptor precursor Btub or Bfe or Cer or DcrC or B3966 SWALL:BTUB-ECOLI (SWALL:P06129) (614 aa) fasta scores: E(): 2.3e-123, 52.7 38d in 628 aa, and to Yersinia pestis putative vitamin B12 receptor protein Ypo3910 SWALL:Q8ZAA1 (EMBL:AJ414159) (625 aa) fasta scores: E(): 5.4e-144, 58.45 38d in 633 aa" /codon-start=1 /transl-table=11 /product="exported vitamin B12 receptor protein" /protein-id="CAL10279.1" /db-xref="GI:122087498" /db-xref="GOA:A1JI41" /db-xref="InterPro:IPR000531" /db-xref="InterPro:IPR010101" /db-xref="InterPro:IPR010917" /db-xref="InterPro:IPR012910" /db-xref="UniProtKB/TrEMBL:A1JI41" /translation="MTTKNTITIKKYTLTALSV TAFSGWAQGNATATGNKDEMVTAS RFKQPVSTVLAPADVVTTRDDIDRWQAKSLNEVMR RLPGV DIAQFGGVGQGSSMYIRGT EARHVLILIDGIPLARTGIVNSVNLDQIPISLVQ RVEYIRGPRSAVYGSGAIGGVINV ITQTDQEGAQINAGIGSKGYQQYDGSVRQRFGDT LATLAGGYQTSNGYNIKPDSPNPI DNDRDGF RNKNFWAGLEHQFSQEISGFIRGYGYT NNSDYDIGSLSSPAYSGDEERLYN HTYDAGLRYASGAYSSQLIGSYQKYKDYNFSSQY GRYGVATTLDNMDQRNVQWGNNTYS FESGTL SAGLDWQQQRLTSSSQTI SDTYKRDNTG LYLSGQQKIGNVTLEASGRGDKDE QFGWHETWQTAAGWEFVPDYRVTL SYGTGFLAPS LGQQYGSQRFDIISNSDLKPEESR QWEAGLEGVTGPLDWRLSAYHNKIENLIDYSFDN

		SIFKGHYYNVNSATIKGVEWTGNL TTGIFTHGVTLQYIDPRNDLNNEVLARRSKQQA YQLDWTMFNLDIDISYQYYGKRYD NSTSAYSSTQRELSSYSTVDVSAGYPVTSHLT VRGRIANLFDKEYETAYGYKTAGREY YLTGSYNF"
misc-feature	158959..159264	/gene="btuB" /locus-tag="YE0139" /inference="protein" motif:PFAM:PF00593" /note="Pfam match to entry PF00593 TonB-boxC, TonB dependent receptor C-terminal region, score 71.2, E-value 1.4e-18"
misc-feature	159211..159264	/gene="btuB" /locus-tag="YE0139" /inference="protein" motif:Prosites:PS01156" /note="PS01156 TonB-dependent receptor proteins signature 2."
gene	159212..160075	/gene="murI" /locus-tag="YE0140" /note="synonyms: dga, glr"
CDS	159212..160075	/gene="murI" /locus-tag="YE0140" /codon-start=1 /transl-table=11 /product="putative glutamate racemase" /protein-id="CAL10280.1" /db-xref="GI:122087499" /db-xref="GOA:A1JI42" /db-xref="InterPro:IPR001920" /db-xref="InterPro:IPR004391" /db-xref="InterPro:IPR015942" /db-xref="UniProtKB/Swiss-Prot:A1J I42" /translation="MAIKPLDESITSREAITSKA DTAPRPTALIFDSGVGGLSVYQEI RQLLPDLHYIYAFDNVAFPYGEKSGEFIVERVLE IVTAVQQRHPLAIVVIACNTASTV SLPALRERFTFPVVGVPVPAIKPAVRLTRNGVVGL LATRGTVHASYTQDLIERFATDCK IELLGSSSELVELAETKLHGGVVPKEALKKILHPW LAMREPPDTIVLGCTHFPLLTEEL AQVLPEGTRMVDSGAAIARRTAWLISSQENVISS DEENIAYCMALNADTDALLPVLQG YGFPSLEKLPI"
misc-feature	159293..159943	/gene="murI" /locus-tag="YE0140" /inference="protein" motif:PFAM:PF01177" /note="Pfam match to entry PF01177 Asp-Glu-race, Asp/Glu/Hydontoin racemase, score 337.7, E-value 8.3e-99"
misc-feature	159488..159514	/gene="murI" /locus-tag="YE0140" /inference="protein" motif:Prosites:PS00923" /note="PS00923 Aspartate and glutamate racemases signature 1."
misc-feature	159821..159853	/gene="murI"

		/locus-tag="YE0140"
		/inference="protein"
		motif:Prosite:PS00924"
		/note="PS00924 Aspartate and glutamate racemases signature 2."
gene	160552..162040	/gene="16S rRNA"
rRNA	160552..162040	/gene="16S rRNA"
		/product="16S ribosomal RNA"
		/note="match to 16S-rRNA 1..1461 (Y.enterocolitica 16S)"
gene	162169..162245	/gene="tRNA-Ile (GAT)"
tRNA	162169..162245	/gene="tRNA-Ile (GAT)"
		/product="tRNA-Ile"
		/note="codon recognized: AUC"
gene	162320..162395	/gene="tRNA-Ala (TGC)"
tRNA	162320..162395	/gene="tRNA-Ala (TGC)"
		/product="tRNA-Ala"
		/note="codon recognized: GCA"
gene	162741..165734	/gene="23S rRNA"
rRNA	162741..165734	/gene="23S rRNA"
		/product="23S ribosomal RNA"
		/note="match to 23S-rRNA 1..2994 (Y. enterocolitica 23S EMBL:U77925, Y.pestis KIM 98 38dentity, Citrobacter freundii 23S EMBL:U77928 94 38dentity)"
gene	165734..165970	/gene="5S rRNA"
rRNA	165734..165970	/gene="5S rRNA"
		/product="5S ribosomal RNA"
		/note="match to 5SrRNA 1..240 Y.enterocolitica"
gene	166090..166166	/gene="tRNA-Asp (GTC)"
tRNA	166090..166166	/gene="tRNA-Asp (GTC)"
		/product="tRNA-Asp"
		/note="codon recognized: GAC"
gene	166220..166295	/gene="tRNA-Trp (CCA)"
tRNA	166220..166295	/gene="tRNA-Trp (CCA)"
		/product="tRNA-Trp"
		/note="codon recognized: UGG"
gene	166814..167770	/locus-tag="YE0141"
CDS	166814..167770	/locus-tag="YE0141"
		/codon-start=1
		/transl-table=11
		/product="putative periplasmic protein precursor"
		/protein-id="CAL10281.1"
		/db-xref="GI:122087500"
		/db-xref="InterPro:IPR001761"
		/db-xref="UniProtKB/TrEMBL:A1JI43"
		/translation="MYRRLLLA AVTAAMCSAVQ AAPLVVGF SQIGSESGWRS AETKV SKQEA EKR GITLKIADAQQQENQIKAVRSFIAQ GVDAIF IAPVVATG WTPVLQEAKE AKIPVFL LDRMIEVNDPSLYTA AVASDSVYEGKV AGEWLLK DVAGKPCNVVELQGT VG SSVAINR KKG FADGIASAPNVK IIRSQSGDFTRS KGKEVMES FIKAEQNGKNICAVYA HNDDMAIGAIQAIKEAGLKPGSEIKIVSIDGV PDI FKAMSSGEANATVELTPNMAGPA FDI ALI ALKKDGTQPPKFIQTESRLLQPD TAKQEY ESKKSLGY"
sig-peptide	166814..166876	/locus-tag="YE0141"

		/note="Signal peptide predicted for YE0141 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.998 between residues 21 and 22" /locus-tag="YE0141" /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted for YE0141 by TMHMM2.0 at aa 5-27"
misc-feature	166826..166894	
misc-feature	166880..167743	/locus-tag="YE0141" /inference="protein motif:PFAM:PF00532" /note="Pfam match to entry PF00532 Peripla-BP-like,Periplasmic binding proteins and sugar binding domain of the LacI family, score 2.7, E-value 1e-05"
gene	167855..169345	/locus-tag="YE0142"
CDS	167855..169345	/locus-tag="YE0142" /codon-start=1 /transl-table=11 /product="putative sugar transport system ATP-binding protein" /protein-id="CAL10282.1" /db-xref="GI:122087501" /db-xref="GOA:A1JI44" /db-xref="InterPro:IPR003439" /db-xref="InterPro:IPR003593" /db-xref="UniProtKB/TrEMBL:A1JI44" /translation="METLLEVRGLSVEFPGVKAL DSVDFSLQRGEVVALLGENGAGKS TLIKALTGVYKRAAGEVYLDVAICPIDTADAQK MGIGTVYQEVNLLPNISIAANLFI GREPLRWGLIDHRAMNQATKLLKGYGLELDVQR PLADFSIAIQQIVAIARAVDLSAK VLILDEPTASLDAKEVSMLLDILRQLRDQGIGMV FVTHFLDQVYRISDRITVLRNGKL VGTKNTTELPRIELVQMMLGHSFDEQLLKRGEHN IAVSNPLVEFKNYSRRGVVENFDL SVSPGEIVGLAGLLGSGRTETAQLIFGVTTPTDTG EAKIQGKPKVIRTTPRKASRYGFGY CPEDRKTDGIVGAATVRENIILALQAQRGWLRLPI SIREQTQIAEDFIQQLGIRTPGPE QQIQYLSGGNQKQVLLARWLATKPRFLILDEPTR GIDVGAAHEIIRLIEKLCNEGLAL LIISSELEELAGYADRVIVLRDRRHIAQLGHDEI SVPAIMQAIQVQ"
misc-feature	167942..168502	/locus-tag="YE0142" /inference="protein motif:PFAM:PF00005" /note="Pfam match to entry PF00005 ABC-tran, ABC transporter, score 196.8, E-value 2.1e-56"
misc-feature	167963..167986	/locus-tag="YE0142" /inference="protein motif:Prosites:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)." /locus-tag="YE0142" /inference="protein
misc-feature	168695..169273	

		motif:PFAM:PF00005"
		/note="Pfam match to entry PF00005
		ABC-tran, ABC transporter, score
		101.9, E-value 8.2e-28"
misc-feature	169046..169090	/locus-tag="YE0142"
		/inference="protein
		motif:Prosite:PS00211"
		/note="PS00211 ABC transporters
		family signature."
gene	169357..170376	/locus-tag="YE0143"
CDS	169357..170376	/locus-tag="YE0143"
		/codon-start=1
		/transl-table=11
		/product="putative sugar transport
		system permease"
		/protein-id="CAL10283.1"
		/db-xref="GI:122087502"
		/db-xref="GOA:A1JI45"
		/db-xref="InterPro:IPR001851"
		/db-xref="UniProtKB/TrEMBL:A1JI45"
		/translation="MGNRSLSMPQRPRKVKWVLP
		KGATQFGALIVILLIDSLVAPHFF
		SIHIQDGRFLFGSVIDILNRGAPVALLALGMTLVI
		ATGGIDLSVGAVMAIAGATAATLT
		SAGHPFFTIVLVAALAVGALCGLWNGFLVAVLQIQ
		PIVATLMLMVAGRGIAQLITEGQI
		VTFDSSGGLAELGSSTLMYMPMSVVIAFSMLIIVW
		LLTRKTALGLFIESVGINLRSARN
		AGVSTRVLVISVYVICGVCAAVAGIIVTADIRGA
		DANNAGLWLELDAILAVVIGGASL
		MGGRFNLLLSVIGALIIQGMNTGILLSGYQPEFN
		LVLKAIVVLAVLVVQSPMISLSHI FRRRK"
misc-feature	join(169432..169500,	/locus-tag="YE0143"
	169561..169629,	
	169687..169755,	
	169768..169836,	
	169879..169947,	
	170029..170097,	
	170125..170184,	
	170203..170271,	
	170299..170361)	
		/inference="protein
		motif:TMHMM:2.0"
		/note="9 probable transmembrane
		helices predicted for YE0143 by
		TMHMM2.0 at aa 26-48, 69-91,
		111-133, 138-160,175-197, 225-247,
		257-276, 283-305 and 315-335"
		/locus-tag="YE0144"
gene	170376..171344	/locus-tag="YE0144"
CDS	170376..171344	/locus-tag="YE0144"
		/codon-start=1
		/transl-table=11
		/product="putative sugar transport
		system permease"
		/protein-id="CAL10284.1"
		/db-xref="GI:122087503"
		/db-xref="GOA:A1JI46"
		/db-xref="InterPro:IPR001851"
		/db-xref="InterPro:IPR006162"
		/db-xref="UniProtKB/TrEMBL:A1JI46"
		/translation="MLKRNIPLLLITIAVFILGYA
		FCLSQFSPFSSTRVWCDLLTDNAF

		LGIVAVGMTFVILSGGIDLSVGSVIAFTGVLLAK LIGTYGIHPMYAFAIVLVMGAMFG AFMGWIIDSLKLPAFIITLAGMFFVRGMSFIVSE ESIPIDHPIYSTLANAWKVPGGG RFTLLALIMLLVVAFGILLAHRTFRGHNHYAIGG NSVSAALMGVPVRQTTIKIYMLSS TLAALSGIVFSLYTSAGYALAASGVELDAIAAVV IGGTLLTGGIGTVFGTLFGVLIQG LIQSYITFDGTLSSWWTIKIVIGILLFSFIAIQKA MSAFYLNRRARP"
sig-peptide	170376..170465	/locus-tag="YE0144" /note="Signal peptide predicted for YE0144 by SignalP 2.0 HMM (Signal peptide probability 0.989) with cleavage site probability 0.851 between residues 30 and 31"
misc-feature	170466..171329	/locus-tag="YE0144" /inference="protein motif:PFAM:PF02653" /note="Pfam match to entry PF02653 BPD-transp-2,Branched-chain amino acid transport system / permease component, score -43.8, E-value 0.00011"
misc-feature	170946..170993	/locus-tag="YE0144" /inference="protein motif:Prosite:PS00012" /note="PS00012 Phosphopantetheine attachment site."
gene	complement(171355..172236)	/locus-tag="YE0145"
CDS	complement(171355..172236)	/locus-tag="YE0145" /codon-start=1 /transl-table=11 /product="LysR-family transcriptional regulatory protein" /protein-id="CAL10285.1" /db-xref="GI:122087504" /db-xref="GOA:A1JI47" /db-xref="InterPro:IPR000847" /db-xref="InterPro:IPR005119" /db-xref="InterPro:IPR011991" /db-xref="UniProtKB/Swiss-Prot:A1JI47" /translation="MDTELLKTFLEVSRTTRHFRGR AAESLYLTQSAVSFRIRQLENQLG ANLFTRHRNNIIRLTPAGERLLPYAETLMSTWQLA KKEVAHSLQHTLSIGATASLWEA YLTPWLQQLYKQRETLRLAARIALRQSLVKQLHE RQLDLLITTEPPKMDELASLLLGH FSLRLFSSIPFELPEKTDGTEHKNANEAPYIKL EWGADFHQQESRLNSEQMPVLTT TSAHLTRQLLDTTGGCAFLPEHWQKEYPELVVNA DIPPIVRPLYAVWLQNSDQQTILIR QLLKTPMNNAQAQAIR"
misc-feature	complement(171376..171987)	/locus-tag="YE0145" /inference="protein motif:PFAM:PF03466" /note="Pfam match to entry PF03466"

		LysR-substrate, LysR substrate binding domain, score 56.9, E-value 3e-14"
misc-feature	complement(172051..172230)	/locus-tag="YE0145"  /inference="protein motif:PFAM:PF00126" /note="Pfam match to entry PF00126 HTH-1, Bacterial regulatory helix-turn-helix protein, lysR family, score 97.3, E-value 2e-26"
misc-feature	complement(172096..172188)	/locus-tag="YE0145"  /inference="protein motif:Prosite:PS00044" /note="PS00044 Bacterial regulatory proteins, lysR family signature."
misc-feature	complement(172126..172191)	/locus-tag="YE0145"  /note="Predicted helix-turn-helix motif with score 1285.000, SD 3.56 at aa 16-37, sequence RHFGRAAESLYLTQSAVSFRIR"
gene	172356..172694	/locus-tag="YE0146"
CDS	172356..172694	/locus-tag="YE0146" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10286.1" /db-xref="GI:122087505" /db-xref="InterPro:IPR007335" /db-xref="UniProtKB/TrEMBL:A1JI48" /translation="MADSFITTNRFFDNKHYPRG FSRHGDFTIKEAQLLERHGYAFNE LDLGKREPVTETEEQLFVAVCRGEREPVSAEEKVW SKYVTRTRRPKRFFHTLSGGKPQMD AVEDYTDSDD"
gene	complement(172798..174321)	/locus-tag="YE0147"
CDS	complement(172798..174321)	/locus-tag="YE0147"  /codon-start=1 /transl-table=11 /product="putative magnesium chelatae family protein" /protein-id="CAL10287.1" /db-xref="GI:122087506" /db-xref="GOA:A1JI49" /db-xref="InterPro:IPR000523" /db-xref="InterPro:IPR001208" /db-xref="InterPro:IPR003593" /db-xref="InterPro:IPR004482" /db-xref="UniProtKB/TrEMBL:A1JI49" /translation="MSLATIYTRATLGIQAPSVT VEVHISNGLPGLVLVGLPETTVKE ARDRVRSALINSGFTEPAKRITVSLAPADLPKEG GRYDLPIALAILAASEQIPADKLA HYEFLGELALSGALRRISGAIPAALASSQAQRQL ILPSENSLEIGLIAQGNSRVADHL LAVCSFLQGENTLAQGQRLEATQDWDNRLDLQDI

		IGQSQAKRALEIAAAGGHNLLLLG PPGTGKTMLANRLTSLPLPLTDQEALAAAINGL SHSNELPAQWRCRAFRAPHHSASM AALIGGGSIPRPGEISLAHNGVLFDELPEFERR VLDSLREPLESGEIIISRAAAKVC FPAKVQLIAAMNPSPSGHYQGIHNRAPPQQVRLRY LAKLSGPFLDRFDLSIEVPLLPAG MLGTQKHQGENSKTVRQRVLQARKKQLDRAGKTN KQLNSQEIAEYCYLPEDAVFLEQ VLLKLGLSVRTWHHILKVARTIADLALEDNIQKN HLSEALSYRCMDRLLSQLHKSLM"
misc-feature	complement(172921..172986)	/locus-tag="YE0147"  /note="Predicted helix-turn-helix motif with score 1104.000, SD 2.95 at aa 446-467, sequence VFLEQVLLKLGLSVRTWHHILK"
misc-feature	complement(173290..174267)	/locus-tag="YE0147"  /inference="protein motif:PFAM:PF01078" /note="Pfam match to entry PF01078 Mg-chelatase, Magnesium chelatase, subunit ChlI, score 299.4, E-value 2.8e-87"
misc-feature	complement(173647..173670)	/locus-tag="YE0147"  /inference="protein motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	174892..176538	/gene="ilvG"
CDS	174892..176538	/locus-tag="YE0148" /gene="ilvG" /locus-tag="YE0148" /codon-start=1 /transl-table=11 /product="acetolactate synthase isozyme II large subunit" /protein-id="CAL10288.1" /db-xref="GI:122087507" /db-xref="GOA:A1JI50" /db-xref="InterPro:IPR000399" /db-xref="InterPro:IPR011766" /db-xref="InterPro:IPR012000" /db-xref="InterPro:IPR012001" /db-xref="InterPro:IPR012846" /db-xref="UniProtKB/TrEMBL:A1JI50" /translation="MNGAQWVVQALRAQGVDTVF GYPGGAIMPVYDALYDGGVEHLLC RHEQGAAIAAIGYARATGKVGVCIAITSGPGATNL ITGLADALLDSVPVIAITGQVGSA LIGTDAFQEIDVLGLSLACTKHSFLVESLDALPA IMAEAFAIATSGRPGPVLIDIPKD IQLAVGELTPHLMPEEHLIDSAAELQQALDMLA TAKKPMLYVGGGVGMAQAVPALRE FIDVTGIPAVATLKGLGAPDTNHPCYLGMLGMHG TKAANFAVQDCDLLIAVGARFDDR VTGKLNTFAAKAKVIHMDIDPAELGKLRQAHVAL QGDLKVLLPALQQPLNIQPWRDEV IALKQQHWSRYDHPGQAIYAPLLLKQISDRKAPQ TVVTTDVGQHQMWTQAQHMNFTRPE



		NFITSSGLGTMGFGVPAAVGAQMARPDDMVICVS GDGSFMMNVQELGTIKRKQLPLKI VLLDNQRLGMVRQWQQLFFDGRYSETNLSNPDF ITLASAFNIPGQRITRKDQVDAAL DALFNSEGPYLLQVSSIDELENVWPLVPPGAGNET MLEKVS"
misc-feature	174892..175401	/gene="ilvG" /locus-tag="YE0148" /inference="protein" motif:PFAM:PF02776" /note="Pfam match to entry PF02776 TPP-enzymes-N, Thiamine pyrophosphate enzyme, N-terminal TPP binding domain ,score 332.6, E-value 3e-97"
misc-feature	175069..175161	/gene="ilvG" /locus-tag="YE0148" /inference="protein" motif:Prosite:PS00044" /note="PS00044 Bacterial regulatory proteins, lysR family signature."
misc-feature	175435..175896	/gene="ilvG" /locus-tag="YE0148" /inference="protein" motif:PFAM:PF00205" /note="Pfam match to entry PF00205 TPP-enzymes, Thiamine pyrophosphate enzyme, central domain, score 229.7,E-value 2.7e-66"
misc-feature	175933..176457	/gene="ilvG" /locus-tag="YE0148" /inference="protein" motif:PFAM:PF02775" /note="Pfam match to entry PF02775 TPP-enzymes-C, Thiamine pyrophosphate enzyme, C-terminal TPP binding domain ,score 300.1, E-value 1.7e-87"
misc-feature	176122..176181	/gene="ilvG" /locus-tag="YE0148" /inference="protein" motif:Prosite:PS00187" /note="PS00187 Thiamine pyrophosphate enzymes signature."
gene	176535..176792	/gene="ilvM"
CDS	176535..176792	/locus-tag="YE0149" /gene="ilvM" /locus-tag="YE0149" /codon-start=1 /transl-table=11 /product="acetolactate synthase isozyme II small subunit" /protein-id="CAL10289.1" /db-xref="GI:122087508" /db-xref="UniProtKB/TrEMBL:A1JI51" /translation="MIQHQISIQARFRPEMLERV LRVVRHRGFQVCAMNMSPMINAEN INIELTVASGRPVDLLSSQLSKLMDVACVEILQP NTLQIRA"
gene	176815..177741	/gene="ilvE"

CDS	176815..177741	/locus-tag="YE0150" /gene="ilvE" /locus-tag="YE0150" /codon-start=1 /transl-table=11 /product="branched-chain amino acid aminotransferase" /protein-id="CAL10290.1" /db-xref="GI:122087509" /db-xref="GOA:A1JI52" /db-xref="InterPro:IPR001544" /db-xref="InterPro:IPR005785" /db-xref="UniProtKB/TrEMBL:A1JI52" /translation="MTKKADFIWFNGEMVPWAEA KVHVMSHALHYGTSVFEGVRCYNS HKGPVVFRHREHMQRLHDSAKIYRMPVSQSVDEL MEACRATLRKNNLTSAYIRPLVFI GDVGMGVNPPDGYKTDVIIAAFPWGAYLGAEALE QGIDAMVSSWNRVAPNTIPTAACA GGNYLSSLVGSEARRHGYQEGIALDIHGFLSEG AGENLFEVKDGILFTPPFTSSALP GITRDAIIKLAKDMGLEVREQVLSRESLYLADEV FMSGTAAEITPVRSDGIQVGIGK RGPITGKIQQAFFGLFTGETEDKWGWLDPINQ"
misc-feature	176845..177681	/gene="ilvE" /locus-tag="YE0150" /inference="protein motif:PFAM:PF01063" /note="Pfam match to entry PF01063 aminotran-4,Aminotransferase class IV, score 460.9, E-value 7e-136"
misc-feature	177391..177480	/gene="ilvE" /locus-tag="YE0150" /inference="protein motif:Prosite:PS00770" /note="PS00770 Aminotransferases class-IV signature."
gene	177853..179703	/gene="ilvD"
CDS	177853..179703	/locus-tag="YE0151" /gene="ilvD" /locus-tag="YE0151" /codon-start=1 /transl-table=11 /product="dihydroxy-acid dehydratase" /protein-id="CAL10291.1" /db-xref="GI:122087510" /db-xref="GOA:A1JI53" /db-xref="InterPro:IPR000581" /db-xref="InterPro:IPR004404" /db-xref="UniProtKB/Swiss-Prot:A1J I53" /translation="MPKYRSHTTTTHGRNMAGARA LWRATGMTDDDFGKPIIAVVNSFT QFVPGHVHLRDLGKLVAEQIEASGGVAKEFNTIA VDDGIAMGHGGMLYSLPSRELIAD SVEYMVNAHCADAMVCISNCDKITPGMLMASLRL NIPVIFVSGGPMEAGKTKLSDKII KLDLVDAMIQGANPNVSDADSEQUIERSACPTCGS CSGMFTANSMNCLNEALGLALPGN GSLLATHADRKQLFLDAGKHIVELTKRYYEQDDI SALPRSIANKAAFENAMTLDIAMG

		GSTNTVLHLLAAQEGDIDFDISDIDRLSRKVPH LCKVAPSTQKYHMEDVHRAGGVVG ILGELDRAGLLNREVKNVLGLNLPQTLEAYDVML TKDEGVKQMYSSAGPAGIRTTKAFS QDCRFPSLDTDRQEGCIRTREHAYSQDGGGLAVLY GNLSENGSIVKTAGVVDKDSLTFRG PAKVYESQDDAVAAAILGGKVAVAGDVVVIRYEGPK GGPGMQEMLYPTTYLKSMGLGKSC ALLTDGRFSGGTSGLSIGHASPEAASGGLIALVQ DGDIIDIDIPNRAMKLDVSDAELA ARREAELARGDAAWTPKARERQVSYALRAYALLA TSADKGAVRDKSKLGG"
misc-feature	177952..179682	/gene="ilvD" /locus-tag="YE0151" /inference="protein motif:PFAM:PF00920" /note="Pfam match to entry PF00920 ILVD-EDD, Dehydratase family, score 1247.3, E-value 0"
misc-feature	178216..178248	/gene="ilvD" /locus-tag="YE0151" /inference="protein motif:Prosite:PS00886" /note="PS00886 Dihydroxy-acid and 6-phosphogluconate dehydratases signature 1."
misc-feature	178288..178311	/gene="ilvD" /locus-tag="YE0151" /inference="protein motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-feature	179377..179412	/gene="ilvD" /locus-tag="YE0151" /inference="protein motif:Prosite:PS00887" /note="PS00887 Dihydroxy-acid and 6-phosphogluconate dehydratases signature 2."
gene	179709..181253	/gene="ilvA" /locus-tag="YE0152"
CDS	179709..181253	/gene="ilvA" /locus-tag="YE0152" /codon-start=1 /transl-table=11 /product="threonine dehydratase" /protein-id="CAL10292.1" /db-xref="GI:122087511" /db-xref="GOA:A1JI54" /db-xref="InterPro:IPR000634" /db-xref="InterPro:IPR001721" /db-xref="InterPro:IPR001926" /db-xref="InterPro:IPR005787" /db-xref="UniProtKB/TrEMBL:A1JI54" /translation="MAVSQPLSTAPDGAEYLRAI LRAPVYEVAQVTPLQVMEKISSRL DNTILVKREDRQPVHSFKLRGAYAMLAGLTAEQK ACGVITASAGNHAQGVALSANKLG IKALIVMPVATADIKVDAVRGFGGEVLLFGANFD EAKGKAIELSQLQGYTFVPPFDHP AVIAGQGTLMELLQQDAHLDRVFVPVGGGLVA GVAVLIKQLMPQIKVIGVEAEDSA

		CLRAALDAGKPVDLARVGLFAEGVAVKRIGDEPF RLCQEYLDEVISVSDAICAIVKD LFEDVRAIAEP SGALALAGLKKYVQQHNIQGERL AHVLSGANVNFHGLRYV SERCELG EQREAL LAVTIPEQKGSFLRFCELLGGRSVTEFN YRYADADNACIFVGVRLTRGYAER AEILAE LQGKG YQVVDLSDDMAKLHVRYMVGG PSKPLRERLFSFEFPESPGALLKF LHTLGTHWNISLFHYRSHGTDGFRVL AGFELSDS EPQFEQHLTALGYDCHDETNNPAF KFFLAG"
misc-feature	179781..180659	/gene="ilvA" /locus-tag="YE0152" /inference="protein" motif:PFAM:PF00291" /note="Pfam match to entry PF00291 PALP, Pyridoxal-phosphate dependent enzyme, score 318.7, E-value 4.4e-93"
misc-feature	179865..179906	/gene="ilvA" /locus-tag="YE0152" /inference="protein" motif:Prosite:PS00165" /note="PS00165 Serine/threonine dehydratases pyridoxal-phosphate attachment site."
misc-feature	180693..180965	/gene="ilvA" /locus-tag="YE0152" /inference="protein" motif:PFAM:PF00585" /note="Pfam match to entry PF00585 Thr-dehydrat-C, C-terminal regulatory domain of Threonine dehydratase ,score 159.3, E-value 4.3e-45"
misc-feature	180978..181244	/gene="ilvA" /locus-tag="YE0152" /inference="protein" motif:PFAM:PF00585" /note="Pfam match to entry PF00585 Thr-dehydrat-C, C-terminal regulatory domain of Threonine dehydratase ,score 151.2, E-value 1.2e-42"
gene	181439..182935	/locus-tag="YE0153"
CDS	181439..182935	/locus-tag="YE0153" /inference="similar to sequence:INSDC:AL035475" /inference="similar to sequence:INSDC:AL445564" /note="Similar in parts to many including: Plasmodium falciparum putative replication A protein Mal4p2.32 SWALL:Q9U0J0 (EMBL:AL035475) (1145 aa) fasta scores: E(): 0.55, 19.25 38d in 483 aa and Mycoplasma pulmonis hypothetical protein Mypu-4790 SWALL:Q98Q87 (EMBL:AL445564) (804 aa) fasta scores: E(): 2, 22.8 38d in 307 aa. Note the abundance of Asn residues in the predicted product of this CDS."

		/codon-start=1 /transl-table=11 /product="putative membrane protein" /protein-id="CAL10293.1" /db-xref="GI:122087512" /db-xref="UniProtKB/TrEMBL:A1JI55" /translation="MMSLLILSYWITLFLLELSNL IITYWSLYMSELITLNFKSTSTYL DWNATSIGARYQYHADGTRFNGGVSVQKINQA IEGDSNYRRFDQM QATIDQGSVS KEGGAGNEIYFIENKANNSAAVSFYKYGLDNKLN ESQSFNYQSNILTSRTKIMPNSIG QITKSQKFNIHDKLVESNVFSYKKDRIGNDLIII QKEKYSGNEVVSTTHKELYDSSGK IIKIDVYDKNDKQLERNEFSYFNNGNKCRTVKST FNISGNLNHQEKIYKNKNGDLRAM VQSNYDNGQSLKDSKSTYYYINGEVDREVVEVEYSA DGKVIVGRIEKAYNITNAILIKET ESSYSMDGKIIIGRINKEYSALDGRLEKITRSNR SDSGQLKREVESYLDINGQESKRI SQYYSNGVTKCFERSFSAGKMTGKVYMEFDNNGN AINIKRLNPEGKMVDVLINASLDT FFKGVTQLADAINSFP TREQAPAAVDTIIGSHAN LRNLVPVMNYASRQ"
misc-feature	181457..181525	/locus-tag="YE0153" /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted for YE0153 by TMHMM2.0 at aa 7-29"
gene	complement(182937..1838 18)	/gene="ilvY"
CDS	complement(182937..1838 18)	/locus-tag="YE0154" /gene="ilvY"  /locus-tag="YE0154" /codon-start=1 /transl-table=11 /product="LysR-family transcriptional regulatory protein" /protein-id="CAL10294.1" /db-xref="GI:122087513" /db-xref="GOA:A1JI56" /db-xref="InterPro:IPR000847" /db-xref="InterPro:IPR005119" /db-xref="InterPro:IPR011991" /db-xref="UniProtKB/TrEMBL:A1JI56" /translation="MDLRDLKLFLHLAESRHFGR SAKAMHVSPSTLSRQIQRL EETIG QPLFLRDNRTVQLTDAGTQLKAFAQQTLLQYQQL RHALGQHGPSLSGELRLFC SVTAA YSHLPPILDRFRARHPLVEIKLTTGDAADAVDKV QSNEADLGIAGRPEVLPTSVAFTQ IGEIPLVLIAPALPCAVRSQVSVDQPDWATIPFI LPEHGPPSRKRIDLWFRQRITNPL IYATVSGHEAIVSMVALGCGVALIPSVVVDNSPE PVRNRISLLDDVSLVEPFELGVCV QKKRLNEPLIEAFWGLL"
misc-feature	complement(182940..1835 63)	/gene="ilvY"

		/locus-tag="YE0154" /inference="protein" motif:PFAM:PF03466" /note="Pfam match to entry PF03466 LysR-substrate, LysR substrate binding domain, score 118.2, E-value 9.9e-33" /gene="ilvY"
misc-feature	complement(183633..183812)	/locus-tag="YE0154" /inference="protein" motif:PFAM:PF00126" /note="Pfam match to entry PF00126 HTH-1, Bacterial regulatory helix-turn-helix protein, lysR family, score 97.4, E-value 1.8e-26" /gene="ilvY"
misc-feature	complement(183678..183770)	/locus-tag="YE0154" /inference="protein" motif:Prosite:PS00044" /note="PS00044 Bacterial regulatory proteins, lysR family signature." /gene="ilvY"
misc-feature	complement(183708..183773)	/locus-tag="YE0154" /note="Predicted helix-turn-helix motif with score 1928.000, SD 5.75 at aa 16-37, sequence RHFGRSAKAMHVSPSTLSRQIQ" /gene="ilvC"
gene	184071..185549	/locus-tag="YE0155"
CDS	184071..185549	/gene="ilvC" /locus-tag="YE0155" /codon-start=1 /transl-table=11 /product="ketol-acid reductoisomerase" /protein-id="CAL10295.1" /db-xref="GI:122087514" /db-xref="GOA:A1JI57" /db-xref="InterPro:IPR000506" /db-xref="InterPro:IPR013023" /db-xref="InterPro:IPR013116" /db-xref="InterPro:IPR014359" /db-xref="InterPro:IPR016040" /db-xref="UniProtKB/Swiss-Prot:A1J I57" /translation="MANYFNTLNLRQQLAQLGKC RFMARDEFAD EAGYLKGKKVVIVG CGAQQLNQGLNMRD SGLDVAYALRKEAIAEKRAS WRKATENGFKVGT YEELIPQADLV VNLT PDKQHS AVVQAVQPLMKDGAALGYSHGFNI VEVGEQVRKDI TVVMVAPKCPGTE VREEYKRGFGVPTLI AVHPENDPKGEGMAIAKAW AAATGGHRAGVLE SSFVAEVKSDL MGEQTILCGMLQAGSLLCFDKLVSEGTDAAYAEK LIQFGWETITEALKQGGITLMMDR LSNPAKL RAYALSEQ LKEIMAPLFQKHMDDIISG EFSSGMMADWANDDKLLNWREET

		GKTAFENAPQFEGKISEQEYFDHGVLMIAMVKAG VELAFETMVDSGIIEESAYYESLH ELPLIANTIARKRLYEMNVVISDTAEYGNLFFAN AAVPLLKGKFMDSLQAGDLGKSV GTAVDNAQLRDVNEAIRNHPIEAVGHKLRGYMTD MKRIAVAG"
misc-feature	184698..185528	/gene="ilvC" /locus-tag="YE0155" /inference="protein" motif:PFAM:PF01450" /note="Pfam match to entry PF01450 IlvC, Acetohydroxy acid isomeroreductase, catalytic domain, score 463.0, E-value 1.6e-136"
gene	complement(185847..186524)	/locus-tag="YE0157"
CDS	complement(185847..186524)	/locus-tag="YE0157"  /codon-start=1 /transl-table=11 /product="putative chaperone protein" /protein-id="CAL10296.1" /db-xref="GI:122087515" /db-xref="GOA:A1JI58" /db-xref="InterPro:IPR001829" /db-xref="InterPro:IPR008962" /db-xref="InterPro:IPR016147" /db-xref="InterPro:IPR016148" /db-xref="UniProtKB/TrEMBL:A1JI58" /translation="MACSVPAMASVVAEKTRIIF SEGSTEESLQLVNSNDYPVAVQVW VDDGDLMATPEKAISPVLVLPPLFRLQPQAQRSL RLILSGASKLPLDRESAFWLNVE IPPKATTKVDESSVTLALRMQYKVFYRPKSLPA PADTVSKALTFVLERNGNTASVRV DNPTPYASLASLTLGLAEGLPDMVAPFSKLDFF LNRVPIADSKTVNFVLIDDLGNRK PFSRELK"
misc-feature	complement(185859..186110)	/locus-tag="YE0157"  /inference="protein" motif:PFAM:PF02753" /note="Pfam match to entry PF02753 pili-assembly-C, Gram-negative pili assembly chaperone, C-terminal domain ,score 28.6, E-value 9.5e-06"
misc-feature	complement(186120..186497)	/locus-tag="YE0157"  /inference="protein" motif:PFAM:PF00345" /note="Pfam match to entry PF00345 pili-assembly, Gram-negative pili assembly chaperone, N-terminal domain ,score 141.8, E-value 8.2e-40"
misc-feature	complement(186210..186263)	/locus-tag="YE0157"  /inference="protein" motif:Prosites:PS00635" /note="PS00635 Gram-negative pili

gene complement(186571..1879 /locus-tag="YE0158"  
38)

CDS complement(186571..1879 /locus-tag="YE0158"  
38)

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/db-xref="UniProtKB/TrEMBL:A1JI59"  
/translation="MLRPTEQLISCEVSRPTMPV  
HCRRSYIVAGTMLLIGLFSTSAWS  
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PGVIDLSTAANFQPDGTLAAATS  
DFTTFALNTSYDPDRVLFRCAAADVQDLFEMYAT  
NGDNDYGGKNEDEGAIAGNVPSGFA  
TYVRNVVIRLTNLSTGEYYSRLWKGRRLTGLDTD  
STGRILVKAKNFSNLYTELFRIDY  
VRAGTNNAASYTYAYTQPNAYIAFKGPGISGPVE  
GTDSVSNWPGWYSTWPASIGLYNY  
VTFRRTTICAVTNFTPTVILPRISVAELNSGSSS  
SAEFSVDFQCQTGITSGVNAGAVA  
MGFLVPAANAAKAQALGLMNGSGGISHLVSDNYG  
AAGMANGVGIRIYRNNNPMYLLSK  
NVTQTGNNGGWYGIFQGAQTITGTVSGGNSYTEN  
FRAELSKISGQTVTAGAVNAHAQV VIRVQ"

misc-feature complement(187801..1878 /locus-tag="YE0158"  
33)

/inference="protein  
motif:Prosite:PS00013"  
/note="PS00013 Prokaryotic  
membrane lipoprotein lipid  
attachment site."

gene complement(187956..1901 /locus-tag="YE0159"  
75)

CDS complement(187956..1901 /locus-tag="YE0159"  
75)

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/product="putative outer membrane  
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/protein-id="CAL10298.1"  
/db-xref="GI:122087517"  
/db-xref="GOA:A1JI60"  
/db-xref="InterPro:IPR000015"  
/db-xref="UniProtKB/TrEMBL:A1JI60"  
/translation="MAERVKGASFHFDQAKLRLE  
LSIPQALLQQRPRGYIERSEWEEG  
EKLAFFVNYSANFYRSDTQTQONSTSDYGFVGLKS  
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DTQWNNIRTYVQRPISQLDSELTTLGETFTDSTLF  
GTMSFRGVKMATDQRMWPESMRGF  
APEVRGVATSNARVVISQNGREIYETNVAPGPFV  
INDLYSTTSQGDNLNVEVIEANGSR  
STFTVPFSAVPDSMRPGVSRYNNAVVGESRDFTN  
DSYFTDFTYERGLTNQLTANSRIR  
LAQDYTALLVGGVIGTSVGAFLNNTTYSHAKVED  
NQTQDGWRMQATYSQTFNETGTSTF  
SLAGYRYSTKGYRDLNDVFGVRSVQKNGGTWDSS



		TYKQRSQFTTTINQTLAGYGQLSA SASTSDYYNDTQRDTQLQLNYSNSYKDISYNVAL SRQRTIYTSTQFGWDADDDTDEMT TTRYGNTENIASLTVSIPLNIGSGNQYLSMSANR NPKSGNNYQTSLSGTAGERNTLNY SVNAGYDDSNVSGSSNNWGANVQKQFPNATVNGS YSRGNNYTQYGAGARGAAVIHSGK VTLGPYLGDTFGLIEADGAQGATVRNAQGARIDK NGFALVPSLTPYNYNTVGLDTKGI NRNTELKENQGRVVPYAGAAVRVKFETLTGYAVL IQTQTADGEGLPLGSDVYNNKDEL VGMVGQGNQIYARVKENKGSLYVRWGENSNEQCE LPYDFASQDTEQDIIHLTGSCRR"
misc-feature	complement(188010..190172)	/locus-tag="YE0159"  /inference="protein motif:PFAM:PF00577" /note="Pfam match to entry PF00577 Usher, Fimbrial Usher protein, score 734.3, E-value 3.4e-218"
misc-feature	complement(189582..189614)	/locus-tag="YE0159"  /inference="protein motif:Prosite:PS01151" /note="PS01151 Fimbrial biogenesis outer membrane usher protein signature."
gene	complement(190653..191330)	/locus-tag="YE0160"
CDS	complement(190653..191330)	/locus-tag="YE0160"  /codon-start=1 /transl-table=11 /product="putative fimbrial chaperone" /protein-id="CAL10299.1" /db-xref="GI:122087518" /db-xref="GOA:A1JI61" /db-xref="InterPro:IPR001829" /db-xref="InterPro:IPR008962" /db-xref="InterPro:IPR016147" /db-xref="InterPro:IPR016148" /db-xref="UniProtKB/TrEMBL:A1JI61" /translation="MGISFANASVMSGSRRIYS AGEKEHSIQLTNNDNFPNAVQVWL DSGDTQSTPETGKAPFIVTPFFRIEANAGQTLR LKYTGSGGLPTDRESVFYLNFLQVP PVNKAENNKMLVLMRNRIKVFYRPENIAGRVDQ VSSALTFNVRQQGKDVVVTGKNPT GFYATIASGEVVGKGKCLKMKSEMIPPMSQAQWV IPNSSVPSNAIVNFLLVNDFGGQD TGSYKIQ"
misc-feature	complement(190665..190928)	/locus-tag="YE0160"  /inference="protein motif:PFAM:PF02753" /note="Pfam match to entry PF02753 pili-assembly-C, Gram-negative pili assembly chaperone, C-terminal domain , score 33.8, E-value 2.6e-07"
misc-feature	complement(190938..191306)	/locus-tag="YE0160"

		/inference="protein motif:PFAM:PF00345" /note="Pfam match to entry PF00345 pili-assembly, Gram-negative pili assembly chaperone, N-terminal domain ,score 179.4, E-value 3.7e-51"
gene	complement(191517..192047)	/locus-tag="YE0161"
CDS	complement(191517..192047)	/locus-tag="YE0161"
		/codon-start=1 /transl-table=11 /product="putative fimbrial protein" /protein-id="CAL10300.1" /db-xref="GI:122087519" /db-xref="GOA:A1JI62" /db-xref="InterPro:IPR000259" /db-xref="InterPro:IPR014779" /db-xref="UniProtKB/TrEMBL:A1JI62" /translation="MNKITLAMALFAASTTVAMA ASNNTITFQGEVTAQTCSVTVNGL DANPMVLLPTVSSGDLASGKTAGKTTFTLGVS CATGAADIDIKTVFVGNQVTTAGN LKNTGTASNVDLQLLKDATTTTGIDLNSSVGQDG IVLKAGDTSAEHDFAVQYFATGQA GPGSVIASVQYAVSYL"
sig-peptide	complement(191988..192047)	/locus-tag="YE0161"
		/note="Signal peptide predicted for YE0161 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.991 between residues 20 and 21"
misc-feature	complement(191520..191978)	/locus-tag="YE0161"
		/inference="protein motif:PFAM:PF00419" /note="Pfam match to entry PF00419 Fimbrial, Fimbrial protein, score 26.4, E-value 3.4e-08"
gene	complement(192664..192945)	/gene="ppiC"
		/locus-tag="YE0162"
CDS	complement(192664..192945)	/gene="ppiC"
		/locus-tag="YE0162" /codon-start=1 /transl-table=11 /product="peptidyl-prolyl cis-trans isomerase C" /protein-id="CAL10301.1" /db-xref="GI:122087520" /db-xref="GOA:A1JI63" /db-xref="InterPro:IPR000297" /db-xref="UniProtKB/TrEMBL:A1JI63" /translation="MANKASALHILVDDEKQAND ILAQLNNGANFQELAKKFSNCPSK RGGDLGEFNKGDMVPAFDKAVFSCELLQPYGPV KTQFGYHIIKVLRYN"
misc-feature	complement(192673..192945)	/gene="ppiC"

42)

		/locus-tag="YE0162" /inference="protein" motif:PFAM:PF00639" /note="Pfam match to entry PF00639 Rotamase, PPIC-type PPIASE domain, score 132.4, E-value 5.3e-37"
gene	193159..195183	/gene="rep"
		/locus-tag="YE0163"
CDS	193159..195183	/gene="rep"
		/locus-tag="YE0163"
		/codon-start=1
		/transl-table=11
		/product="ATP-dependent DNA helicase Rep"
		/protein-id="CAL10302.1"
		/db-xref="GI:122087521"
		/db-xref="GOA:A1JI64"
		/db-xref="InterPro:IPR000212"
		/db-xref="InterPro:IPR005752"
		/db-xref="InterPro:IPR014016"
		/db-xref="InterPro:IPR014017"
		/db-xref="UniProtKB/TrEMBL:A1JI64"
		/translation="MRLNPSQQQAVEFVTGPCLV LAGAGSGKTRVITNKIAHLIRQCG YQPKHIAAVTFTNKAAREMKERVAQTLGRKEARG LMIATFHTLGLLEIIKKEYKALGMK SNFSLFDAQDQLGLLKDLTHKWLEDDKTLQQLI SQISNWKNDLLDPAAAAALARSER DKLFVHCYGLYDAHLKACNVLDFDDLISLPTLLL QKDLEVRERWQNRLRYLLVDEYQD TNTSQYQMVKLLVGSRRARFTVVGDDQSIYSWRG ARPQNLVLLNEDFPQLQVIKLEQN YRSSGRILKAANILIANNPVFEKKLFSELEYGD ELKVITANNEDHEAERVVGELIAH HFVKKTKQYSDYAILYRGNHQSRLFEEKLLMQNRIP YRISGGDSFFSRPEIKDLLAYLRV LTNQDDDSAFLRIVNTPKREIGSATIQKLGewan VRNKS LFRASFDLGLGEHLKGRGL ESLQRFTHWMEGIIRLVEREPIAAVRDLIHGIDY ESWLFETSPSPKAAEMRMKNVNL FSWMTEMLEGSELNEPMTLTQVVTRFTLRDMMER GESDEELDQVQLMTLHASKGLEFP YVFLVGMEEGLLPHQSSIDEDNVDEERRLAYVGI TRAQRELFFTLCKERRQYGE LIRP EPSRFLMELPQDDLKWENERKAVSPEERMQKGQS HLANIRAQLANAKKPQ"
misc-feature	193165..194610	/gene="rep"
		/locus-tag="YE0163"
		/inference="protein"
		motif:PFAM:PF00580"
		/note="Pfam match to entry PF00580 UvrD-helicase, UvrD/REP helicase, score 718.8, E-value 1.6e-213"
misc-feature	193222..193245	/gene="rep"
		/locus-tag="YE0163"
		/inference="protein"
		motif:Prosite:PS00017"
		/note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	complement (195239..197065)	/gene="pehX"

CDS	complement(195239..197065)	/locus-tag="YE0164" /gene="pehX"  /locus-tag="YE0164" /EC-number="3.2.1.82" /inference="similar to sequence:INSDC:AF059505" /inference="similar to sequence:UniProtKB:P15922" /note="Highly similar to the plant pathogenic Erwinia chrysanthemi exo-poly-alpha-D-galacturonosidase PehX SWALL:PEHX-ERWCH (SWALL:P15922) (602 aa) fasta scores: E(): 3.6e-145, 61.23 38d in 601 aa. This CDS was previously sequenced as: Yersinia enterocolitica exopolygalacturonase SWALL:O68975 (EMBL:AF059505) (601 aa) fasta scores: E(): 0, 98.83 38d in 600 aa" /codon-start=1 /transl-table=11 /product="exo-poly-alpha-D-galactu ronosidase precursor" /protein-id="CAL10303.1" /db-xref="GI:122087522" /db-xref="GOA:A1JI65" /db-xref="InterPro:IPR000743" /db-xref="InterPro:IPR003961" /db-xref="InterPro:IPR008957" /db-xref="InterPro:IPR012334" /db-xref="UniProtKB/TrEMBL:A1JI65" /translation="MQAQLQRPRTTGMLVIMASL MVGTPMAMAAKSSSLDAPQQQLQVP TLAYDESSIVLVWKAPEDTRKIVDYQIFSAGKLL GKASDNNDKFSPAKPYIDHIFYVND KDNFQHKIVMQNFTVIGLKPETSYQFTVKAQYAD GLSLVASKPITAKTSAKPQIVNVR DFGAIDDGKTLNTKAIQQAIDSCKPGCRVEIPAG TYKSGALWLKSDMTLNLQAGAILL GSENPNDYPAGYRLYPYSTIERPASLINAI DPNN SKPGTFRNIRITGSGVIDGNGWLR AKTAEITDELGRSLPQYVASKNSKVHEDGILAKN QVEKAVSDGMDLKNAYGQRRSSLM TLRGVENVYLAGFTVRNPAFHGIMNLENHNVVAN GLIHQTYDANNGDGIEFGNSQNVN VFNNFFDTGDDCINFAAGTGEKAQEPEPMKGAWL FNNYFRMGHGAIVTGSHTGAWIED ILAENNVMYLTDIGLRAKSTSTIGGGARNVTFRN NAMRDLAKQVMVMTLDYADSNANI DYPPAKIPAQFYDFTLKNVTVDNSTGKNPSIEIK GDTANKAWHRLVHVNNVQLNNVTP TAISDLRDSEFNKVTFTELRGDTPWHFSEVKNVK VDGKPVAP"
sig-peptide	complement(196979..197065)	/locus-tag="YE0164" /note="Signal peptide predicted for YE0164 by SignalP 2.0 HMM (Signal peptide probabilty 1.000)

		with cleavage site probability 0.985 between residues 29 and 30"
misc-feature	complement(195356..196519)	/gene="pehX"  /locus-tag="YE0164" /inference="protein motif:PFAM:PF00295" /note="Pfam match to entry PF00295 Glyco-hydro-28,Polygalacturonase (pectinase), score -27.9, E-value 7.2e-09"
misc-feature	complement(196556..196579)	/gene="pehX"  /locus-tag="YE0164" /inference="protein motif:Prosit:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-feature	complement(196637..196963)	/gene="pehX"  /locus-tag="YE0164" /inference="protein motif:PFAM:PF00041" /note="Pfam match to entry PF00041 fn3, Fibronectin type III domain, score 28.4, E-value 1.1e-05"
misc-feature	complement(196979..197032)	/gene="pehX"  /locus-tag="YE0164" /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted for YE0164 by TMHMM2.0 at aa 12-29"
gene	complement(197407..198903)	/gene="gppA"
CDS	complement(197407..198903)	/locus-tag="YE0165" /gene="gppA"  /locus-tag="YE0165" /EC-number="3.6.1.40" /codon-start=1 /transl-table=11 /product="guanosine-5'-triphosphat e,3'-diphosphate pyrophosphatase" /protein-id="CAL10304.1" /db-xref="GI:122087523" /db-xref="GOA:A1JI66" /db-xref="InterPro:IPR003695" /db-xref="UniProtKB/Swiss-Prot:A1J I66" /translation="MMLSSTSLYAAIDLGSNSFH MLVVREVAGSIQTLARIKRVRLA AGLDTQNHLSQEAMERGWCCLKFSERLQDIPLD QIRVVATATLRLASNAEEFLQTAT EILGCPIQVISGEEEARLIYHGVAHTTGGPEQRL VVDIGGGSTELVTGNGAQANILVS LPMGCVTWLERYFSDRNLAKNFDRSESAAREML KPVAQRFREHGWQICVGASGTVQA LQEIMVAQGMDELITLAKLQQLKQRAIQCGKLEE LEIPGLTLERALVFPSGLSILIAI FQELAIESMTLAGGALREGLVYGMLHLPVEQDIR

SRTVRNIQRRYLLDTEQAKRVSKL  
 ADNFLQVEKEWRLDSRCRELLQNACLIHEIGLS  
 IDFKRAPQHAAYLIRNLDLPGFTP  
 AQKLLLAALLQNQSDTLDLSSLNQNALPVDMAQ  
 HLCRLRLAIIFSSRRRDDTLPAV  
 RLRANGETLYVLLPHGWLQQHPYRAEAEQESHW  
 QSYVQWPLLLLEEFN"

misc-feature complement(197992..1988 /gene="gppA"  
 40)  
 /locus-tag="YE0165"  
 /inference="protein  
 motif:PFAM:PF02541"  
 /note="Pfam match to entry PF02541  
 Ppx-GppA, Ppx/GppA phosphatase  
 family, score 427.6, E-value  
 7.2e-126"

gene complement(198907..1999 /gene="rhlB"  
 83)  
 /locus-tag="YE0166"  
 /note="synonym: mmrA"

CDS complement(198907..1999 /gene="rhlB"  
 83)  
 /locus-tag="YE0166"  
 /codon-start=1  
 /transl-table=11  
 /product="putative DEAD-box  
 helicase"  
 /protein-id="CAL10305.1"  
 /db-xref="GI:122087524"  
 /db-xref="GOA:A1JI67"  
 /db-xref="InterPro:IPR000629"  
 /db-xref="InterPro:IPR001650"  
 /db-xref="InterPro:IPR011545"  
 /db-xref="InterPro:IPR014001"  
 /db-xref="InterPro:IPR014021"  
 /db-xref="UniProtKB/TrEMBL:A1JI67"  
 /translation="MLSHPAEEGRQTNQPRALIM  
 APTRELAVQIHSDAESLSQVTGLK  
 LGLAYGGDGYDKQLKVLESGVDILIGTTGRLIDY  
 AKQNYINLGAIQVVVLDEADRMVD  
 LGFIKDIRWLFRRMPVSDKRLNMLFSATLSYRVR  
 ELAFEQMNNAEYVEVEPLQKTGHR  
 IQEELFYPSNEEKMRLLQTLIEEEWPDRCIIFAN  
 TKHRCEEIWGHLAADGHRVGLLTG  
 DVAQKKRLRILEDFTKGDLILVATDVAAAGLHI  
 PLVTHVFNYDLPDDCEDYVHRIGR  
 TGRAGESGHSISLACEEYALNLPAIETYTGHSIP  
 VSKYNSDALLTDLPAKRLARTRT  
 GNGPRNSAPRRSGAPRNNRKRPS"

misc-feature complement(199141..1993 /gene="rhlB"  
 56)  
 /locus-tag="YE0166"  
 /inference="protein  
 motif:PFAM:PF00271"  
 /note="Pfam match to entry PF00271  
 helicase-C, Helicase conserved  
 C-terminal domain, score 116.3,  
 E-value 3.7e-32"

misc-feature complement(199492..1999 /gene="rhlB"  
 83)  
 /locus-tag="YE0166"  
 /inference="protein"

		motif:PFAM:PF00270"
		/note="Pfam match to entry PF00270
		DEAD, DEAD/DEAH box helicase,
		score 94.6, E-value 1.3e-25"
misc-feature	complement(199681..199707)	/gene="rhlB"
		/locus-tag="YE0166"
		/inference="protein"
		motif:Prosite:PS00039"
		/note="PS00039 DEAD-box subfamily
		ATP-dependent helicases
		signature."
gene	200312..200638	/gene="trxA"
		/locus-tag="YE0167"
		/note="synonyms: fipA, tsnC"
CDS	200312..200638	/gene="trxA"
		/locus-tag="YE0167"
		/codon-start=1
		/transl-table=11
		/product="thioredoxin 1"
		/protein-id="CAL10306.1"
		/db-xref="GI:122087525"
		/db-xref="GOA:A1JI68"
		/db-xref="InterPro:IPR005746"
		/db-xref="InterPro:IPR006662"
		/db-xref="InterPro:IPR012335"
		/db-xref="InterPro:IPR013766"
		/db-xref="InterPro:IPR015467"
		/db-xref="UniProtKB/TrEMBL:A1JI68"
		/translation="MSDKIIHLSDDSFDTDLKA
		SGLVLVDFWAEWCGPCKMIAPILD
		EIAEEYEGRLTITKLNIDDNQGTAPKYGIRGIPT
		LLLFRDGEVVATKVGALSKGQLKE FLDANL"
misc-feature	200315..200635	/gene="trxA"
		/locus-tag="YE0167"
		/inference="protein"
		motif:PFAM:PF00085"
		/note="Pfam match to entry PF00085
		thiore, Thioredoxin ,score 168.2,
		E-value 8.7e-48"
misc-feature	200384..200440	/gene="trxA"
		/locus-tag="YE0167"
		/inference="protein"
		motif:Prosite:PS00194"
		/note="PS00194 Thioredoxin family
		active site."
gene	201295..202554	/gene="rho"
		/locus-tag="YE0168"
		/note="synonyms: nitA, psuA, rnsC,
		sbaA, tsu"
CDS	201295..202554	/gene="rho"
		/locus-tag="YE0168"
		/codon-start=1
		/transl-table=11
		/product="transcription
		termination factor"
		/protein-id="CAL10307.1"
		/db-xref="GI:122087526"
		/db-xref="GOA:A1JI69"
		/db-xref="InterPro:IPR000194"
		/db-xref="InterPro:IPR003593"
		/db-xref="InterPro:IPR004665"

		/db-xref="InterPro:IPR011112"
		/db-xref="InterPro:IPR011113"
		/db-xref="InterPro:IPR011129"
		/db-xref="UniProtKB/TrEMBL:A1JI69"
		/translation="MNLTELKNTPVSDLITLGEN MGLLENLARMRKQDIIFSILKQHAK SGEDIFGDGVLEILQDGFGLRSADSSYLAGPDD IYVSPSQIRRFNLRGTGDTVAGKIR PPKEGERYFALLKVNEVNYDKPENARNKILFENL TPLHANSRLRMERGNSTEDLTAR VLDLASPIGRGQRGLIVAPPKAGKTMLLQNIATS IAYNHPDCVLMVLLIDERPEEVTE MQRLVKGEVIASTFDEPASRHHVQVAEMVIEKAKR LVEHKKDVIILLDSITRLARAYNT VVPASGKVLTTGGVDANALHRPKRFFGAARNVEEG GSLTIIATALVDTGSKMDEVIYEE FKGTGNMELHLSRKIAEKRVFPAIDFNRSCTRKE ELLTTTEELQKMWILRRILHPMGE IDAMEFLISKLATAKTNDQFFDNMRRS"
misc-feature	201523..202407	/gene="rho" /locus-tag="YE0168" /inference="protein" motif:PFAM:PF00006" /note="Pfam match to entry PF00006 ATP-synt-ab, ATP synthase alpha/beta family, nucleotide-binding domain ,score 290.0, E-value 1.9e-84"
misc-feature	201724..201798	/gene="rho" /locus-tag="YE0168" /inference="protein" motif:Prosite:PS00464" /note="PS00464 Ribosomal protein L22 signature."
misc-feature	201826..201849	/gene="rho" /locus-tag="YE0168" /inference="protein" motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	202836..203933	/gene="rfe" /locus-tag="YE0169" /note="synonym: b3784"
CDS	202836..203933	/gene="rfe" /locus-tag="YE0169" /codon-start=1 /transl-table=11 /product="putative undecaprenyl-phosphate alpha-N-acetylglucosaminyltransfer ase" /protein-id="CAL10308.1" /db-xref="GI:122087527" /db-xref="GOA:A1JI70" /db-xref="InterPro:IPR000715" /db-xref="InterPro:IPR012750" /db-xref="UniProtKB/TrEMBL:A1JI70" /translation="MNL LTMSTEIFVIFMFSLAF LFVARKVAKKIGLVDPNYRKRHQ GLIPLVGGISVFAGICFTFLITNQHIPHFRLYLG CAGLLVFVGALDDRFDISVKIRAF VQALVGIAMMAVAGLYLRS LGHAFGPWEMILGPF"



		GYVVTLFAVWAAINAFNMVDGIDG LLGGLSCVSFGAMGILLYQSGQMALALWCFAMIA AILPYILLNLGLLGRRYKVFMGDA GSTLIGFTAIWILLQTTQGNAHPINPVTALWIIA IPLMDMIAIMYRRLRKGMSPFSPD RQHIHHLIMRAGFTSRQAFVLITLAAALLAAGV IGERLTFVPEWVMLALFLLAFILY GYCIKRAWRVARFIKRTKRRMRRASQNKHES" /gene="rfe"
misc-feature	join(202848..202907, 202968..203036, 203049..203102, 203139..203198, 203226..203294, 203313..203372, 203385..203453, 203472..203540, 203568..203624, 203715..203768, 203796..203849)	/locus-tag="YE0169" /inference="protein motif:TMHMM:2.0" /note="11 probable transmembrane helices predicted for YE0169 by TMHMM2.0 at aa 5-24, 45-67, 72-89, 102-121,131-153, 160-179, 184-206, 213-235, 245-263, 294-311 and 321-338"
misc-feature	203052..203543	/gene="rfe" /locus-tag="YE0169" /inference="protein motif:PFAM:PF00953" /note="Pfam match to entry PF00953 Glycos-transf-4,Glycosyl transferase, score 20.2, E-value 9.7e-08"
gene	203969..205030	/gene="wzzE" /locus-tag="YE0170" /note="synonyms: b3785, wzz"
CDS	203969..205030	/gene="wzzE" /locus-tag="YE0170" /codon-start=1 /transl-table=11 /product="putative lipopolysaccharide biosynthesis protein" /protein-id="CAL10309.1" /db-xref="GI:122087528" /db-xref="GOA:A1JI71" /db-xref="InterPro:IPR003856" /db-xref="UniProtKB/TrEMBL:A1JI71" /translation="MSTDKTGSTHNEPSVDNELD IRSLCRTLWRGKVWIIIGMAILFAA IALGVSYLVKQQWSATAITDRPTVNNLGGYYSQQ QFLRNLNDRINSAASSEQPGISDE AYGEFITQLAAYDTRDFWLQTDYYKQVEGDAK ADAALLDELVNNIVFTPRDDKKML NDSIKLTAETASDSNKLLRSYIDFASQRAASHLN DEIEGAWAARTQSMKAQVKRQEAV AKAVFDREVTAVTQALKVASQQGINRNQTDTPAE QLPDSKMFMLGKPMLEARLETLQA TGPSFDIDYDQNRAMLATLNVGPTLDKTFQTYRY

		L RTPEDPVTRDSPRRVFLLIMWGA IGALVGAGVVLVRRTSRTE"
misc-feature	204017..204520	/gene="wzzE" /locus-tag="YE0170" /inference="protein motif:PFAM:PF02706" /note="Pfam match to entry PF02706 wzz, Chain length determinant protein, score 45.5, E-value 7.8e-11"
misc-feature	join(204059..204127, 204947..205006)	/gene="wzzE"  /locus-tag="YE0170" /inference="protein motif:TMHMM:2.0" /note="2 probable transmembrane helices predicted for YE0170 by TMHMM2.0 at aa 31-53 and 327-346"
gene	205110..206240	/gene="rffE" /locus-tag="YE0171" /note="synonyms: nfrC, wecB"
CDS	205110..206240	/gene="rffE" /locus-tag="YE0171" /codon-start=1 /transl-table=11 /product="UDP-N-acetylglucosamine 2-epimerase" /protein-id="CAL10310.1" /db-xref="GI:122087529" /db-xref="GOA:A1JI72" /db-xref="InterPro:IPR003331" /db-xref="UniProtKB/TrEMBL:A1JI72" /translation="MKVLTVFGTRPEAIKMAPLV HALAQDEAFESRVCVTAQHREMLD QVLRLEFIQPDYDLNIMKPGQGLTEITCRILEGL KPVLAEFKPDVILVHGDTTTLST SLAAFYHRIPVGHVEAGLRTGNLYSPWPPEANRQ LTGHLAMYHFAPTENSQRNLLREM VPDNRIFVTGNTVIDALFWVRDRVMNNPQLRASL AERYPFIDTNKKMILVTGHRRESF GGGFERICSALAEIALKHPEVQVVYPVHLNPNVS EPVNRILKGIDNIIILDPQDYLPF VYLMNHAYLILTDSGGIQEEAPSLGKPVLMRDT TERPEAVDSGTVLLVGTNINKIVD AVTRLLTDEYAHQMTRAHNPYGDGHACQRILEA LKNHQVTL"
misc-feature	205233..206219	/gene="rffE" /locus-tag="YE0171" /inference="protein motif:PFAM:PF02350" /note="Pfam match to entry PF02350 Epimerase-2, UDP-N-acetylglucosamin e 2-epimerase, score 723.5, E-value 6e-215"
gene	206237..207499	/gene="rffD" /locus-tag="YE0172" /note="synonyms: b3787, wecC"
CDS	206237..207499	/gene="rffD" /locus-tag="YE0172" /codon-start=1 /transl-table=11 /product="putative

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sig-peptide	206237..206305	
misc-feature	206246..206827	/gene="rffD" /locus-tag="YE0172" /inference="protein motif:PFAM:PF03721" /note="Pfam match to entry PF03721 UDPG-MGDP-dh-N,UDP-glucose/GDP-man nose dehydrogenase family, NAD binding domain, score 299.1, E-value 3.6e-87"
misc-feature	206849..207127	/gene="rffD" /locus-tag="YE0172" /inference="protein motif:PFAM:PF00984" /note="Pfam match to entry PF00984 UDPG-MGDP-dh,UDP-glucose/GDP-manno se dehydrogenase family, central domain, score 153.9, E-value 1.9e-43"
misc-feature	207206..207481	/gene="rffD" /locus-tag="YE0172" /inference="protein motif:PFAM:PF03720" /note="Pfam match to entry PF03720 UDPG-MGDP-dh-C,UDP-glucose/GDP-man nose dehydrogenase family, UDP binding domain, score 91.3, E-value 1.2e-24"
gene	207496..208563	/gene="rffG"

CDS	207496..208563	/locus-tag="YE0173" /gene="rffG" /locus-tag="YE0173" /codon-start=1 /transl-table=11 /product="dTDP-D-glucose-4,6-dehyd ratase" /protein-id="CAL10312.1" /db-xref="GI:122087531" /db-xref="GOA:A1JI74" /db-xref="InterPro:IPR001509" /db-xref="InterPro:IPR005888" /db-xref="InterPro:IPR016040" /db-xref="UniProtKB/TrEMBL:A1JI74" /translation="MRRILVTGGAGFIGSAVVRH IIDGTSDSVVVVDKLTLYAGNLESL AVVAHSERYAFEQVDICDRAELDRVFAQYQPDVV MHLAAESHVDRSIDGPAAFIETNV VGTIYQMLEAARHYWQPLDAKKKLAFRFHISTDE VYGDHLGTTDDLFTETTPYAPSSPY SASKASSDHLVRAWLRTYGLPTLVTNCSNNYGPY HFPEKLIPLVILNALAGKPLPVYG NGAQVRDWLFVEDHARALYQVVTEGVVGETYNIG GHNERKNIEVVETICALLDELVPE KPAGIARYRDLITFVKDRPGHDMRYAIDASKIER ELGWRPQETFESGIRKTVLWYLN KSWWQVRVQDGSYAGERLGLGD"
misc-feature	207505..208500	/gene="rffG" /locus-tag="YE0173" /inference="protein motif:PFAM:PF01370" /note="Pfam match to entry PF01370 Epimerase, NAD dependent epimerase/dehydratase family, score 720.1,E-value 6.4e-214"
gene	208794..209675	/gene="rffH"
CDS	208794..209675	/locus-tag="YE0174" /gene="rffH" /locus-tag="YE0174" /codon-start=1 /transl-table=11 /product="glucose-1-phosphate thymidyltransferase" /protein-id="CAL10313.1" /db-xref="GI:122087532" /db-xref="GOA:A1JI75" /db-xref="InterPro:IPR005835" /db-xref="InterPro:IPR005907" /db-xref="UniProtKB/TrEMBL:A1JI75" /translation="MKGIILAGGSGTRLHPITRG VSKQLLPVYDKPMIYYPLSVLMLA GIRDILIIISTPEDLPSFQRLGNGDEFGINLSYA AQPSPDGLAQAFIIGEEFIGNEPC CLVLGDNIYFGQGFSKPKLKAVAAREHGATVFGYQ VMDPERFGVVEFDDDFRALSIEEK PTQPKSNWAVTGLYFYDNQVVDFAKKVKPSSRGE LEITSINQMYLDRGELTVELLGRG FAWLDTGTGTHDSLIEASTFVQTVEKRQGFKIACLE EISWRNGWLDDDGVRRAATALAKT GYGKYLDDLHARPRQY"
misc-feature	208797..209513	/gene="rffH" /locus-tag="YE0174"

		/inference="protein motif:PFAM:PF00483" /note="Pfam match to entry PF00483 NTP-transferase,Nucleotidyl transferase, score 390.3, E-value 1.2e-114"
gene	209764..210390	/gene="rffC" /locus-tag="YE0175" /note="synonyms: b3790, wecD"
CDS	209764..210390	/gene="rffC" /locus-tag="YE0175" /codon-start=1 /transl-table=11 /product="putative lipopolysaccharide biosynthesis protein" /protein-id="CAL10314.1" /db-xref="GI:122087533" /db-xref="GOA:A1JI76" /db-xref="InterPro:IPR000182" /db-xref="InterPro:IPR012752" /db-xref="InterPro:IPR016181" /db-xref="UniProtKB/TrEMBL:A1JI76" /translation="MDAFTLTQAKVPTHRLDLID SLGQLGFKLVEGEVDLVLLVEEKD RVGTENASSAIDTGTYYQRLATTADIPLLRSVAA QAFALSRFRAPWYDPQDSGRFYAL WAEKAVLGTFDHQCLLVMDTFGQPAGFVTLRDLQ DGSARIGLLAVFPDAQGKGIGSLL MSAAKQWCQSHGLHRLRVATQMSNVAALRLYIRS GASIESTAYWLCRG"
misc-feature	210115..210354	/gene="rffC" /locus-tag="YE0175" /inference="protein motif:PFAM:PF00583" /note="Pfam match to entry PF00583 Acetyltransf,Acetyltransferase (GNAT) family, score 73.5, E-value 2.9e-19"
gene	210392..211522	/gene="rffA" /locus-tag="YE0176" /note="synonyms: b3791, wecE"
CDS	210392..211522	/gene="rffA" /locus-tag="YE0176" /codon-start=1 /transl-table=11 /product="putative lipopolysaccharide biosynthesis protein" /protein-id="CAL10315.1" /db-xref="GI:122087534" /db-xref="GOA:A1JI77" /db-xref="InterPro:IPR000653" /db-xref="InterPro:IPR012749" /db-xref="InterPro:IPR015421" /db-xref="InterPro:IPR015422" /db-xref="UniProtKB/TrEMBL:A1JI77" /translation="MIPFNAPPVVGTGLGYMQAA ITSGKLCGDGGFTRRCQQWMEKRF DCPKVLLTPSCTASLEMAALLLDIKPGDEVIMPS FTFVSTANAFVLRGAKMVFVDIRP DTMNIDETKIEAAITDKTKVIVPVHYAGVACEMD

		TIMALAKKHNLFFVEDAAQGVMS YKGKALGTIGHIGCFSFHETKNYTAGGEGGATLI NDPSLIDRAEIIREKGTNRSQFFR GQVDKYTWTDIGSSYLMSDLQAAYLWGQLEAADQ INQRRLLALWHTYYDAFKPLADAGR IDLPVIPGNLAQNAHMFYIKLRDIEDRSKFISFL KEAEIMAVFHYIPLHACPAGEEFG RMDGEDRFTTKESERLVRPLIFYNLTDVNQSTVI NTVLSFFA"
misc-feature	210410..211507	/gene="rffA" /locus-tag="YE0176" /inference="protein" motif:PFAM:PF01041" /note="Pfam match to entry PF01041 DegT-DnrJ-EryC1, DegT/DnrJ/EryC1/St rS aminotransferase family, score 291.1, E-value 9.2e-85"
misc-feature	210758..210790	/gene="rffA" /locus-tag="YE0176" /inference="protein" motif:Prosite:PS00013" /note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site."
gene	211524..212780	/gene="wzxE" /locus-tag="YE0177" /note="synonyms: b3792, wzx"
CDS	211524..212780	/gene="wzxE" /locus-tag="YE0177" /codon-start=1 /transl-table=11 /product="putative lipopolysaccharide biosynthesis protein" /protein-id="CAL10316.1" /db-xref="GI:122087535" /db-xref="GOA:A1JI78" /db-xref="InterPro:IPR002797" /db-xref="UniProtKB/TrEMBL:A1JI78" /translation="MSLAKASIWTAGSTLIKIGV GLLVVKLLAVTFGPSGVGQAGNFR QLITVLGVLSGAGIFNGITKYVAEYHQQPERLRA VLGTSSAIVLGFSTLLALIFLLAA KPVSIALFGHADYQNVVRAVAFIQMGIAVANLFL AILKGYRDAMGNALAVIGGSLIGV VAYYICFRIGGYPGALVGLALVPALVVIPAAAML IRRKTIPLSYLKLSWDKALASHLG KFTIMALITSVTLVPVAYVMMRNLLADRYGWDAVG IWQGVSSISDAYLQFITASFTVYL LPTLSRLKAKADISREILRSLKFVLPVAVATASLI VWLLRDFAIWLLFSHQFTAMRDLF AWQLVGDVCLKVGSYVFGYLVIAKASLRFYILTEV SQFLLLTGFAHWLIPMNGSLGAAQ AYMATYIVYFALCSCVFLMYRRHSSP"
misc-feature	211530..212375	/gene="wzxE" /locus-tag="YE0177" /inference="protein" motif:PFAM:PF01943" /note="Pfam match to entry PF01943 Polysacc-synt, Polysaccharide biosynthesis protein, score 36.7, E-value 3.4e-08"

misc-feature	join(211560..211628, 211656..211724, 211761..211829, 211872..211940, 211959..212027, 212040..212108, 212169..212237, 212280..212348, 212409..212477, 212520..212588, 212607..212675, 212685..212753)	/gene="wzxE"  /locus-tag="YE0177" /inference="protein" motif:TMHMM:2.0" /note="12 probable transmembrane helices predicted for YE0177 by TMHMM2.0 at aa 13-35, 45-67, 80-102, 117-139,146-168, 173-195, 216-238, 253-275, 296-318, 333-355,362-384 and 388-410"
misc-feature	212712..212744	/gene="wzxE" /locus-tag="YE0177" /inference="protein" motif:Prosite:PS00013" /note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site."
gene	212803..213888	/locus-tag="YE0178"
CDS	212803..213888	/locus-tag="YE0178" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10317.1" /db-xref="GI:122087536" /db-xref="GOA:A1JI79" /db-xref="InterPro:IPR009993" /db-xref="UniProtKB/Swiss-Prot:A1J I79" /translation="MTTLIHVLGSDIPHHNLTVL RFFNDVLTTRVPAEQARHFMVAAK ETAPFSSFPQLEIETHSNKKTAEAVITRAQASR DTRFFWHGQFNATLWLALLSGKIK PHQVYWHIWGADLYEDAKSLKFRLFYLLRRIAQG RVGHVFATRGDLIYFQQRHPRVPA SLLYFPTRMDAALTGVNIDKPLAGPMTILVGNSG DSTNRHIEALKAIHQFGPDARVI LPMGYPANNELYIEKVRQAGLALFAADNLRILTE QIPFDDYLNILRECDLG YFIFNRQ QGIGTLCLLTQFGVPFVLSRKNPFWQDLAEQHIP VLFYGDSDLDEPLIREAQRQLAGLD KHAI AFFNP NYIEGWQQALALAAGEHP"
gene	213885..215261	/gene="wecF" /locus-tag="YE0179"
CDS	213885..215261	/note="synonym: rfft" /gene="wecF" /locus-tag="YE0179" /codon-start=1 /transl-table=11 /product="probable 4-alpha-L-fucosyltransferase"

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                    214557..214616,
                    214893..214961,
                    215022..215075,
                    215103..215171)
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                    /db-xref="GOA:A1JI80"
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                    PVFTMNRVETNLTWMLLALVAIGTVGIFFMQNGF
                    LLFKLDSYSKIFSSDVSGVALKRF
                    FYFFIPAMLVVYFLRQDMRAWFFFLASTVAFGIL
                    TYVIVGGTRANIIIAFSLFLFIGI
                    VRGWITLWMLAAAGVFGIVGMFWLALKRYGLDVN
                    GAEAFYTFLYLTRDTFSPWENLGL
                    LLQNYDKIDFQGLAPIIRDIFYVIPSSLWPAPD
                    LVLNTANYFTWDVLDNHSGLAISP
                    TLIGSLVVMGGVLFIPLGAIVVGLIIKWFDWLYE
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/misc-feature      214716..214763
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                    /inference="protein"
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                    /note="11 probable transmembrane
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                    110-132,152-174, 181-200, 204-223,
                    225-244, 337-359, 380-397 and
                    407-429"
                    /gene="wecF"
                    /locus-tag="YE0179"
                    /inference="protein"
                    motif:Prosite:PS00225"
                    /note="PS00225 Crystallins beta
                    and gamma 'Greek key' motif
                    signature."

/misc-feature      215106..215138
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                    /locus-tag="YE0179"
                    /inference="protein"
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                    membrane lipoprotein lipid
                    attachment site."

gene              215354..216028
                    /gene="wecG"
                    /locus-tag="YE0180"
                    /note="synonym: rffM"

CDS               215354..216028
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                    /locus-tag="YE0180"
                    /codon-start=1
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misc-feature	215465..215980	/gene="wecG" /locus-tag="YE0180" /inference="protein" motif:PFAM:PF03808" /note="Pfam match to entry PF03808 Glyco-tran-WecB, Glycosyl transferase WecB/TagA/CpsF family, score 292.2, E-value 4.2e-85"
gene	216379..217770	/locus-tag="YE0181"
CDS	216379..217770	/locus-tag="YE0181" /codon-start=1 /transl-table=11 /product="putative permease protein" /protein-id="CAL10320.1" /db-xref="GI:122087539" /db-xref="GOA:A1JI82" /db-xref="InterPro:IPR002293" /db-xref="InterPro:IPR004840" /db-xref="InterPro:IPR004841" /db-xref="UniProtKB/TrEMBL:A1JI82" /translation="MADNEEKKGLHRGLEARHIE LIALGGTIGVGLFMGSASTLKWAG PSVLLAYIIAGLFVFFIMRSMGEMLYLEPVAGSF AVYAHKYLSPYFGYLTAWGYWFMW IAVGISEITAIGVYVQFWFPEIPQWLPAIAGVAI VALANLAAVRLYGELEFWFAMIKV TTIIVMILVGLGVIFFGFGNHGQPIGFDNLTAHG GFFAGGWKGFMFALCIVVASYQGV ELVGITAGEARNPQVTLKRAINILWRILIFYVG AIFVIVTIFPWDGIGTGGSPFVLT FAKIGIVSAAGIINFVVLTAALSGCNSGMYSGGR MLYALAKNRQLPACLTKLSASGVP VYCIAVTILCLMVGSSLNYIIPNPQQVFVYVYSA SVLPGMVPWFVVLVSQLRFRQAHV EALKQHPFKSIMFPYVNYLTIAFLICVLVGMGLN PDTRLSSLVGVIFLGLVTACYFCL GMHNKVPVEIKRR"
misc-feature	216406..217737	/locus-tag="YE0181" /inference="protein" motif:PFAM:PF00324" /note="Pfam match to entry PF00324 aa-permeases, Amino acid permease, score 500.3, E-value 9.3e-148"
misc-feature	join(216439..216492, 216502..216561,	/locus-tag="YE0181"

	216661..216729, 216757..216825, 216844..216912, 216955..217023, 217099..217167, 217195..217263, 217375..217443, 217456..217524, 217585..217653, 217663..217731)	/inference="protein motif:TMHMM:2.0" /note="12 probable transmembrane helices predicted for YE0181 by TMHMM2.0 at aa 21-38, 42-61, 95-117, 127-149,156-178, 193-215, 241-263, 273-295, 333-355, 360-382,403-425 and 429-451"
misc-feature	216505..216597	/locus-tag="YE0181" /inference="protein motif:Prosite:PS00218" /note="PS00218 Amino acid permeases signature."
misc-feature	217249..217281	/locus-tag="YE0181" /inference="protein motif:Prosite:PS00013" /note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site."
misc-feature	217684..217716	/locus-tag="YE0181" /inference="protein motif:Prosite:PS00013" /note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site."
gene	217919..217995	/gene="tRNA-Arg (CCG)"
tRNA	217919..217995	/gene="tRNA-Arg (CCG)" /product="tRNA-Arg" /note="codon recognized: CGG"
gene	218079..218154	/gene="tRNA-His (GTG)"
tRNA	218079..218154	/gene="tRNA-His (GTG)" /product="tRNA-His" /note="codon recognized: CAC"
gene	218170..218256	/gene="tRNA-Leu (CAG)"
tRNA	218170..218256	/gene="tRNA-Leu (CAG)" /product="tRNA-Leu" /note="codon recognized: CUG"
gene	218332..218408	/gene="tRNA-Pro (TGG)"
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gene	complement(219361..2205 60)	/gene="hemY" /locus-tag="YE0184"
CDS	complement(219361..2205 60)	/gene="hemY" /locus-tag="YE0184" /codon-start=1 /transl-table=11 /product="putative protoheme IX biogenesis protein" /protein-id="CAL10321.1"

		/db-xref="GI:122087540" /db-xref="GOA:A1JI83" /db-xref="InterPro:IPR005254" /db-xref="InterPro:IPR010817" /db-xref="InterPro:IPR011990" /db-xref="InterPro:IPR013026" /db-xref="InterPro:IPR013105" /db-xref="UniProtKB/TrEMBL:A1JI83" /translation="MLRVLLLFLILTAGIVLGPM LAGHQGYVLIQTDNYNVETSVTGL VIMLVLVLVAFLIVEWILRRIFRTGARTRGWFLG RKRTRARKQTKAALIKLAEGDFKQ VEKLLTRNADHAEQPMVNYLLAAEAAQQRGDEFR TNQYLERAAEVADTDQLPVDITRV RIQLAQGHVHAARHGVDRLLDQAPRHPEVLRRLAE QAYLRSGAYSSLLEILPAMSKVQV HTAEETIAALEQQAYIGMMNQCMEEGSDGLKRWW KDQSRKVRNEIPLQVALAEHLIEC DDSDVAAQQIILDGLKRQYDERLVLLIPRLKSGNP EPIEKSLRQHIKQHGATPLLNSTL GQLMLKHGEWEKASEAFKAALAQRPDGYDYAWLA DALDKLHRPEDAAQARREGLLLTL RQNGESL"
sig-peptide	complement(220492..220560)	/gene="hemY"  /locus-tag="YE0184" /note="Signal peptide predicted for YE0184 by SignalP 2.0 HMM (Signal peptide probability 0.919) with cleavage site probability 0.457 between residues 23 and 24"
misc-feature	complement(220072..220101)	/gene="hemY"  /locus-tag="YE0184" /inference="protein motif:Prosite:PS00215" /note="PS00215 Mitochondrial energy transfer proteins signature."
misc-feature	complement(join(220375..220443, 220480..220548))	/gene="hemY"  /locus-tag="YE0184" /inference="protein motif:TMHMM:2.0" /note="2 probable transmembrane helices predicted for YE0184 by TMHMM2.0 at aa 5-27 and 40-62"
gene	complement(220563..221687)	/gene="hemX"
CDS	complement(220563..221687)	/locus-tag="YE0185" /gene="hemX"  /locus-tag="YE0185" /codon-start=1 /transl-table=11 /product="putative uroporphyrin-III C-methyltransferase" /protein-id="CAL10322.1" /db-xref="GI:122087541" /db-xref="GOA:A1JI84" /db-xref="InterPro:IPR007470"

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misc-feature	complement (221517..221585)	/gene="hemX"  /locus-tag="YE0185" /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted for YE0185 by TMHMM2.0 at aa 35-57"
gene	complement (221720..222466)	/gene="hemD"  /locus-tag="YE0186"
CDS	complement (221720..222466)	/gene="hemD"  /locus-tag="YE0186" /codon-start=1 /transl-table=11 /product="uroporphyrinogen-III synthase" /protein-id="CAL10323.1" /db-xref="GI:122087542" /db-xref="GOA:A1JI85" /db-xref="InterPro:IPR003754" /db-xref="UniProtKB/TrEMBL:A1JI85" /translation="MTILVTRPSPAGEQLVSRLR ALGRVAYHAPLIDFSPGDDL PKLP ALLQDMQAGDLVFALSQNAVRYANPLLKRNNLSW PAQLSYAIGRNTALALHTASRLH VTFPPTGETSEMLLSLPDLQQLTGKKALLLRNG GRELLGESLRERGATVTFCECYQR SPIFYDGSEQSAHWQRSGVDILVVTSGEMLQQIY TLVPDYRSSWLLRCRLVVVSDRL AALAAQMGSNIRVAENADNDALIRALQDF"
misc-feature	complement (221735..222439)	/gene="hemD"  /locus-tag="YE0186" /inference="protein motif:PFAM:PF02602" /note="Pfam match to entry PF02602 HEM4,Uroporphyrinogen-III synthase HemD, score 165.6, E-value 5.5e-47"
gene	complement (222463..223404)	/gene="hemC"  /locus-tag="YE0187"
CDS	complement (222463..223404)	/note="synonym: popE" /gene="hemC"

		/locus-tag="YE0187" /codon-start=1 /transl-table=11 /product="porphobilinogen deaminase" /protein-id="CAL10324.1" /db-xref="GI:122087543" /db-xref="GOA:A1JI86" /db-xref="InterPro:IPR000860" /db-xref="UniProtKB/Swiss-Prot:A1J I86" /translation="MLDKIIRIATRQSPLALWQA HYVQHLLQANHPGLQVELVPMVTR GDIILDTPLAKVGGKGLFVKELELALLEGRADIA VHSMKDVPIAFPEGLGLVTICERD DPRDAFVSINYAHLDELPAQSIVGTSSLRRQCQL RERRPDLIIRDLRGNVGTIRLAKLD KGEYHAIILAVAGLKRLGLETRIRYAMPAEESLP AVGQGAVGIECRLDDNFTRQLLAP LNHRETELRVCAERAMNTRLEGGCQVPIGSYael DGDTLWLRALVGAPDGSEIIRGER RGPAAENAEQMGVELADELLSRGAREILAEVYQDN PPL"
misc-feature	complement (222511..222732)	/gene="hemC"  /locus-tag="YE0187" /inference="protein motif:PFAM:PF03900" /note="Pfam match to entry PF03900 Porphobil-deamC, Porphobilinogen deaminase, C-terminal domain, score 117.1, E-value 2.1e-32"
misc-feature	complement (222664..222714)	/gene="hemC"  /locus-tag="YE0187" /inference="protein motif:Prosites:PS00533" /note="PS00533 Porphobilinogen deaminase cofactor-binding site."
misc-feature	complement (222754..223392)	/gene="hemC"  /locus-tag="YE0187" /inference="protein motif:PFAM:PF01379" /note="Pfam match to entry PF01379 Porphobil-deam, Porphobilinogen deaminase, dipyromethane cofactor binding domain, score 471.6, E-value 4.3e-139"
gene	223809..226355	/gene="cyaA" /locus-tag="YE0189" /note="synonym: cya"
CDS	223809..226355	/gene="cyaA" /locus-tag="YE0189" /codon-start=1 /transl-table=11 /product="adenylate cyclase" /protein-id="CAL10325.1" /db-xref="GI:122087544" /db-xref="GOA:A1JI87" /db-xref="InterPro:IPR000274" /db-xref="UniProtKB/TrEMBL:A1JI87"

		/translation="MYLYIETLKQRLDAINQLRV DRALAAMGPAFQKVYSLPTLLHC HHPLMPGYLDGNVPHGICLFTPNETQQDYLSEVE AKWGQPLQQSVGGELPITGVYSMG STSSIGQCHTSDLDIWVCHQAWLDAEERNRLQKK CSLLEKWAASMGVEVSFFLIDENR FRHNASGSLGGEDCGSTQHILLLDEFYRSAVRLA GKRILWNMVPVEEENNYDDYVLSL YAQGVLTNPNEWLDLGGSTLSAEYFGASLWQLY KSIDSPYKAVLKTVLLEAYSWEYP NSQLLAMEIKQRLHAGEIVAFGLDAYCMMLDRV RYLTQINDTTRLNLVRRCFYLVKVC EKLSRTPASVGWRREILSQLVSEWGSDES DNRANWKIERVREAHNELLDAMMQ SYRNLIRFARRNNLSVSASPQDIGVLRKLYAAF EALPGKVTLVNPQISPDLSEEHLT FIHVPAGRANRPGWYLYNQAPSMETIVSHQPLEY NRYLNKLVSWAYFNGLLTSKTHLH IKSANLCDTVKLQELVTDISHHFPLRLPAPTPKA LYSPEIRHLAIIIVNLEHDPTAAF RNQVVHFD FRKLDVFSFGEQQCLVGSIDLLYRN SWNEVRTLHFSGEQAVLEALKTIL GKMHQDAAPPESDVFCYSQHLRGLIRTRIQQLV SECIELRLSSTRQEPGRFKAVRVA GQTWGLFFERLSVSVQKLENAIEFYGAISNNKLH GLSIQVETDQIHLPPVVDGFASEG IIQFFFEGTADEKGFNIYILDETNRVEVYHHCEG SKEELVRDVSRYSSSHDRFTYGS SFINFNLPQFYQIVQLDGRTQVIPFRSNALSHLH IADKETSAPAQQFQLH"
misc-feature	223809..226298	/gene="cyaA" /locus-tag="YE0189" /inference="protein" motif:PFAM:PF01295" /note="Pfam match to entry PF01295 Adenylate-cyclase, Adenylate cyclase, class-I, score 2160.8, E-value 0"
misc-feature	224085..224102	/gene="cyaA" /locus-tag="YE0189" /inference="protein" motif:Prosites:PS00343" /note="PS00343 Gram-positive cocci surface proteins 'anchoring' hexapeptide."
misc-feature	224532..224567	/gene="cyaA" /locus-tag="YE0189" /inference="protein" motif:Prosites:PS01092" /note="PS01092 Adenylate cyclases class-I signature 1."
misc-feature	225600..225644	/gene="cyaA" /locus-tag="YE0189" /inference="protein" motif:Prosites:PS01093" /note="PS01093 Adenylate cyclases class-I signature 2."
gene	complement(226526..226846)	/gene="cyaY"
CDS	complement(226526..226846)	/locus-tag="YE0190" /gene="cyaY" /locus-tag="YE0190"

		/codon-start=1 /transl-table=11 /product="frataxin-like protein" /protein-id="CAL10326.1" /db-xref="GI:122087545" /db-xref="InterPro:IPR002908" /db-xref="UniProtKB/Swiss-Prot:A1J I88" /translation="MNDSEFHQLADQLMLCIEET LDGFSGSDSIDYETNGGVMTLTFE NGSKIVINRQEPLHQVWLATKAGGYHFDYREGHW YCSRSGEFFTKLSEAATAQAGEV VSFS"
misc-feature	complement(226529..226846)	/gene="cyaY"  /locus-tag="YE0190" /inference="protein motif:PFAM:PF01491" /note="Pfam match to entry PF01491 Frataxin-Cyay,Frataxin-like domain, score 242.5, E-value 3.8e-70"
gene	226960..227163	/locus-tag="YE0191"
CDS	226960..227163	/locus-tag="YE0191" /codon-start=1 /transl-table=11 /product="putative lipoprotein" /protein-id="CAL10327.1" /db-xref="GI:122087546" /db-xref="UniProtKB/TrEMBL:A1JI89" /translation="MKKKLCWSLTAMMVFALSGC GLKGPLYFPPSDKPKVETTKQDSG QVDKNQQGLPGDSKPTQSIAGPQ"
sig-peptide	226960..227028	/locus-tag="YE0191" /note="Signal peptide predicted for YE0191 by SignalP 2.0 HMM (Signal peptide probabiltiy 0.994) with cleavage site probability 0.378 between residues 23 and 24"
misc-feature	226972..227040	/locus-tag="YE0191" /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted for YE0191 by TMHMM2.0 at aa 5-27"
misc-feature	226987..227019	/locus-tag="YE0191" /inference="protein motif:Prosite:PS00013" /note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site."
gene	227252..228076	/gene="dapF"
CDS	227252..228076	/locus-tag="YE0192" /gene="dapF" /locus-tag="YE0192" /codon-start=1 /transl-table=11 /product="diaminopimelate epimerase" /protein-id="CAL10328.1" /db-xref="GI:122087547" /db-xref="GOA:A1JI90" /db-xref="InterPro:IPR001653"

		/db-xref="UniProtKB/Swiss-Prot:A1J I90" /translation="MQFSKMHG LGNDFMVVDAVT QNVYFSP ELIRRLADRHTGVGFDQ MLVVEPPYDPELDFHYRIFNADGSEVSQCGNGAR CFARFVRLKGLTNKRDISVSTQTG RMILSVTEDELVCVNMGEPNFEPQSVPFRAAKAE KTYILRAAEHTVLCGVVSMGNPHC VMQVDDVSVANVALLGPVLESHERFPERANIGFM QVVSREHIRLRVYERGAGETQACG SGACAAVAVGIQQELLGEEVHVELPGGSLHISWK GPGHPLYMTGPATHVYDGF IHL"
misc-feature	227258..227623	/gene="dapF" /locus-tag="YE0192" /inference="protein" motif:PFAM:PF01678" /note="Pfam match to entry PF01678 DAP-epimerase, Diaminopimelate epimerase, score 179.5, E-value 3.5e-51"
misc-feature	227441..227485	/gene="dapF" /locus-tag="YE0192" /inference="protein" motif:Prosite:PS01326" /note="PS01326 Diaminopimelate epimerase signature."
misc-feature	227702..228052	/gene="dapF" /locus-tag="YE0192" /inference="protein" motif:PFAM:PF01678" /note="Pfam match to entry PF01678 DAP-epimerase, Diaminopimelate epimerase, score 182.3, E-value 5.2e-52"
gene	228170..228874	/locus-tag="YE0193"
CDS	228170..228874	/locus-tag="YE0193" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10329.1" /db-xref="GI:122087548" /db-xref="InterPro:IPR007435" /db-xref="UniProtKB/TrEMBL:A1JI91" /translation="MKSSEEQALAGIELDDDAVM QYLLQNPDDFFIRNARLVEQMHIPH PVRGTVSLVEWQLGRQRNQIGQLEEEITLLMEQA GLNEVLFNRLQLQGNLAAASSLQ DMLNRLQRWARDFFLAGANVRLFTDRWQIGAPSD FTHLGLSRHAF EPMRIQRLGNARH YLGSLNGPELLLLLPQAKQVGSVALSLLGKEGDL GVIVFSSRDIQHYQQGMGTVM LNQ LSMLLP SLLERWIEPV"
gene	228871..229782	/gene="xerC"
CDS	228871..229782	/locus-tag="YE0194" /gene="xerC" /locus-tag="YE0194" /codon-start=1 /transl-table=11 /product="putative integrase/recombinase" /protein-id="CAL10330.1"



		/db-xref="GI:122087549" /db-xref="GOA:A1JI92" /db-xref="InterPro:IPR002104" /db-xref="InterPro:IPR004107" /db-xref="InterPro:IPR011931" /db-xref="InterPro:IPR013762" /db-xref="UniProtKB/TrEMBL:A1JI92" /translation="MTDFSTSLAPQVEAFLRYLK VERQLSPLTITSYRRQLQALMEMG EQMGLAHWQTLDAAQVRSLSRSKRAGLHSSSLA LRLSALRSFLNWLVSQGVQLANPA KGVSTPRSGRHLPKNIDVDEVAKLLDIDLNDPLA VRDRAMLEVMYGAGLRLSELVGMN CKHVDLASGEVWVMGKGSKERKVPIGKTAVKWLD HWLELRELFEPQDDAIFLANTGKR ISARNVQKRFAEWGVKQGVSSHIHPKLRHSFAT HMLESSGDLRAVQELLGHANLTTT QIYTHLDFQHLATVYDAAHPRAKRGKS"
misc-feature	228898..229158	/gene="xerC" /locus-tag="YE0194" /inference="protein motif:PFAM:PF02899" /note="Pfam match to entry PF02899 Phage-integr-N, Phage integrase, N-terminal SAM-like domain, score 104.1, E-value 1.8e-28"
misc-feature	229222..229737	/gene="xerC" /locus-tag="YE0194" /inference="protein motif:PFAM:PF00589" /note="Pfam match to entry PF00589 Phage-integrase, Phage integrase family, score 208.0, E-value 9.4e-60"
gene	229782..230498	/locus-tag="YE0195"
CDS	229782..230498	/locus-tag="YE0195" /codon-start=1 /transl-table=11 /product="putative haloacid dehalogenase-like hydrolase" /protein-id="CAL10331.1" /db-xref="GI:122087550" /db-xref="GOA:A1JI93" /db-xref="InterPro:IPR005834" /db-xref="InterPro:IPR006439" /db-xref="UniProtKB/TrEMBL:A1JI93" /translation="MHFYRPLERISAITFDLDDT LYDNRPVISRTEQESVAFLLQYHP NLAQLQAADLHRFRRELLEQDPDIYHDVTQWRWH AIELGLMRHGLSKSEAQCGADAAM ENFALWRSRIYVPPATHDTLSALAEHYPLVAITN GNADPKACGLDNYFQFVLRSGPHG RAKPFDRMYHKAANHLDIPLKNILHVGDDLTTDV AGSLRCGMQACWVNDRQQSLMTAS DSRLLPHEISQLASLTALL"
misc-feature	229809..230411	/locus-tag="YE0195" /inference="protein motif:PFAM:PF00702" /note="Pfam match to entry PF00702 Hydrolase, haloacid dehalogenase-like hydrolase, score 92.0, E-value 7.7e-25"

gene	230599..232761	/gene="uvrD" /locus-tag="YE0196" /note="synonyms: mutU, pdeB, rad, recL"
CDS	230599..232761	/gene="uvrD" /locus-tag="YE0196" /codon-start=1 /transl-table=11 /product="DNA helicase II" /protein-id="CAL10332.1" /db-xref="GI:122087551" /db-xref="GOA:A1JI94" /db-xref="InterPro:IPR000212" /db-xref="InterPro:IPR005753" /db-xref="InterPro:IPR014016" /db-xref="InterPro:IPR014017" /db-xref="UniProtKB/TrEMBL:A1JI94" /translation="MDVSDLLDSLNEKQREAVAA PRCNLLVLGAGSGKTRVLVHRIA WLLSVENASPYSIIVTFTNKAAAEMRHRHRIEHLI GTSQGGMWIGTFHGLAHRLLRAHH MDANLPQDFQILDSDDQLRLKRLVKALNLDEKQ WPPRQAMWYINGKKDEGLRPQHIE SYGNPVEATWLRIYQAYQEACDRAGLVDFAEALL RAHELWLNKPHILNHYRERFTNIL VDEFQDTNNIQYAWIRLLAGDRSNVMIVGDDQDS IYGWRGAQVENIQRFKDFPGAET IRLEQNYRSTSNILTAANTLIANNDGRMGKNLWT DGAQGEPISLYCAFNELDEARFVV NRIKAWQDNGGALNDCAILYRSNAQSRVLEEALL QTAMPYRIYGGQRFFERQEIKDAL AYLRLISNRNDDAAFERVVNTPTRGIGDRTL DVI RQTARDRQLTLWQSTRAMLQEKVL AGRAASALQRFVELVDSL AHETADMPLHVQTD RV IRDSGLWSMYEQEKGEKQARVEN LEELVNATRQYSYQDEDQDLMPLQAFLSHAALEA GEGQADAYQDAVQLMTIHSAGLE FPQVFIVGMEEGMFPSQMSLDEGGRLEEERRLAY VGVTRAMQKLTLCYAESRRLYGKE VNHRPSRFIGELPQECVEEVRLRATVSRPVNHR MGTPMNENDSGFSLGQVRVHPKFG EGTIVNLEGSGEHSRLQVAFPGEGIKWLVAAYAR LEAV"
misc-feature	230626..232068	/gene="uvrD" /locus-tag="YE0196" /inference="protein" motif:PFAM:PF00580" /note="Pfam match to entry PF00580 UvrD-helicase, UvrD/REP helicase, score 747.8, E-value 2.9e-222"
misc-feature	230683..230706	/gene="uvrD" /locus-tag="YE0196" /inference="protein" motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-feature	232705..232734	/gene="uvrD" /locus-tag="YE0196" /inference="protein" motif:Prosite:PS00215" /note="PS00215 Mitochondrial energy transfer proteins"

gene complement(233186..2337 /locus-tag="YE0197"  
58) signature."

CDS complement(233186..2337 /locus-tag="YE0197"  
58)  
/codon-start=1  
/transl-table=11  
/product="putative TetR-family  
regulatory protein"  
/protein-id="CAL10333.1"  
/db-xref="GI:122087552"  
/db-xref="GOA:A1JI95"  
/db-xref="InterPro:IPR001647"  
/db-xref="UniProtKB/TrEMBL:A1JI95"  
/translation="MSMYEQGAFPSIIEVANAAQ  
LSRATAYRYFPTQSALVSAMVDES  
LGPILAWQPTQPDAGQRIAELLSFAYPRMLQHEG  
VLRAALHLSLQQWADNRSNPNNNEE  
KLIRGNRKRLCLKAVEPLEGKLTPEALQRVIHAF  
SLIYGSEVFMVLKDIWHLDDAGIQ  
DVTQWMGKAILLQAETDAKQAAQDESRMNK"

misc-feature complement(233639..2337 /locus-tag="YE0197"  
19)  
/inference="protein  
motif:PFAM:PF00440"  
/note="Pfam match to entry PF00440  
tetR, Bacterial regulatory  
proteins, tetR family, score 22.2,  
E-value 3.4e-05"

misc-feature complement(233666..2337 /locus-tag="YE0197"  
31)  
/note="Predicted helix-turn-helix  
motif with score 1464.000, SD 4.17  
at aa 10-31, sequence  
PSIIEVANAAQLSRATAYRYFP"

gene 234065..235297 /locus-tag="YE0198"

CDS 234065..235297 /locus-tag="YE0198"  
/codon-start=1  
/transl-table=11  
/product="conserved hypothetical  
protein"  
/protein-id="CAL10334.1"  
/db-xref="GI:122087553"  
/db-xref="InterPro:IPR003006"  
/db-xref="InterPro:IPR008322"  
/db-xref="InterPro:IPR010647"  
/db-xref="UniProtKB/TrEMBL:A1JI96"  
/translation="MPRHIFIATTTDTKGDELAY  
VSELIKATGLKTVTVDLSTKEARR  
AGGADITAETVASHHPDGRQAVFCGDRGRAISAM  
AVAFAERFIASRDDVAALLGLGGSG  
GTALITPAMQSLPIGIPKLMVSTMASGDVSGYIG  
ASDIAMMYSVTDIAGLNRISRRVL  
SNAAHQIAGAVYFAKEVFAQAELATDDKPALGLT  
MFGVTTPCIQAVSAALSAEYDCLV  
FHATGSGGKAMEKLAESGLLAGALDLTTTEVCDL  
LFDGVLACGPERFDAIAHSQIPYV  
GSCGALDMVNFSGPATIPVKYADRLFYEHNQVIT  
LMRTTKQENIEMARWIGEKLNRC  
GEVRFLIPQGGFSALDAPGQPFWDEKALQAFIHT  
LQETVIQTDKRRLVHYFPNINDPQ  
FAQAAVENFKEIAKTPSH"

misc-feature	234704..234724	/locus-tag="YE0198" /inference="protein motif:Prosite:PS00290" /note="PS00290 Immunoglobulins and major histocompatibility complex proteins signature."
gene	235324..236154	/locus-tag="YE0199"
CDS	235324..236154	/locus-tag="YE0199" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10335.1" /db-xref="GI:122087554" /db-xref="InterPro:IPR009215" /db-xref="UniProtKB/TrEMBL:A1JI97" /translation="MPKFQRQAILAKFREMIARR EPIIGGGAGTGLSAKCEEAGGIDL IVIYNSGRYRMAGRGLAGLLAYGNANEIVVDMA KEVLPVVKHTPVLAGVNGTDPFCQ FDQFLDQLKALGFSGVQNFPTVGLIDGNFRANLE ETGMGYGLEVDMIRLAHEKDLLTT PYVFS AEDAVAMTQAGADIIVPHMGLTTGGNIGA DTALKLADCVPLINKWAAA KAVR EDVIVLCHGGPISTPQDAQYIMDNCPQCDGFYGA SSMERLPTEIALTDTTKQFKNIKR"
gene	236657..237607	/gene="corA"
CDS	236657..237607	/locus-tag="YE0200" /gene="corA" /locus-tag="YE0200" /codon-start=1 /transl-table=11 /product="magnesium and cobalt transport protein" /protein-id="CAL10336.1" /db-xref="GI:122087555" /db-xref="GOA:A1JI98" /db-xref="InterPro:IPR002523" /db-xref="InterPro:IPR004488" /db-xref="UniProtKB/TrEMBL:A1JI98" /translation="MLSAFKLSNNRLSRLELDES DDLTTSLWVDLVEPEEGERERVQN ELGQSLATRPELDDIEASARFFEDDGLHIHSFF YYEDAEDHAGNSTVAFTIRDGRLY TLRERELPAFRLYMRARNQTLVDGNAYELLLDL FETKIEQLADEIENIYSDLEALSR VIMEGQQGDEYDAALSTLAEQEDIGWKVRLCLMD TQRALNFLVRKARLP SGQLEQARE VLRDIESLLPHNESLFQKVNFLMQAAMGFINIEQ NRIIKIFSVSVVFLPPTLVASSY GMNFEFMPELRWSFGYPAAIGLMIIAGLAPYLYF KRKNWL"
misc-feature	236717..237604	/gene="corA" /locus-tag="YE0200" /inference="protein motif:PFAM:PF01544" /note="Pfam match to entry PF01544 CorA, CorA-like Mg2+ transporter protein, score 394.8, E-value 5.5e-116"
misc-feature	join(237419..237475, 237518..237586)	/gene="corA"

		/locus-tag="YE0200" /inference="protein motif:TMHMM:2.0" /note="2 probable transmembrane helices predicted for YE0200 by TMHMM2.0 at aa 255-273 and 288-310"
gene	complement(237795..238685)	/gene="rarD"
CDS	complement(237795..238685)	/locus-tag="YE0201" /gene="rarD"  /locus-tag="YE0201" /codon-start=1 /transl-table=11 /product="putative membrane protein" /protein-id="CAL10337.1" /db-xref="GI:122087556" /db-xref="GOA:A1JI99" /db-xref="InterPro:IPR000620" /db-xref="InterPro:IPR004626" /db-xref="UniProtKB/TrEMBL:A1JI99" /translation="MDKQRTTRQGIFFALAAFYIW GIAPAYFKLIQQVPADEILTHRII WSFFFMLILLTVSRNWPQVRSIAIKNRKRLLLAV TAVLIASNWLLFIWAVNNHNMLEA SLGYFINPLVNVLFGLMFLGERFRMQWVAVALA FGGVLIQLWQFGSLPVI GLGLAIT FALYGLIRKKLGIDAQTGMLVETMWLLPIAAVYL FFIADSP TSHMGANAWSLNVLLAA AGVITTIPLLFFTAATRLRLSTLGFFQYLGPTL MFILAVTFYGETIGNDKMVTFVFI WAALLLFTLDALYTQRKLRG"
misc-feature	complement(join(237819..237878,237891..237959,237996..238064,238092..238151,238185..238238,238251..238304,238323..238391,238401..238469,238506..238574,238602..238661))	/gene="rarD"
		/locus-tag="YE0201" /inference="protein motif:TMHMM:2.0" /note="10 probable transmembrane helices predicted for YE0201 by TMHMM2.0 at aa 9-28, 38-60, 73-95, 99-121,128-145, 150-167, 179-198, 208-230, 243-265 and 270-289"
misc-feature	complement(237831..238211)	/gene="rarD"
		/locus-tag="YE0201" /inference="protein motif:PFAM:PF00892" /note="Pfam match to entry PF00892 DUF6, Integral membrane protein DUF6, score 21.2, E-value 0.0016"
misc-feature	complement(238251..238634)	/gene="rarD"

		/locus-tag="YE0201" /inference="protein" motif:PFAM:PF00892" /note="Pfam match to entry PF00892 DUF6, Integral membrane protein DUF6, score 53.9, E-value 2.3e-13"
gene	complement(238765..239235)	/locus-tag="YE0202"
CDS	complement(238765..239235)	/locus-tag="YE0202"  /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10338.1" /db-xref="GI:122087557" /db-xref="InterPro:IPR003736" /db-xref="InterPro:IPR006683" /db-xref="UniProtKB/TrEMBL:A1JIA0" /translation="MPVTPLTLESARNLIGEIVF YHMPFNRELGLKLTRFEQDFAEIT FDNNDKLVGNIAQRILHGGVIAAVLDVAAGLVCV GNSLVRHEPLIQEQQLQMKLAKMGT IDLRVDYLRPGRGEHFIASSCILRSGNKVSVARV ELHNENQMHIASATATYLVG"
misc-feature	complement(238768..239181)	/locus-tag="YE0202"
		/inference="protein" motif:PFAM:PF02584" /note="Pfam match to entry PF02584 DUF157, Uncharacterized protein PaaI, COG2050, score -2.7, E-value 0.00013"
gene	239416..240294	/gene="pldA"
		/locus-tag="YE0203"
CDS	239416..240294	/gene="pldA" /locus-tag="YE0203" /codon-start=1 /transl-table=11 /product="phospholipase A" /protein-id="CAL10339.1" /db-xref="GI:122087558" /db-xref="GOA:A1JIA1" /db-xref="InterPro:IPR003187" /db-xref="UniProtKB/TrEMBL:A1JIA1" /translation="MGRFWQILIALLLVPTLVQA EEATVEKIHDAPTVRGSIIAAMLQ DHDNPFLLYPYETNYLLYTYTSDINKDAISSYDW AQNANKDEVKQSLGFPPIWRGIA GDNSLLGASYTQRSWWQASNKDESSPFRETNYEP QLFLAWATDYELAGWTFREVEFGY NHQSNKGADPTSRSWDRVYTRLMAQRGNLEIDLK PWYRLPESDSKDDNPDINKYMGYY RLKVGYALGESVFSLDGRYNWNTGYGGAEMGWSY PITKHVRFYTTQVFSGYGESMIDYN FRQTRVGVGIMLNDVL"
sig-peptide	239416..239475	/gene="pldA" /locus-tag="YE0203" /note="Signal peptide predicted for YE0203 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability

misc-feature	239479..240282	0.998 between residues 20 and 21" /gene="pldA" /locus-tag="YE0203" /inference="protein motif:PFAM:PF02253" /note="Pfam match to entry PF02253 PLA1, Phospholipase A1, score 651.6, E-value 2.7e-193"
gene	240371..242221	/gene="recQ"
CDS	240371..242221	/locus-tag="YE0204" /gene="recQ" /locus-tag="YE0204" /codon-start=1 /transl-table=11 /product="ATP-dependent DNA helicase" /protein-id="CAL10340.1" /db-xref="GI:122087559" /db-xref="GOA:A1JIA2" /db-xref="InterPro:IPR001650" /db-xref="InterPro:IPR002121" /db-xref="InterPro:IPR004589" /db-xref="InterPro:IPR006293" /db-xref="InterPro:IPR011545" /db-xref="InterPro:IPR014001" /db-xref="InterPro:IPR014021" /db-xref="UniProtKB/TrEMBL:A1JIA2" /translation="MSTAAVINRELLAEQVLRDT FGYQQFRPGQQEIINATLSGQDCL VVMPTGGGKSLCYQIPALVTDGLTLVVSPLISLM KDQVDQLLAYGVGAGCLNSSQTRE QQLAVMGCRSGQIKLLYIAPERLVMESFLDQLH QWRPALLAVDEAHCISQWGHDFRP EYRALGQLKQRFPNLPVIALTATADEATRGDIVR LLNLDQPLIQVSSFDRPNIRYTLV EKFKPLDQLWRFVQDQRGKSGIIYCNSRAKVEDT TARLQSRGLSVAAYHAGLDNERRA QVQEAQFQRDDLQVVVATVAFGMGINKPNVRFVVH FDIPRTIESYYQETGRAGRDGLPA EAMLLYDPADMAWLRRCLEEKPAGAQQDIERHKL NAMGAFAEAQTCRRLVLLNYFGEG KQQSCGNCDICLDPPKRYDGLADAQKALSCVYRV GQRFGLGYIVEVLRGANNQRIREF DHDKLSVYGIGREQSHEHWVSVLRQLIHLGLLSQ NIAMFSALQLTEAAPVLRaelPL QLAVPRIQSLKVRSSANQKSYGGNYDRKLFakLR KLRKSIADegNIppyVVFNDATLL EMAEQMPITASELLSVNGVGQRKLERFGAPFMAM IRDHVDNIHVDNNVDD"
misc-feature	240416..241024	/gene="recQ" /locus-tag="YE0204" /inference="protein motif:PFAM:PF00270" /note="Pfam match to entry PF00270 DEAD, DEAD/DEAH box helicase, score 152.1, E-value 6.2e-43"
misc-feature	240620..240652	/gene="recQ" /locus-tag="YE0204" /inference="protein motif:Prosites:PS00013" /note="PS00013 Prokaryotic membrane lipoprotein lipid"

misc-feature	241148..241363	attachment site." /gene="recQ" /locus-tag="YE0204" /inference="protein motif:PFAM:PF00271" /note="Pfam match to entry PF00271 helicase-C, Helicase conserved C-terminal domain, score 103.7, E-value 2.4e-28"
misc-feature	241961..242203	/gene="recQ" /locus-tag="YE0204" /inference="protein motif:PFAM:PF00570" /note="Pfam match to entry PF00570 HRDC, HRDC domain ,score 116.3, E-value 3.7e-32"
gene	242284..242904	/gene="rhtC"
CDS	242284..242904	/locus-tag="YE0205" /gene="rhtC" /locus-tag="YE0205" /codon-start=1 /transl-table=11 /product="threonine efflux protein" /protein-id="CAL10341.1" /db-xref="GI:122087560" /db-xref="GOA:A1JIA3" /db-xref="InterPro:IPR001123" /db-xref="InterPro:IPR004778" /db-xref="UniProtKB/TrEMBL:A1JIA3" /translation="MLMLFLTVALVHLVALMSPG PDFFFVSQTAASRSRREAMMGVTG ISLGIVVWAGVALMGLNLILHKMAWLHQIIMVGG GLYLCWMGWQLLKSARSKRDTSEA EVQVALPARGRTFLRGFLTNLSNPKAVIYFGSVF SLFVGDNVTAGARWGLFVLIVAET FVWFSIVACVFALPVMRRGYQRLSKWIDGLAGVL FAGFGIHLILSR"
sig-peptide	242284..242373	/gene="rhtC" /locus-tag="YE0205" /note="Signal peptide predicted for YE0205 by SignalP 2.0 HMM (Signal peptide probabiltiy 0.709) with cleavage site probability 0.229 between residues 30 and 31"
misc-feature	join(242293..242361, 242407..242475, 242485..242553, 242638..242706, 242734..242802, 242839..242898)	/gene="rhtC"
		/locus-tag="YE0205" /inference="protein motif:TMHMM:2.0" /note="6 probable transmembrane helices predicted for YE0205 by TMHMM2.0 at aa 4-26, 42-64, 68-90, 119-141,151-173 and 186-205"
misc-feature	242485..242811	/gene="rhtC" /locus-tag="YE0205" /inference="protein motif:PFAM:PF01810"



		/note="Pfam match to entry PF01810 LysE, LysE type translocator, score 115.7, E-value 5.8e-32"
gene	complement(242954..243574)	/gene="rhtB"
CDS	complement(242954..243574)	/locus-tag="YE0206" /gene="rhtB"
		/locus-tag="YE0206" /codon-start=1 /transl-table=11 /product="putative homoserine/homoserine lactone efflux protein" /protein-id="CAL10342.1" /db-xref="GI:122087561" /db-xref="GOA:A1JIA4" /db-xref="InterPro:IPR001123" /db-xref="InterPro:IPR004778" /db-xref="UniProtKB/TrEMBL:A1JIA4" /translation="MTLDWWLTYLLTTLILSLSP GSGAINTMSTAISHGTRGVASIC GLQLGLAVHIVLVGVGLGALISQSLLAFELLKWL GAAYLIWLGIIQQWRAAGALDLHAL ANSMPRRKLFKRAVFVNLTNPKSIVFLAALFPQF VLPHQPQVAQYLILGSTSVIVDII VMMGYATLATRIAGWIKSPQQMKLLNRIFGGLFM LVGALLATARKV"
sig-peptide	complement(243503..243574)	/gene="rhtB"
		/locus-tag="YE0206" /note="Signal peptide predicted for YE0206 by SignalP 2.0 HMM (Signal peptide probability 0.803) with cleavage site probability 0.440 between residues 24 and 25"
misc-feature	complement(join(242966.. .243025,243050..243118, 243161..243229, 243317..243385, 243395..243463, 243500..243562))	/gene="rhtB"
		/locus-tag="YE0206" /inference="protein motif:TMHMM:2.0" /note="6 probable transmembrane helices predicted for YE0206 by TMHMM2.0 at aa 5-25, 38-60, 64-86, 116-138,153-175 and 184-203"
misc-feature	complement(243056..243364)	/gene="rhtB"
		/locus-tag="YE0206" /inference="protein motif:PFAM:PF01810" /note="Pfam match to entry PF01810 LysE, LysE type translocator, score 112.4, E-value 5.6e-31"
gene	243778..244833	/gene="pldB"
CDS	243778..244833	/locus-tag="YE0207" /gene="pldB" /locus-tag="YE0207" /codon-start=1

		/transl-table=11 /product="putative lysophospholipase" /protein-id="CAL10343.1" /db-xref="GI:122087562" /db-xref="InterPro:IPR000073" /db-xref="UniProtKB/TrEMBL:A1JIA5" /translation="MPLDNHMNNWLTRREEQFAAF VNGPLLDWFQQRDEDEFMGVDNIP IRYVRFCSQPQHTRVVVVVPGRIESYVKYPEVAYD LFQQGYDVIVLDHRGQGRSGRILD DRNRGHVIKFDDYIEDFAQLVQREITGSHYQQRF ALAHSMGGAILTRYLAREPTVFNA VALCAPMFGIHLPMPGWLAHRIVDWTEKHQKLRD YYAIGTGQWRPLPYVNNMLTHSRE RYRRYLRYADSPEIRVGGPTYHWVRESLLVGEQ IIAQADKITTPLLQASEDRVVH NPAHNAFTQAMTLAGHPCEGEQPKLIKARHEIL FERDTLRAEALSAILRFFAQHHSS LQHKKPVGPQDSDTTRG" /gene="pldB" /locus-tag="YE0207" /inference="protein" motif:PFAM:PF00561" /note="Pfam match to entry PF00561 abhydrolase, alpha/beta hydrolase fold, score 94.9, E-value 1e-25"
misc-feature	244027..244752	
gene	244845..245654	/locus-tag="YE0208" /locus-tag="YE0208" /codon-start=1 /transl-table=11 /product="putative haloacid dehalogenase-like hydrolase" /protein-id="CAL10344.1" /db-xref="GI:122087563" /db-xref="GOA:A1JIA6" /db-xref="InterPro:IPR000150" /db-xref="InterPro:IPR006379" /db-xref="InterPro:IPR013200" /db-xref="UniProtKB/TrEMBL:A1JIA6" /translation="MYHVVASDLTGTLSPDHIL TPYTKETLKLTTQRDVHFVFATGR HHIDVAQIRDNLEISAFMITSNGARVHNTAGELI FSHNLDADIARDLYNIEHHNPDIL TNVYLNDEWYMNRESPAQEEFFRESVFQYQVFEP ALLPTDGVCKVYFTCDDHDKLLIL EEAINARWGDRVNVVSFSFPTCLEVMGGGVSKGHA LEQVAKIIGYSLKECIAFGDGMND LEMLSMSGKGCIMRDAHQRLKDMLPNLEVIGSNA DDAVPHYLRKMFLGSDK" /locus-tag="YE0208" /inference="protein" motif:PFAM:PF00702" /note="Pfam match to entry PF00702 Hydrolase, haloacid dehalogenase-like hydrolase, score 31.2, E-value 1.6e-06"
CDS	244845..245654	
misc-feature	244848..245549	/locus-tag="YE0208" /inference="protein" motif:PFAM:PF00702" /note="PS01228 Hypothetical cof family signature 1."
misc-feature	244854..244889	

gene complement(245866..2468 /gene="glpQ"  
64)

CDS complement(245866..2468 /gene="glpQ"  
64)  
/locus-tag="YE0209"  
/codon-start=1  
/transl-table=11  
/product="glycerophosphoryl  
diester phosphodiesterase"  
/protein-id="CAL10345.1"  
/db-xref="GI:122087564"  
/db-xref="GOA:A1JIA7"  
/db-xref="InterPro:IPR004129"  
/db-xref="UniProtKB/TrEMBL:A1JIA7"  
/translation="MVIAHRGASGYLPEHSLPAK  
AMAYAQQGADYLEQDLVMTKDNELV  
VLHDHYLDRVTDVAERFPDRARKDGRYYAIDFTL  
PEIKSLKFTEGFDIDKEGKKVQSY  
PGRFPMGKADFRVHTFQEEIEFVQGLNHSTGKNI  
GIYPEIKAPWFHKQEGKDISTKVL  
EVLKQYGYTTKADKVYLQCFDANELKRIKNELEP  
KMGMNLLKLVQLVAYTDWNETYEQK  
PDGKWVNYSYDWMFKPGAMQVAQYADGIGPDYH  
MLVVETSTPNNIKLTNMVKEAHAN  
NMMVHPFTIRADKLPKYATDVNQLFDIIYNQAGV  
DGVFTDFPDKGVQFLQKQGQHQ"

misc-feature complement(245899..2468 /gene="glpQ"  
52)  
/locus-tag="YE0209"  
/inference="protein  
motif:PFAM:PF03009"  
/note="Pfam match to entry PF03009  
GDPD, Glycerophosphoryl diester  
phosphodiesterase family, score  
317.6, E-value 9.4e-93"

gene complement(247088..2484 /gene="glpT"  
52)

CDS complement(247088..2484 /gene="glpT"  
52)  
/locus-tag="YE0210"  
/inference="similar to  
sequence:INSDC:AE008802"  
/inference="similar to  
sequence:UniProtKB:P08194"  
/note="Highly similar to  
Escherichia coli  
glycerol-3-phosphate transporter  
glpT or b2240 SWALL:GLPT-ECOLI  
(SWALL:P08194) (452 aa) fasta  
scores: E(): 2.3e-165, 91.29 38d  
in 448 aa and to Salmonella  
typhimurium MFS family,  
Sn-glycerol-3-phosphate transport  
protein GlpT or stm2283  
SWALL:Q8ZNG6 (EMBL:AE008802) (452  
aa) fasta scores: E(): 2.8e-167,  
92.58 38d in 445 aa"  
/codon-start=1  
/transl-table=11  
/product="glycerol-3-phosphate"

		transporter" /protein-id="CAL10346.1" /db-xref="GI:122087565" /db-xref="GOA:A1JIA8" /db-xref="InterPro:IPR000849" /db-xref="InterPro:IPR005267" /db-xref="InterPro:IPR007114" /db-xref="InterPro:IPR011701" /db-xref="UniProtKB/TrEMBL:A1JIA8" /translation="MLSIFKPAPHVARLPADQVD PTYRRLRWQIFMGIFFGYAAYLV RKNFTLAMPYLIQQFSRGDLGFALSGISIAYGF SKFIMGSVSDRSNPRVFLSAGLIL AAAVMLFMGFVPWATSSIAVMFVLLFLCGWFQGM GWPPCGRTMVHWWSKKERGSIVSV WNCAHNVGGGLPPLLFLLGMAWFNDWKAALYMPA FGAILVALIVFGLMRDTPQSVGLP PIEEYKNDYPDDYSEEAEEEELTAKQIFMQYILPN KLLWYIAIANVFVYLLRYGILDWS PTYLKEVKHFALDKSSWAYFLYEYAGIPGTLLCG WMSDKVFKGNRGATGVFFMTLVTI ATIVYWLNPVGNPGIDMACMITIGFLIYGPVMLI GLHALELAPKKAAGTAAGFTGLFG YLGGSSVAASAIVGYTVDYFGWDGGFMVMIGGSIL AVLLLIVVMFSEKKHHEELARQAE MDKK"
misc-feature	complement(247106..248368)	/gene="glpT"  /locus-tag="YE0210" /inference="protein motif:PFAM:PF00083" /note="Pfam match to entry PF00083 sugar-tr, Sugar (and other) transporter, score -109.0, E-value 0.00052"
misc-feature	complement(join(247142. .247201,247229..247297, 247334..247402, 247430..247498, 247517..247576, 247634..247693, 247832..247891, 247904..247972, 248027..248095, 248105..248173, 248192..248260, 248318..248377))	/gene="glpT"  /locus-tag="YE0210" /inference="protein motif:TMHMM:2.0" /note="12 probable transmembrane helices predicted for YE0210 by TMHMM2.0 at aa 26-45, 65-87, 94-116, 120-142,161-183, 188-207, 254-273, 293-312, 319-341, 351-373,386-408 and 418-437"
misc-feature	complement(247946..247996)	/gene="glpT"  /locus-tag="YE0210" /inference="protein motif:Prosite:PS00942" /note="PS00942 glpT family of transporters signature."

gene	248974..250629	/gene="glpA" /locus-tag="YE0212"
CDS	248974..250629	/gene="glpA" /locus-tag="YE0212" /codon-start=1 /transl-table=11 /product="anaerobic glycerol-3-phosphate dehydrogenase subunit A" /protein-id="CAL10347.1" /db-xref="GI:122087566" /db-xref="GOA:A1JIA9" /db-xref="InterPro:IPR000447" /db-xref="InterPro:IPR006076" /db-xref="InterPro:IPR007419" /db-xref="InterPro:IPR017752" /db-xref="UniProtKB/TrEMBL:A1JIA9" /translation="MTNSSPYTETDVIIIGGGAT GAGIARDCARRGLACTLLERHDIA TGATGRNHGLLHSGARYAVTDGESARECIEENRI LKRIARHCIEQTDGLFITLPEDSL EYQQQFIARCQEAGIEAEAIDPKQALRLEPAANP TLIAAVRVPDGTVDPFRLTAANML DAREHGANVLTYYHEVIGLLRHGDRVSGVRVFDHK NQRQYDIHAQIVVNAAGIWQHIA EYADLRIRMFPKAGALLILGHRINNMVINRCRK ADADILVPGDTISLIGTTSTHIEY DQIDNMVVTAQEVDTLIREGSKLSPQLAQTRILR AYAGVRPLVASDDDPSGRNVSRGI VLLDHASRDGLEGFITITGGKLMTYRLMAEWATD KVCEKLGVTAACTTAQEPLPGSQQ SAEQTLISKVISLPASIRGSAVYRHGDRATQLLAG NRLDNSLVCECEAVTAGEVRYAIE SLSVNNLLDLRRRTRVGMGTCQGELCACRAAGLL SRFKVTTPQQSREQLRQFLNERWK GVRPIAWGDALRESEFTHWVYQGLCGLDDSPNTA NVQEKPDEI"
misc-feature	249001..250074	/gene="glpA" /locus-tag="YE0212" /inference="protein motif:PFAM:PF01266" /note="Pfam match to entry PF01266 DAO, FAD dependent oxidoreductase, score 408.8, E-value 3.2e-120"
misc-feature	249016..249069	/gene="glpA" /locus-tag="YE0212" /inference="protein motif:Prosites:PS00977" /note="PS00977 FAD-dependent glycerol-3-phosphate dehydrogenase signature 1."
misc-feature	250030..250062	/gene="glpA" /locus-tag="YE0212" /inference="protein motif:Prosites:PS00978" /note="PS00978 FAD-dependent glycerol-3-phosphate dehydrogenase signature 2."
gene	250619..251893	/gene="glpB" /locus-tag="YE0213"
CDS	250619..251893	/gene="glpB" /locus-tag="YE0213"

		/codon-start=1 /transl-table=11 /product="putative anaerobic glycerol-3-phosphate dehydrogenase subunit B" /protein-id="CAL10348.1" /db-xref="GI:122087567" /db-xref="GOA:A1JIB0" /db-xref="InterPro:IPR003953" /db-xref="InterPro:IPR009158" /db-xref="UniProtKB/Swiss-Prot:A1J IB0" /translation="MKFDVIIIGGGLAGLVCGIR LAEQGYCAIVSAGQNALHFSSGS LDLLAKLPNGQAVSQPLSAETLAELAPEHPYSK MGQTGQVGELAQQAESLLSRCGLS LVGSAAKNHLRLTPLGNCRPTWLSPADIPVAPLE GPLPWQKVAVIGIEGFLDFQPQMV ASALQEQGVEVTSYDLHLPALDRLRDNPSEFRAV NIARVLDLPENLQPLADELARLSS TAEMILLPACIGLDESAPLEALRAAVGKPIQLLP TLPPSLLGMRLHQALRHRFQQLGG IVMPGDAVLRAELVGNRITGLYSRNHGDIPLRRA QMVLASGSFFSNGLVATFEHVYEP ILDLDILSLPNRADWSNSNMFAQPYLQFGVNTD NRLRALRGGVALDNLHVIGAVLGG YDPLQQGCGAGVSLTSALFVAEQIVSAMEVTL" /gene="glpB" /locus-tag="YE0213" /note="Signal peptide predicted for YE0213 by SignalP 2.0 HMM (Signal peptide probability 0.893) with cleavage site probability 0.891 between residues 22 and 23"
sig-peptide	250619..250684	
gene	251932..253155	/gene="glpC" /locus-tag="YE0214"
CDS	251932..253155	/gene="glpC" /locus-tag="YE0214" /codon-start=1 /transl-table=11 /product="anaerobic glycerol-3-phosphate dehydrogenase subunit C" /protein-id="CAL10349.1" /db-xref="GI:122087568" /db-xref="GOA:A1JIB1" /db-xref="InterPro:IPR001450" /db-xref="InterPro:IPR004017" /db-xref="InterPro:IPR012285" /db-xref="InterPro:IPR017753" /db-xref="UniProtKB/TrEMBL:A1JIB1" /translation="MARDKSFESCIKTVCTTYC PVAKVNPPLYPGPKQAGPDGERLRL KDPALYDDALKYCTNCKRCEVACPSDVKIGDIIQ RAKASYSSNKPCLRDAILSHTDLM GTLSTPFAPVINAVTGLKPVRVLLDKALKIDHRR ELPKYSFGTFRRWYRKQAEKQQQY AEQVAFFHGCFFVYNHPQLGKDLVSVFAMNIGV QLLKREKCCGVPLIANGFIEQAKK QARVNLES LTDAVIDRDIPVATSSSCTFTLRDE YPHLLDVD TAPVRDRVELATRYLY RLLDQGRELPLKPLLSNQNKPLRIAYHTPCHMEK

		MGWTAYTLALLQRIPGIELVVLD QCCGIAGTYGFKSENYATSQGIGASLFQQIEESG VDLVITDCETCKWQIEMSTSKKCE HPITLLAQALNPLCP"
misc-feature	251959..251994	/gene="glpC" /locus-tag="YE0214" /inference="protein motif:Prosite:PS00198" /note="PS00198 4Fe-4S ferredoxins, iron-sulfur binding region signature."
misc-feature	252079..252150	/gene="glpC" /locus-tag="YE0214" /inference="protein motif:PFAM:PF00037" /note="Pfam match to entry PF00037 fer4, 4Fe-4S binding domain, score 13.2, E-value 0.0015"
misc-feature	252100..252135	/gene="glpC" /locus-tag="YE0214" /inference="protein motif:Prosite:PS00198" /note="PS00198 4Fe-4S ferredoxins, iron-sulfur binding region signature."
misc-feature	252490..252681	/gene="glpC" /locus-tag="YE0214" /inference="protein motif:PFAM:PF02754" /note="Pfam match to entry PF02754 DUF224, Domain of unknown function (DUF224), score 35.2, E-value 9.6e-08"
misc-feature	252895..253083	/gene="glpC" /locus-tag="YE0214" /inference="protein motif:PFAM:PF02754" /note="Pfam match to entry PF02754 DUF224, Domain of unknown function (DUF224), score 61.2, E-value 1.5e-15"
gene	complement(253311..253754)	/gene="dcrB"
CDS	complement(253311..253754)	/locus-tag="YE0215" /gene="dcrB"  /locus-tag="YE0215" /codon-start=1 /transl-table=11 /product="putative lipoprotein" /protein-id="CAL10350.1" /db-xref="GI:122087569" /db-xref="UniProtKB/TrEMBL:A1JIB2" /translation="MGQPVSLLLEGKVAFLPADL SDQSGKMGSQANNMHVYANKTGDK AVIVILGDDTNEALNVLTDRLAQQRRARDANLQV VTNKAIKVDGHPFQQLDSIITSGG QKAYSSVLMGQVDNHLMTIQITLPADNQQQAQTE AESIISTLKLK"
gene	complement(253896..254576)	/gene="yhhQ"  /locus-tag="YE0216"

CDS	complement(253896..254576)	/gene="yhhQ" /locus-tag="YE0216" /codon-start=1 /transl-table=11 /product="putative membrane protein" /protein-id="CAL10351.1" /db-xref="GI:122087570" /db-xref="InterPro:IPR003744" /db-xref="UniProtKB/TrEMBL:A1JIB3" /translation="MFSFTAQQRMTALVWLSLFH IVIITSSNYLVQLPISIFGFHTTW GAFTFPFIFLATDLTVRIFGAPLARRIILSVMVP ALLISYLISALFYQGSWQGFLALS SFNLFVARIAAASF MAYVLGQILDVQVFNRLRQR SAWWVAPTAAAMFFGNISDTMAFFF IAFYRSSDPFMAANWVEIALVDYSFKLLICMLFF LPAYGMMLNVLLKYFARKTEQQTL MQANTAEQ"
misc-feature	complement(253947..254564)	/gene="yhhQ" /locus-tag="YE0216" /inference="protein" motif:PFAM:PF02592" /note="Pfam match to entry PF02592 DUF165, Uncharacterized ACR, YhhQ family COG1738, score 254.3, E-value 1.1e-73"
misc-feature	complement(join(253959..254027,254085..254153,254187..254255,254298..254366,254385..254444,254472..254540))	/gene="yhhQ" /locus-tag="YE0216" /inference="protein" motif:TMHMM:2.0" /note="6 probable transmembrane helices predicted for YE0216 by TMHMM2.0 at aa 13-35, 45-64, 71-93, 108-130,142-164 and 184-206"
gene	254823..255077	/locus-tag="YE0217"
CDS	254823..255077	/locus-tag="YE0217" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10352.1" /db-xref="GI:122087571" /db-xref="GOA:A1JIB4" /db-xref="InterPro:IPR001455" /db-xref="UniProtKB/Swiss-Prot:A1JIB4" /translation="MTDIFANPDKTLDALGLRCP EPVMMVRKTVRHMEDGQTLLIIAD DPATTRDIPGFCRFMDHQLLAQDTGQTPYRYLVK KGAKAE"
misc-feature	254838..255059	/locus-tag="YE0217" /inference="protein" motif:PFAM:PF01206" /note="Pfam match to entry PF01206"



		UPF0033, Uncharacterized protein family UPF0033, score 136.2, E-value 3.8e-38"
misc-feature	254856..254894	/locus-tag="YE0217" /inference="protein motif:Prosites:PS01148" /note="PS01148 Uncharacterized protein family UPF0033 signature."
gene	complement(255099..257429)	/locus-tag="YE0218"
CDS	complement(255099..257429)	/locus-tag="YE0218"  /codon-start=1 /transl-table=11 /product="putative P-type cation-translocating membrane ATPase" /protein-id="CAL10353.1" /db-xref="GI:122087572" /db-xref="GOA:A1JIB5" /db-xref="InterPro:IPR000150" /db-xref="InterPro:IPR001366" /db-xref="InterPro:IPR001757" /db-xref="InterPro:IPR001969" /db-xref="InterPro:IPR005834" /db-xref="InterPro:IPR006121" /db-xref="InterPro:IPR006404" /db-xref="InterPro:IPR006416" /db-xref="InterPro:IPR008250" /db-xref="UniProtKB/TrEMBL:A1JIB5" /translation="MHSHEHRHSTETQSHCGCG HDHAKKQTGCSSQPAANISHDSSN SVSEHSHQEGGCCSQSSHTDDGDEESDRLANATP AGSQHFWSQVKGMDPCSCARKIEN AVSNLVGIIENVKVLFAATEKLVVDARSDIRLQVQQ AVIQAGFSLIDTQSPGAGKNTSE SRFREYLPIALLTTLMLLSWGISLFSVELSELAF TVTTIVGLPIVTKAWKLIRSGTP FAIETLMSVAAIGAMFIGATAEAMVLLLFMVGE LLESYAANRARRGVTALMALVPEE ALLLKEGERRQVSVASLRPGDIEVSPGGRLPAD AELMTPFASFDESALTGESVPVER VQGEKVAAGSLSVDRATEMRVISEPGNNAIDRIL QLIELAEERRAPIERFIDRFSRIY TPAIMFLSALVILVPPLAFAEPWETWIYRGLTLL LIGCPCALVISTPAAITSALAAAT RRGALIKGGALEQLGRIQTVAFDKTGTLTGKGP QVTDILPISGVSETRLLSLAAAVE AGSHHPLAVAIMQRAQQNTPMLPLAEERRALAGI GVEGRVNGLVVRVSAPSKISPELL TAEWLAQFDELESSGKTAVAVLENEKFIGVVALR DTLRDAKQAIKALKKLGIQGVML TGDNPRAAAAIAAGELGIDYRAGLLPADKVQAVMA LNATHPTVMVGDGINDAPAMKAAS IGIAMGSGTDVALETADAALTNRLTGLAEIILL SRAANANIRQNITIALGLKGIFLV TTLGLTGLWLAVLADSGATALVTANALRLLRKR DI"
misc-feature	complement(255138..255173)	/locus-tag="YE0218"  /inference="protein motif:Prosites:PS00141"

		/note="PS00141 Eukaryotic and viral aspartyl proteases active site."
misc-feature	complement(join(255168..255236,256089..256157,256200..256268,256677..256745,256788..256856,256875..256934))	/locus-tag="YE0218"
		/inference="protein motif:TMHMM:2.0" /note="6 probable transmembrane helices predicted for YE0218 by TMHMM2.0 at aa 166-185, 192-214, 229-251,388-410, 425-447 and 732-754"
misc-feature	complement(255357..256028)	/locus-tag="YE0218"
		/inference="protein motif:PFAM:PF00702" /note="Pfam match to entry PF00702 Hydrolase, haloacid dehalogenase-like hydrolase, score 106.1, E-value 4.4e-29"
misc-feature	complement(255360..255428)	/locus-tag="YE0218"
		/inference="protein motif:Prosite:PS01229" /note="PS01229 Hypothetical cof family signature 2."
misc-feature	complement(255990..256010)	/locus-tag="YE0218"
		/inference="protein motif:Prosite:PS00154" /note="PS00154 E1-E2 ATPases phosphorylation site."
misc-feature	complement(256038..256703)	/locus-tag="YE0218"
		/inference="protein motif:PFAM:PF00122" /note="Pfam match to entry PF00122 E1-E2-ATPase, E1-E2 ATPase, score 295.6, E-value 4e-86"
misc-feature	complement(256989..257180)	/locus-tag="YE0218"
		/inference="protein motif:PFAM:PF00403" /note="Pfam match to entry PF00403 HMA,Heavy-metal-associated domain, score 53.8, E-value 2.5e-13"
misc-feature	complement(257079..257168)	/locus-tag="YE0218"
		/inference="protein motif:Prosite:PS01047" /note="PS01047 Heavy-metal-associated domain."
gene	complement(257713..258339)	/gene="yhhN"
		/locus-tag="YE0219"
CDS	complement(257713..258339)	/gene="yhhN"
		/locus-tag="YE0219"

		/codon-start=1 /transl-table=11 /product="putative membrane protein" /protein-id="CAL10354.1" /db-xref="GI:122087573" /db-xref="GOA:A1JIB6" /db-xref="InterPro:IPR012506" /db-xref="UniProtKB/TrEMBL:A1JIB6" /translation="MSWPFLAVFFSGWLFVDATY RGPRWQRWVFKPVTLLLLLLLLLAWQ APILGPAGYLIVLGLLATLVADALLLPSERLLY ALGAFFLSHLLYTISFASQMTFTL FWPLPLVLIIVGALLLATIWTRLDEMWPVVAFV GMTLLMVWMAGEQYFARSTDMSFS LLTGTVLLLVSHTIWLNLNRYRFSFRASDAIVAGC YFVGHFLLIVRSLYL"
misc-feature	complement(join(257719.. .257775,257812..257871, 257899..257955, 257974..258042, 258055..258114, 258127..258186, 258199..258258))	/gene="yhhN"
		/locus-tag="YE0219" /inference="protein motif:TMHMM:2.0" /note="7 probable transmembrane helices predicted for YE0219 by TMHMM2.0 at aa 28-47, 52-71, 76-95, 100-122,129-147, 157-176 and 189-207"
gene CDS	258627..258947 258627..258947	/locus-tag="YE0221" /locus-tag="YE0221" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10355.1" /db-xref="GI:122087574" /db-xref="InterPro:IPR014949" /db-xref="UniProtKB/TrEMBL:A1JIB7" /translation="MANEQLLYRIQFINNGKNYQ LYVREVGPSALFGFIEIADFVFD QSTLLVDPSTEKLKTEFSGVNRSYIPLHSVIRID AVTEKGSARISELGSNVMSFPYLP GNKP"
gene CDS	258986..259369 258986..259369	/locus-tag="YE0222" /locus-tag="YE0222" /codon-start=1 /transl-table=11 /product="putative membrane protein" /protein-id="CAL10356.1" /db-xref="GI:122087575" /db-xref="UniProtKB/TrEMBL:A1JIB8" /translation="MNKPPLLFIAVVVLIVVLAT RQYWQKKRQDAENDRSPVRSQVE VIDKREVLAPNRRSRQREEIVAAEEKRYEVYFQPL LSGVEVKKSNEIKIVLPQQEYNRI EQGAKGTLRLQGTRYISFVPNSVAK"
sig-peptide	258986..259042	/locus-tag="YE0222" /note="Signal peptide predicted

		for YE0222 by SignalP 2.0 HMM (Signal peptide probability 0.802) with cleavage site probability 0.534 between residues 19 and 20"
misc-feature	258998..259057	/locus-tag="YE0222" /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted for YE0222 by TMHMM2.0 at aa 5-24"
gene	complement(259410..259682)	/gene="yhhL"
CDS	complement(259410..259682)	/locus-tag="YE0223" /gene="yhhL"  /locus-tag="YE0223" /codon-start=1 /transl-table=11 /product="putative membrane protein" /protein-id="CAL10357.1" /db-xref="GI:122087576" /db-xref="InterPro:IPR009525" /db-xref="UniProtKB/TrEMBL:A1JIB9" /translation="MWINIGRLLMLGVWFFLLLN LFQFPFKPLRYFIDVAMIFMVLMLH GLQLILLKSTQPKDQPIISGLQQFKIFVFGVFELL AWQKKQPPLPKK"
misc-feature	complement(join(259443.. .259502,259530..259598, 259617..259670))	/gene="yhhL"  /locus-tag="YE0223" /inference="protein motif:TMHMM:2.0" /note="3 probable transmembrane helices predicted for YE0223 by TMHMM2.0 at aa 5-22, 29-51 and 61-80"
gene	complement(259672..260226)	/locus-tag="YE0224"
CDS	complement(259672..260226)	/locus-tag="YE0224"  /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10358.1" /db-xref="GI:122087577" /db-xref="InterPro:IPR002052" /db-xref="InterPro:IPR004398" /db-xref="InterPro:IPR016065" /db-xref="UniProtKB/TrEMBL:A1JIC0" /translation="MPVSPGLRPTTDRVRETLFN WLAPMIQGARCCLDCFAGSGALGLE ALSRYAGFTVLLEADRHVAKQLSNNLALLSADNG QVVNTNSLQWLAQPGQPFDLVFLD PPFRKGLLAETVNLLEQFNWLTADAWIYVEAEAE SAAADVPASWQLHREKIAGQVAYR LYIRNKDVPQDRVSVEEQEQHHVD"
misc-feature	complement(259738..260223)	/locus-tag="YE0224"  /inference="protein"

		motif:PFAM:PF03602"
		/note="Pfam match to entry PF03602
		Cons-hypoth95,Conserved
		hypothetical protein 95, score
		223.8, E-value 1.6e-64"
misc-feature	complement (259912..259932)	/locus-tag="YE0224"
		/inference="protein
		motif:Prosite:PS00092"
		/note="PS00092 N-6
		Adenine-specific DNA methylases
		signature."
gene	260574..262097	/gene="ftsY"
		/locus-tag="YE0225"
CDS	260574..262097	/gene="ftsY"
		/locus-tag="YE0225"
		/codon-start=1
		/transl-table=11
		/product="cell division protein"
		/protein-id="CAL10359.1"
		/db-xref="GI:122087578"
		/db-xref="GOA:A1JIC1"
		/db-xref="InterPro:IPR000897"
		/db-xref="InterPro:IPR003593"
		/db-xref="InterPro:IPR004390"
		/db-xref="InterPro:IPR013822"
		/db-xref="UniProtKB/TreMBL:A1JIC1"
		/translation="MAKEKKRGFFSWLGLGRQNE
		EHTAEPLATEKEETAEQVVENPAI
		EEQVLSEKQAEIAPDNTSVEAEARESVAEHSTLA
		PGEWDSTAISEVAAETLPEVGAEP
		AAQSVEEPINFAEDPQYLQHHFSQNHDDKDKVDS
		WDEGTVSAPELPLTEHHVVIDTPA
		PQAIVEESQAEVIEEPVVLEEEIEAEVEEVVAVVA
		QEQRPTKEGFFARLKRSLIKTKQ
		NLGSGFMGLFSGKKIDDDLFEELQLLIADVG
		ETTRKIITSLTEHASRKQLKDAEA
		LYGKLKEEMSEILSKVDKPLDVSGKNPFVILMVG
		VNGVGKTTTIGKLARQFQAEKSV
		MLAAGDTFRAAAVEQLQVWGDRNKIAVVAQHTGA
		DSASVIFDAIQAAKARGIDVLLAD
		TAGRLQNKAHLMEELKKIVRVMKKLDGDAPHEVM
		LTLDASTGQNAVSQAKLFNEAVGL
		TGITLTKLDGTAKGGVIFAIADQFGIPIRYIGVG
		EGIEDLRPFKADDFIEALFARED"
misc-feature	261198..261443	/gene="ftsY"
		/locus-tag="YE0225"
		/inference="protein
		motif:PFAM:PF02881"
		/note="Pfam match to entry PF02881
		SRP54-N, SRP54-type protein,
		helical bundle domain, score 81.0,
		E-value 1.6e-21"
misc-feature	261474..262088	/gene="ftsY"
		/locus-tag="YE0225"
		/inference="protein
		motif:PFAM:PF00448"
		/note="Pfam match to entry PF00448
		SRP54, SRP54-type protein, GTPase
		domain, score 416.8, E-value
		1.3e-122"
misc-feature	261501..261524	/gene="ftsY"

		/locus-tag="YE0225"
		/inference="protein"
		motif:Prosite:PS00017"
		/note="PS00017 ATP/GTP-binding
		site motif A (P-loop)."
misc-feature	262002..262043	/gene="ftsY"
		/locus-tag="YE0225"
		/inference="protein"
		motif:Prosite:PS00300"
		/note="PS00300 SRP54-type proteins
		GTP-binding domain signature."
gene	262103..262771	/gene="ftsE"
		/locus-tag="YE0226"
CDS	262103..262771	/gene="ftsE"
		/locus-tag="YE0226"
		/codon-start=1
		/transl-table=11
		/product="cell division
		ATP-binding protein"
		/protein-id="CAL10360.1"
		/db-xref="GI:122087579"
		/db-xref="GOA:A1JIC2"
		/db-xref="InterPro:IPR003439"
		/db-xref="InterPro:IPR003593"
		/db-xref="InterPro:IPR005286"
		/db-xref="InterPro:IPR013505"
		/db-xref="UniProtKB/TrEMBL:A1JIC2"
		/translation="MIRFEQVSKAYLGGRQALQG
		VDFHLRPAEMAFLTGHSAGKSTL
		LKLICGIERPSAGHIWFGGHDISRLKNREVPFLR
		RQIGMIFQDHLLLDRTVYDNVAM
		PLIIAGASTEDIRRRVSAALDKVGLLDKAKNFPI
		QLSGGEQQRVGARAVVNKPAVLL
		ADEPTGNLDDALSEGILRLFEEFNRVGVTVLMAT
		HDTSLIARRRYPILTLSQGRMSGH HHGE"
misc-feature	262184..262741	/gene="ftsE"
		/locus-tag="YE0226"
		/inference="protein"
		motif:PFAM:PF00005"
		/note="Pfam match to entry PF00005
		ABC-tran, ABC transporter, score
		239.0, E-value 4.5e-69"
misc-feature	262205..262228	/gene="ftsE"
		/locus-tag="YE0226"
		/inference="protein"
		motif:Prosite:PS00017"
		/note="PS00017 ATP/GTP-binding
		site motif A (P-loop)."
misc-feature	262514..262558	/gene="ftsE"
		/locus-tag="YE0226"
		/inference="protein"
		motif:Prosite:PS00211"
		/note="PS00211 ABC transporters
		family signature."
gene	262860..263720	/gene="ftsX"
		/locus-tag="YE0227"
		/note="synonym: ftsS"
CDS	262860..263720	/gene="ftsX"
		/locus-tag="YE0227"
		/codon-start=1
		/transl-table=11
		/product="cell division protein"

		/protein-id="CAL10361.1" /db-xref="GI:122087580" /db-xref="GOA:A1JIC3" /db-xref="InterPro:IPR003838" /db-xref="InterPro:IPR004513" /db-xref="UniProtKB/TrEMBL:A1JIC3" /translation="MMRQPLATLLTVMVIAISLT LPSVCYIVWKNVSQAADQWYPTPQ LTVYLDKALDDNAAENVVTTLKTEAGVEKVNYS REEAMGEFRNWSGFGGALDMLEEN PLPAVAIIITPKLDFQSSGTLDTLRDRVSKVEGVA EVRMDDSWFARLAALTGLVGQVAA MIGVLMVVAVFLVIGNSVRLSIFSRRTINVMKL IGATDGFILRPFLNGGAMLGFGGA VLSLILSEALVWKLGSVVTQVATVFGTSFTLHGL SWDECLLLVLISAMIGWIAAWLAT VQHLRRFTPQ"
sig-peptide	262860..262964	/gene="ftsX" /locus-tag="YE0227" /note="Signal peptide predicted for YE0227 by SignalP 2.0 HMM (Signal peptide probability 0.865) with cleavage site probability 0.331 between residues 35 and 36"
misc-feature	join(262878..262946, 263331..263399, 263460..263528, 263631..263690)	/gene="ftsX"
		/locus-tag="YE0227" /inference="protein motif:TMHMM:2.0" /note="4 probable transmembrane helices predicted for YE0227 by TMHMM2.0 at aa 7-29, 158-180, 201-223 and 258-277"
misc-feature	263310..263699	/gene="ftsX" /locus-tag="YE0227" /inference="protein motif:PFAM:PF02687" /note="Pfam match to entry PF02687 DUF214, Predicted permease, score 74.6, E-value 1.4e-19"
gene	264131..264988	/gene="rpoH" /locus-tag="YE0228" /note="synonyms: fam, hin, httpR"
CDS	264131..264988	/gene="rpoH" /locus-tag="YE0228" /codon-start=1 /transl-table=11 /product="RNA polymerase sigma-32 factor" /protein-id="CAL10362.1" /db-xref="GI:122087581" /db-xref="GOA:A1JIC4" /db-xref="InterPro:IPR000943" /db-xref="InterPro:IPR007627" /db-xref="InterPro:IPR007630" /db-xref="InterPro:IPR011991" /db-xref="InterPro:IPR012759" /db-xref="InterPro:IPR014284" /db-xref="UniProtKB/TrEMBL:A1JIC4" /translation="MTKEMQTLALVPQGSLEAYI

		RAANAYPMLTAEERELAERLHYQ GDLEAAKQLILSHLRFVAHVARNYSGYGLPQADL IQEGNIGLMKAVRRFNPEVGVRLV SFAVHWIKAEIHEYVLNRNWRIVKVATTKAQRKLF FNLRKTKQRLGWFNQDEVELVAKE LGVTSKDVREMESRMSAQDMTFDPTPDDEV RDGQ SMAPVLYLQDKTSDFADGIEEDNW DNHAADKLTYALEGLDERSQHIIRARWLDDD NKS TLQELADQYGVSAERVRQLEKNAM KKLRMAIEA"
misc-feature	264359..264400	/gene="rpoH" /locus-tag="YE0228" /inference="protein" motif:Prosite:PS00715" /note="PS00715 Sigma-70 factors family signature 1."
misc-feature	264884..264949	/gene="rpoH" /locus-tag="YE0228" /note="Predicted helix-turn-helix motif with score 2068.000, SD 6.23 at aa 252-273, sequence STLQELADQYGVSAERVRQLEK"
misc-feature	264887..264967	/gene="rpoH" /locus-tag="YE0228" /inference="protein" motif:Prosite:PS00716" /note="PS00716 Sigma-70 factors family signature 2."
gene	complement(265084..265476)	/gene="yhhK"
CDS	complement(265084..265476)	/locus-tag="YE0229" /gene="yhhK"  /locus-tag="YE0229" /codon-start=1 /transl-table=11 /product="putative acetyltransferase" /protein-id="CAL10363.1" /db-xref="GI:122087582" /db-xref="GOA:A1JIC5" /db-xref="InterPro:IPR000182" /db-xref="InterPro:IPR016181" /db-xref="UniProtKB/TrEMBL:A1JIC5" /translation="MKLTIERLTNLTHQDLIDLA KIWPEQQQTTLWLQWINDGKPLFAA RFNERLLGAVKVMVDGQQAELEDLYVREVTRRRG VGLYLIETLRQLPTIQQWYLSDK QVVAANYEAMGSFMLACGFSRNKQGWQR"
misc-feature	complement(265111..265353)	/gene="yhhK"  /locus-tag="YE0229" /inference="protein" motif:PFAM:PF00583" /note="Pfam match to entry PF00583 Acetyltransf,Acetyltransferase (GNAT) family, score 23.4, E-value 0.00035"
gene	265898..267013	/gene="livK"
CDS	265898..267013	/locus-tag="YE0230" /note="synonym: livJ" /gene="livK"



		/locus-tag="YE0230" /codon-start=1 /transl-table=11 /product="branched-chain amino acid-binding protein" /protein-id="CAL10364.1" /db-xref="GI:122087583" /db-xref="GOA:A1JIC6" /db-xref="InterPro:IPR000709" /db-xref="InterPro:IPR001828" /db-xref="UniProtKB/TrEMBL:A1JIC6" /translation="MKLTGKGVLLAGCIAMAMSH SVLAKDIKVAIVGAMSGPVAQYGD MEFTGARQAIADINAKGGIKGDKLVGVEYDDACD PKQAVAVANKVINDGIRYVIGHLC SSSTQPASDIYEDEGVIMITPAATNADLTTRGYK MIMRTTGLDSDQGPTAAKYILETI KPKRIAVVHDKQQYGEGLARSVRDSLKKQGTEPV LFEGVTAGDKDFSTLVARLKKENV DFVYFGGYPEMGQILRQAKQAGLTARFMGPEGV GNSSLNIAGDASEGMLVTLPKRY DQVPANQPIVDALKAKKLDPTGPFVWTTYAALQS LTTAMERSGSQEPADLVKDLKTGK PVETVMGPLSWDEKGD LKGF EFGIF EWHADGSST AVK"
sig-peptide	265898..265969	/gene="livK" /locus-tag="YE0230" /note="Signal peptide predicted for YE0230 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 1.000 between residues 24 and 25"
misc-feature	265958..267007	/gene="livK" /locus-tag="YE0230" /inference="protein motif:PFAM:PF01094" /note="Pfam match to entry PF01094 ANF-receptor, Receptor family ligand binding region, score 175.3, E-value 6.6e-50"
gene	267172..268098	/gene="livH"
CDS	267172..268098	/locus-tag="YE0231" /gene="livH" /locus-tag="YE0231" /codon-start=1 /transl-table=11 /product="high-affinity branched-chain amino acid transport system, permease protein" /protein-id="CAL10365.1" /db-xref="GI:122087584" /db-xref="GOA:A1JIC7" /db-xref="InterPro:IPR001851" /db-xref="UniProtKB/TrEMBL:A1JIC7" /translation="MSEQFLYFLQQMFNGVTLGS TYALIAIGYTMVYGIIGMINFAHG EVYMISSYVSFIVIAALMMVGIDASWLLIGSAFL VSIVIASTYGWSIERVAYKPVRSS KRLIALISAIGMSIFLQNYVSLNQGSRD LALPSL VTGQWTLAETNGFAATISTMQLTI WIVTFLAMLALTIFIRYSRMGRACRACAEDLKMA

		SLLGINTDRVISLTFVIGALMAAV AGVLLGQFYGVINPYIGFMAGMKAFTAAVLGGIG SIPGAMIGGLILGIAEALTSAYLS TEYKDAVSFALLIVVLLVMPTGILGRPEVEKV" /gene="livH" /locus-tag="YE0231" /inference="protein" motif:PFAM:PF02653" /note="Pfam match to entry PF02653 BPD-transp-2,Branched-chain amino acid transport system / permease component, score 323.1, E-value 2e-94" 
misc-feature	267193..268083	
misc-feature	join(267214..267282, 267301..267369, 267379..267447, 267484..267543, 267628..267696, 267790..267858, 267901..267969, 268015..268074) 	/gene="livH"  /locus-tag="YE0231" /inference="protein" motif:TMHMM:2.0" /note="8 probable transmembrane helices predicted for YE0231 by TMHMM2.0 at aa 15-37, 44-66, 70-92, 105-124,153-175, 207-229, 244-266 and 282-301" 
gene	268095..269381	/gene="livM"
CDS	268095..269381	/locus-tag="YE0232" /gene="livM" /locus-tag="YE0232" /codon-start=1 /transl-table=11 /product="high-affinity branched-chain amino acid transport system, permease protein" /protein-id="CAL10366.1" /db-xref="GI:122087585" /db-xref="GOA:A1JIC8" /db-xref="InterPro:IPR001851" /db-xref="UniProtKB/TrEMBL:A1JIC8" /translation="MKQLNFLNAIISSFVLLVLA SFVMGLQLQLDGTKLIVQGASEVR WLWIGAACIVVFFFQLVRPLIQQGIKKVSGPAWV LPSFDGTTPRQKLLAAAIILIAAIA WPFLVSRGSVDIATLTLIYVMLGLGLNVVVGLSG LLVLGYGGFYAIGAYTYALLNHYY GLGFWESESLPLAGIVAALSGFLLGFPVLRRLRGDYL AIVTLGFGEIVRILLNNTTEITGG PNGISQIPKPTLFGLEFSRTAKDGGWDTFHNFFG LTYDPSDRIIFLYMVALLLVILTL FVINRLLRMPLGRAWEALREDEIACRSLGLSPTK IKLTAFTISAAFAGFAGTLFAARQ GFVSPESFTFVESAFVLAIVVLGGMGSQFAVILA AVLLVVSRELMRDLNAYSMLLLGA LMVLMMIWRPQGLLPMKRPQLKLKVADIKAKQGE QA" 
sig-peptide	268095..268169	/gene="livM" /locus-tag="YE0232" 

		/note="Signal peptide predicted for YE0232 by SignalP 2.0 HMM (Signal peptide probability 0.996) with cleavage site probability 0.812 between residues 25 and 26" /gene="livM"
misc-feature	join(268113..268181, 268224..268277, 268365..268424, 268434..268502, 268506..268574, 268584..268652, 268671..268724, 268875..268943, 269037..269105, 269148..269216, 269235..269294)	
		/locus-tag="YE0232" /inference="protein" motif:TMHMM:2.0" /note="11 probable transmembrane helices predicted for YE0232 by TMHMM2.0 at aa 7-29, 44-61, 91-110, 114-136, 138-160, 164-186, 193-210, 261-283, 315-337, 352-374 and 381-400" /gene="livM"
misc-feature	268314..269351	/locus-tag="YE0232" /inference="protein" motif:PFAM:PF02653" /note="Pfam match to entry PF02653 BPD-transp-2, Branched-chain amino acid transport system / permease component, score 357.7, E-value 8.3e-105"
gene	269378..270145	/gene="livG"
CDS	269378..270145	/locus-tag="YE0233" /gene="livG" /locus-tag="YE0233" /codon-start=1 /transl-table=11 /product="high-affinity branched-chain amino acid transport, ATP-binding protein" /protein-id="CAL10367.1" /db-xref="GI:122087586" /db-xref="GOA:A1JIC9" /db-xref="InterPro:IPR003439" /db-xref="InterPro:IPR003593" /db-xref="UniProtKB/TrEMBL:A1JIC9" /translation="MSTQPLLAVEGLSMRFGGLL AVNNVGLNLNQGEIVSLIGPNGAG KTTIFNCLTGfYRPTGGTIKLRDRHIEGLPGQVI ARMGVIRTFQHVRFLFREMTVVENL LVAQHQHLKSGVFAGLLKTPGFRRAEADALERAA TWLERVGLLELANRQAGNLAYGQQ RRLEIARCMVTRPELLMLDEPAAGLNPKETDELN QLIMELRDQHQVSVLLIEHDMKLV MGISDRIYVVNQGTPLAQGSPIEIRNNPDVIRAY LGE"
misc-feature	269471..270070	/gene="livG" /locus-tag="YE0233" /inference="protein"

		motif:PFAM:PF00005"
		/note="Pfam match to entry PF00005
		ABC-tran, ABC transporter, score
		230.2, E-value 1.9e-66"
misc-feature	269492..269515	/gene="livG"
		/locus-tag="YE0233"
		/inference="protein
		motif:Prosite:PS00017"
		/note="PS00017 ATP/GTP-binding
		site motif A (P-loop)."
misc-feature	269840..269884	/gene="livG"
		/locus-tag="YE0233"
		/inference="protein
		motif:Prosite:PS00211"
		/note="PS00211 ABC transporters
		family signature."
gene	270190..270891	/gene="livF"
		/locus-tag="YE0234"
CDS	270190..270891	/gene="livF"
		/locus-tag="YE0234"
		/codon-start=1
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		branched-chain amino acid
		transport, ATP-binding protein"
		/protein-id="CAL10368.1"
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		/db-xref="InterPro:IPR003593"
		/db-xref="UniProtKB/TrEMBL:A1JID0"
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		SLHIQQGEIVTLIGANGAGKTTLL
		GTLCGEPRATEGSIIIFGEQDITSWQTARIMREAI
		AIVPEGRRVFSRMTVEENLAMGGF
		FADRQQYQQRIERVYDLFPRLFERRAQRAGTMSG
		GEQQMLAIGRALMSQPKLLLLLDEP
		SLGLAPIIILQIFDTIQQLREEGMTIFLVEQNAN
		QALKLADRGYVLENGRIVLEDTGA
		ALLANEAVRSAYLGG"
misc-feature	270268..270816	/gene="livF"
		/locus-tag="YE0234"
		/inference="protein
		motif:PFAM:PF00005"
		/note="Pfam match to entry PF00005
		ABC-tran, ABC transporter, score
		200.5, E-value 1.7e-57"
misc-feature	270289..270312	/gene="livF"
		/locus-tag="YE0234"
		/inference="protein
		motif:Prosite:PS00017"
		/note="PS00017 ATP/GTP-binding
		site motif A (P-loop)."
misc-feature	270589..270633	/gene="livF"
		/locus-tag="YE0234"
		/inference="protein
		motif:Prosite:PS00211"
		/note="PS00211 ABC transporters
		family signature."
gene	complement(270952..2720	/locus-tag="YE0235"
	22)	
CDS	complement(270952..2720	/locus-tag="YE0235"

22)

/codon-start=1  
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protein"  
/protein-id="CAL10369.1"  
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/translation="MNIKSKLLLLILMLFIMQPI  
AMANPSFYPIKYNISNCSTVLED  
SSIAVSFRAHLVNDLFSDVNPHEQWKQLIKIPD  
DESIKLIPHHAISLYFYNYNGEE  
NHSINIRNISNIFLDGANSSHASNNIKEIKFDSS  
PGTFSHTHYDVSFTIAANTLKNIR  
IGATVGGVLNRGEQQYSLSSKGLSFGSTGKQCE  
IFDPQAGVAPEAVKIDPKFRLSSA  
RWQLKPLDLLDLNTANGAGLDASLENAENNR  
CIHYQSMGVRPVLHRIQANNLNL  
SADRNHFQKDKDKIINYQVILMTEGINYAFFLP  
EDNYINYLLKDAEKMCWTPKIKLF  
STNTTDKGSYSDTLNFTITPLA"

sig-peptide complement(271954..2720  
22)

/locus-tag="YE0235"  
  
/note="Signal peptide predicted  
for YE0235 by SignalP 2.0 HMM  
(Signal peptide probability 1.000)  
with cleavage site probability  
0.977 between residues 23 and 24"

misc-feature complement(271930..2719  
98)

/locus-tag="YE0235"  
  
/inference="protein  
motif:TMHMM:2.0"  
/note="1 probable transmembrane  
helix predicted for YE0235 by  
TMHMM2.0 at aa 9-31"

gene complement(272084..2726  
02)

/locus-tag="YE0236"

CDS complement(272084..2726  
02)

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/transl-table=11  
/product="putative exported  
protein"  
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/db-xref="GI:122087589"  
/db-xref="UniProtKB/TrEMBL:A1JID2"  
/translation="MNTLKIALILLLLPLQARAD  
TIPLGDIDVTLEVTAQPRIIEKP  
QGGWYHSITLTSTPENPSLYQAEVPITVKLRRLE  
GYRISVKKPLVLTRRSGVVYSPVK  
EFSPANISWGTDHASLKLLSDNPQTFTVAKSTSS  
QSTTDYLLQISAQAPSGLDITGKY  
YQGLTLLFETNS"

sig-peptide complement(272546..2726  
02)

/locus-tag="YE0236"  
  
/note="Signal peptide predicted  
for YE0236 by SignalP 2.0 HMM  
(Signal peptide probability 1.000)  
with cleavage site probability  
0.995 between residues 19 and 20"

gene complement(272611..2732  
40)

/locus-tag="YE0237"

CDS complement(272611..2732 /locus-tag="YE0237"  
40)  
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/transl-table=11  
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protein"  
/protein-id="CAL10371.1"  
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EVQKSAVVTVTNHGTETETVQ  
LYQLNNPGELPEQESLTPVSEQVPALFAAPAKM  
TLGPQQSGKILLNALSSPDKEQVY  
RLAVTPVNNRSVSGNGAVLGVQLSYMGLIRHLPA  
SQQHQQWTHHCINGSVKLHNTGNTR  
LQWYQLEAQGRVIDDFNLYPGKQRQLAVRDVRGM  
VESETFNLRCPAGKK"

gene complement(273233..2739 /locus-tag="YE0238"  
19)

CDS complement(273233..2739 /locus-tag="YE0238"  
19)  
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/product="putative exported  
protein"  
/protein-id="CAL10372.1"  
/db-xref="GI:122087591"  
/db-xref="UniProtKB/TrEMBL:A1JID4"  
/translation="MKYVYLLSTIALLAAPAIATT  
YAQLVAIPARTTVEALDQHRTVQV  
YNSGDKPLYLDITLQRVDPNGINPEQKTLISDIT  
QPEMIFNPNRITLGPQKQKRDIKLL  
PLKAPAQETLYRLYINPIVDIKAIGNSEDKSKIH  
APMTVSIGYGVLVHHLPPHAEQIR  
HWQHQCCLSGGNLMLTSTGTIHSKFKQLKSADNSA  
LTDSLNLYPGTPVTLSAQQLMGEV  
DNETFSIRCG"

sig-peptide complement(273854..2739 /locus-tag="YE0238"  
19)  
/note="Signal peptide predicted  
for YE0238 by SignalP 2.0 HMM  
(Signal peptide probability 0.998)  
with cleavage site probability  
0.796 between residues 22 and 23"

misc-feature complement(273839..2739 /locus-tag="YE0238"  
07)  
/inference="protein  
motif:TMHMM:2.0"  
/note="1 probable transmembrane  
helix predicted for YE0238 by  
TMHMM2.0 at aa 5-27"

gene complement(273937..2762 /locus-tag="YE0239"  
49)

CDS complement(273937..2762 /locus-tag="YE0239"  
49)  
/codon-start=1  
/transl-table=11  
/product="putative exported  
protein"  
/protein-id="CAL10373.1"  
/db-xref="GI:122087592"  
/db-xref="UniProtKB/TrEMBL:A1JID5"

		/translation="MEWNPMTKTPSIIDKAVLVAL LLTSFNSVGSEDIIEHLVPAGFS AAEEHNTLQLLGILDGKTLPSPLFFSEEKQQLSF DQQQYRDNHIDESSITLLAGILPQ IPYLQCCQNGCDYILSNHRITVDKVNHVVTITNNN NRYLMPVTTWGLVHNQSFDLRLAT EQYRAVSARGQGYLGLPYQSFAFAHWFYNAARIK NNNSYAHQSGYQQQTQIGVGSWYL QKNFQAHYLRAGRQNNLDNSAGSIHTLVNPALDQ FVTLSQSXYLAIDKPSAGSLVLYA TSDGDFEIRDNQLIRRIPAQLGRNEIDYSQLPG GYYTVEIRLVDRTGKVINQESQTI SNIGTQTNNGWFLTLGKGAVRSNNAPHLMQFGRS MNLKSLQTNITLLKDTASHWTAEG NASHPLGIYDLNITPTLGLMSGEKRSGGYLRLTG GNSGLGYASLARYQTPDVSIYAPN AGSTSASYSRRFGPTQLSYQFNQYKNNRQHRIQS RWDWRRPQYGMALSLGVQKGGQWN SQNNYGVFLNTTSLFLKNSASINSAYARQQLTTS ASYQKEFSNDNYGTSTFGIDGSTSG KNSVGSFAHRSGSRGDVSARAGVDNKIANGGIS YNGMLAISPQGIALGRSSYSGTAL LIETPDLAGTPYSFTAEGQPISGSGVYAIPIPRY QDRFFVVRTHSNHSDVEMNIQLPVN ITRAHPGQVFSSQANITLNLHYHGFLKGPQGQPV SGVIDETGDTVHPNGLFSIQSDVI LKNITVQSTSARYRCDMRQQRDHIYLCNLN"
sig-peptide	complement(276163..276249)	/locus-tag="YE0239"
		/note="Signal peptide predicted for YE0239 by SignalP 2.0 HMM (Signal peptide probability 0.973) with cleavage site probability 0.733 between residues 29 and 30"
misc-feature	complement(273940..273951)	/locus-tag="YE0239"
		/inference="protein motif:Prosite:PS00294" /note="PS00294 Prenyl group binding site (CAAX box)." /locus-tag="YE0239"
misc-feature	complement(275722..275745)	/locus-tag="YE0239"
		/inference="protein motif:Prosite:PS00030" /note="PS00030 Eukaryotic putative RNA-binding region RNP-1 signature."
gene	complement(276430..276906)	/locus-tag="YE0240"
CDS	complement(276430..276906)	/locus-tag="YE0240"
		/codon-start=1 /transl-table=11 /product="putative exported protein" /protein-id="CAL10374.1" /db-xref="GI:122087593" /db-xref="UniProtKB/TrEMBL:A1JID6" /translation="MKKTLLSIVTIAILASSSAN AAPVEKDIAIEAKIVSAIKLTKNS GRALDAIKMTYDPVKNDGHFTHTTEQIKFTSLGGT KIKVSLREAFAMLNSNNKTFTDYK"

		VNIEGKELKNGSAAEFFDLTNTDFSGSLNISAKQ PIDAVDGEIYTGVCLKLSIEAEA"
sig-peptide	complement(276844..276906)	/locus-tag="YE0240"  /note="Signal peptide predicted for YE0240 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.999 between residues 21 and 22"
gene	277469..278788	/gene="ugpB" /locus-tag="YE0241"
CDS	277469..278788	/gene="ugpB" /locus-tag="YE0241" /codon-start=1 /translation-table=11 /product="glycerol-3-phosphate-binding periplasmic protein" /protein-id="CAL10375.1" /db-xref="GI:122087594" /db-xref="GOA:A1JID7" /db-xref="InterPro:IPR006059" /db-xref="InterPro:IPR006061" /db-xref="UniProtKB/Swiss-Prot:A1JID7" /translation="MFNNAIRKTSICVALTLAFS ANAMAVTEIPFWHSMEGELGVEVN SLADRFNQSHSDYKIVPVYKGNYESLAAGIAAF RSGKAPAILQVYEVGTATMMASKA IKPVFQVFKDANINFDES FVPTVAGYYTDAKTG HLLSQPFNSSTPVLYYNKDAFKKA GLNPDQPPKTWQELAEDTAKLRAAGSSCGYASGW QGWIQIENFSAWHGQPIASRNNGF DGTDAVLEFNKPLQVKHIQLLSDMNKKGDFTYFG RKDESTAKFYNGDCAITTASSGSL ADIRHYAKFNYGVGMMPYDADAKDAPQNAIIGGA SLWVMDGKDKDITYKGVAEFLQFLT QPEIAAEWHQKTGYLPITTAAYELTKQQGFYDKN PGADVATRQMLNKPPLPYTKGLRL GNMPQIRTVVDEELEGVWTGKKTTPQQALDTAVSR GDVLLHRFEQTNK"
sig-peptide	277469..277543	/gene="ugpB" /locus-tag="YE0241" /note="Signal peptide predicted for YE0241 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.966 between residues 25 and 26"
misc-feature	277571..278731	/gene="ugpB" /locus-tag="YE0241" /inference="protein motif:PFAM:PF01547" /note="Pfam match to entry PF01547 SBP-bac-1, Bacterial extracellular solute-binding protein, score 217.0, E-value 1.9e-62"
misc-feature	277892..277945	/gene="ugpB" /locus-tag="YE0241" /inference="protein motif:Prosite:PS01037" /note="PS01037 Bacterial extracellular solute-binding proteins, family 1 signature."



gene 278898..279785 /gene="ugpA"  
 /locus-tag="YE0242"  
 CDS 278898..279785 /gene="ugpA"  
 /locus-tag="YE0242"  
 /codon-start=1  
 /transl-table=11  
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 transport system, permease protein"  
 /protein-id="CAL10376.1"  
 /db-xref="GI:122087595"  
 /db-xref="GOA:A1JID8"  
 /db-xref="InterPro:IPR000515"  
 /db-xref="UniProtKB/Swiss-Prot:A1J  
 ID8"  
 /translation="MSSSRPGFSCSWLPYLLVLP  
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 DPFGLSSEFVGLSNFIALFHDEYYLASFYTTLIF  
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 GSRIYQTLMILPYAVAPAAVLWIFLFPGLGL  
 ITHFLASLGYNWNHAQNSGQAMFL  
 VVLASVWKQISYNFLFFLAALQSIPRSLVEAAAI  
 DGAGPVRRFFNLVLPVLPVVSFFL  
 LVVNLVYAFFDTFPVIDAATGGGPMQATTTLIYK  
 IYREGFAGLDLSSSAAQSVVLMML  
 VIGLTVIQFRFVERKVRVYQ"  
 misc-feature join(278931..278999,  
 279111..279179,  
 279240..279308,  
 279366..279434,  
 279513..279581,  
 279693..279761) /gene="ugpA"  
 /locus-tag="YE0242"  
 /inference="protein  
 motif:TMHMM:2.0"  
 /note="6 probable transmembrane  
 helices predicted for YE0242 by  
 TMHMM2.0 at aa 12-34, 72-94,  
 115-137, 157-179, 206-228 and  
 266-288"

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LOCUS (LOC): AM236080 GenBank (R)  
 GenBank ACC. NO. (GBN): AM236080  
 GenBank VERSION (VER): AM236080.1 GI:115254414  
 CAS REGISTRY NO. (RN): 906734-09-6  
 SEQUENCE LENGTH (SQL): 5057142  
 MOLECULE TYPE (CI): DNA; circular  
 DIVISION CODE (CI): Bacteria  
 DATE (DATE): 14 Nov 2006  
 DEFINITION (DEF): Rhizobium leguminosarum bv. viciae chromosome complete  
 genome, strain 3841.  
 KEYWORDS (ST): complete genome  
 SOURCE: Rhizobium leguminosarum bv. viciae 3841  
 ORGANISM (ORGN): Rhizobium leguminosarum bv. viciae 3841  
 Bacteria; Proteobacteria; Alphaproteobacteria;  
 Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium  
 group; Rhizobium  
 REFERENCE: 1  
 AUTHOR (AU): Young, J.W.; Crossman, L.C.; Johnston, A.W.B.;  
 Thomson, N.R.; Ghazoui, Z.F.; Hull, K.H.; Wexler, M.;

Curson,A.R.J.; Todd,J.D.; Poole,P.S.; Mauchline,T.H.;  
 East,A.K.; Quail,M.A.; Churcher,C.; Arrowsmith,C.;  
 Cherevach,A.; Chillingworth,T.; Clarke,K.; Cronin,A.;  
 Davis,P.; Fraser,A.; Hance,Z.; Hauser,H.; Jagels,K.;  
 Moule,S.; Mungall,K.; Norbertczak,H.; Rabbinowitsch,E.;  
 Sanders,M.; Simmonds,M.; Whitehead,S.; Parkhill,J.

TITLE (TI): The genome of *Rhizobium leguminosarum* has recognizable  
 core and accessory components

JOURNAL (SO): Genome Biol., 7, R4-R4 (2006)

OTHER SOURCE (OS): CA 145:307927

REFERENCE: 2 (bases 1 to 5057142)

AUTHOR (AU): Crossman,L.C.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (21-FEB-2006) Crossman L.C., Pathogen  
 Sequencing Unit, The Wellcome Trust Sanger Institute,  
 Hinxton, Cambridge, Cambridgeshire, CB10 1SA, UNITED  
 KINGDOM

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..5057142	/organism="Rhizobium leguminosarum bv. viciae 3841" /mol-type="genomic DNA" /strain="3841" /db-xref="taxon:216596" /country="United Kingdom" /note="biovar: viciae 3841"
gene	complement(join(5056183 ..5057142,1..72))	/gene="hemE"
CDS	complement(join(5056183 ..5057142,1..72))	/locus-tag="RL4742" /gene="hemE" /locus-tag="RL4742" /EC-number="4.1.1.37" /inference="similar to sequence:INSDC:RC16796" /inference="similar to sequence:INSDC:SME591793" /note="similarity:fasta; with=UniProt:DCUP-RHOCA (EMBL:RC16796); Rhodobacter capsulatus (Rhodopseudomonas capsulata).; hemE; Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD). Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD).; length=344; id 50.621; 322 aa overlap; query 1-318; subject 23-344 similarity:fasta; with=UniProt:Q92KV8-RHIME (EMBL:SME591793); Rhizobium meliloti (Sinorhizobium meliloti).; PROBABLE UROPORPHYRINOGEN DECARBOXYLASE PROTEIN (EC 4.1.1.37).; length=319; id 81.073; 317 aa overlap; query 1-317; subject 1-317; uroporphyrinogen decarboxylase" /codon-start=1

		/transl-table=11 /product="putative uroporphyrinogen decarboxylase" /protein-id="CAK10225.2" /db-xref="GI:115259114" /db-xref="GOA:Q1MA15" /db-xref="UniProtKB/TrEMBL:Q1MA15" /translation="MSDTGRKIMRVLSGESLSPP PLWLMRQAGRYLPEYRETRAKAGS FLDLCYTPEHAVEVTLQPIRRYGFDAAILFSDIL VIPDAMKRNVRFTEGHGPEMDPID EAGIGSLNGEEVVDYLRPVLETVRRLREELPAET TLLGFCGAPWTVATYMIAGHGTPD QAPARLFAYKHARAFEHLLMLLADVSA DYLV AQI DAGADAVQIFDSWAGVLGEKEFEA FAIRPVARMIASVKSRRPHARI IAFAKGAGYQLK TYRQKTGADAIGLDWSVPLAFAAE LQKDGFPVQGNLDPMRVVAGGRALEEGIDDILQHL GNGPLIFNLGHGITPQADPEHVRL LVDRVRGGA" /locus-tag="RL0001" /locus-tag="RL0001" /inference="similar to sequence:INSDC:SME591782" /note="similarity:blastp; with=UniProt:Y001-RHIME (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; Hypothetical UPF0085 protein R00001.; length=273; E()=0e-120; conserved hypothetical protein" /codon-start=1 /transl-table=11 /product="Hypothetical UPF0085 protein R00001." /protein-id="CAK05489.1" /db-xref="GI:115254415" /db-xref="UniProtKB/TrEMBL:Q1MNF6" /translation="MENRTNFFHLHLISDSTGET LISAGRAASQFRSAQPIEHVYPL IRNRKQLLPVLQAIDDA PGIVLYTIVDRELASLI DERCIEMGVASVNVLEPVMNAFQI YLGAPSRRRVGAQHVMNAGYFARIEALNFTMDHD DGQMPDDYNDADVVIIGISRTSKT PTSIYLANRGIKTANIPIVYGVPLPESLFVASKP LIVCLIATTDRI SQVREN RV LGVT QGFDREHYTDRAAISEELKYARSLCARHNWPLID VTRRSIEETAAAI VALRPKLR" /locus-tag="RL0001" /inference="protein motif:Pfam:PF03618.4" /note="Pfam match to entry PF03618.4 DUF299" /locus-tag="RL0002" /locus-tag="RL0002" /inference="similar to sequence:INSDC:SME591782" /inference="similar to sequence:UniProtKB:Q92TF1" /note="similarity:fasta; SWALL:Y002-RHIME (SWALL:Q92TF1);
gene	474..1295	
CDS	474..1295	
misc-feature	486..1286	
gene	1329..1928	
CDS	1329..1928	

		Rhizobium meliloti; maf-like protein r00002; length 199 aa; 198 aa overlap; query 1-198 aa; subject 1-198 aa similarity:fasta; with=UniProt:Y002-RHIME (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; Maf-like protein R00002.; length=199; id 68.687; 198 aa overlap; query 1-198; subject 1-198" /codon-start=1 /transl-table=11 /product="putative septum formation protein" /protein-id="CAK05490.1" /db-xref="GI:115254416" /db-xref="UniProtKB/TrEMBL:Q1MNF5" /translation="MTPKLILASSSPFRRMLMEN AGLSFEAHAARIDERAVEAPLENA GAKPDAVALVLARAKAEVSSRFPDSLVIQSDQT MSLGDSVVFHKPTDLADAASHLQAL SGVTHRLNSAVAIVSDGVVLWEHLAHAQLTMRPL TVEFIARHLARVGERALSSVGAYQ LEGEGIQLFIEKIEGDYFTILGLPMLPLLKKLREL GAIDG"
misc-feature	1335..1919	/locus-tag="RL0002" /inference="protein motif: Pfam:PF02545.4" /note="Pfam match to entry PF02545.4 Maf"
gene	1921..2778	/locus-tag="RL0003"
CDS	1921..2778	/locus-tag="RL0003" /inference="similar to sequence:INSDC:ECUW67" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:AROE-ECOLI (EMBL:ECUW67); Escherichia coli.; aroE; Shikimate dehydrogenase (EC 1.1.1.25).; length=EC 1 ( 272; id 38.095; 273 aa overlap; query 14-277; subject 6-266 similarity:fasta; with=UniProt:AROE-RHIME (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; aroE; Shikimate dehydrogenase (EC 1.1.1.25).; length=EC 1 ( 286; id 75.439; 285 aa overlap; query 1-285; subject 1-285" /codon-start=1 /transl-table=11 /product="putative shikimate dehydrogenase" /protein-id="CAK05491.1" /db-xref="GI:115254417" /db-xref="GOA:Q1MNF4" /db-xref="UniProtKB/TrEMBL:Q1MNF4" /translation="MGDSRETFGPKAFVTGFPIK

		HSRSPLIHGYWLKTLGLLGSYRAH EVTPEAFADFIHSLKDGSSGFTGGNVTIPHKELA FRLADKPDALSQELGASNTLWRED GALHATNTDGRGFIANLDERHPGWDHRGTAUVVF AGGASRAIIQAVRDRGFKEIHVVN RTVERARELADRFGPRVQAHPAGALVEVMKGAGL FINTTSLGMDGEPAPQLDFSPLAA DAVVTDIVYVPLKTPILAQAEEQGFPIDGLGML LHQAVPGFEKWFGQRPIDAPLRA LIIADMEAH"
misc-feature	1999..2718	/locus-tag="RL0003" /inference="protein motif: Pfam: PF01488.5" /note="Pfam match to entry PF01488.5 Shikimate-DH"
gene	2778..3389	/locus-tag="RL0004"
CDS	2778..3389	/locus-tag="RL0004" /inference="similar to sequence: UniProtKB: Q92TE9" /inference="similar to sequence: UniProtKB: Q98DY2" /note="similarity: fasta; SWALL: COAE-RHILO (SWALL: Q98DY2); Rhizobium loti; dephospho-coa kinase; coaE; length 197 aa; 192 aa overlap; query 1-192 aa; subject 1-192 aa similarity: fasta; SWALL: COAE-RHIME (SWALL: Q92TE9); Rhizobium meliloti; dephospho-coa kinase; coaE; length 194 aa; 192 aa overlap; query 1-192 aa; subject 1-192 aa" /codon-start=1 /transl-table=11 /product="putative dephospho-CoA kinase" /protein-id="CAK05492.1" /db-xref="GI:115254418" /db-xref="GOA:Q1MNF3" /db-xref="UniProtKB/TrEMBL:Q1MNF3" /translation="MLKIGLTGSIGMGKSTAAKL FADAGIPVNDSDAVVHDLYAGEAA PLVNAAFPGTMKDGAVDRRELGRQLALDPDGFKC LEAIVHPLVRKRETEFLKRQRATG ADMVLLDIPLL FETGAEARVDVVVVVSTDPQIQ RVLAREGMTEEKFDMLSRQTPD AEKRRRADYLDITSHSIATTRERVFEIVADLKTR IAKGDFRNA"
misc-feature	2781..3314	/locus-tag="RL0004" /inference="protein motif: Pfam: PF01121.8" /note="Pfam match to entry PF01121.8 CoaE"
gene	3382..4104	/locus-tag="RL0005"
CDS	3382..4104	/locus-tag="RL0005" /inference="similar to sequence: INSDC: AL591782" /inference="similar to sequence: UniProtKB: P03007" /note="similarity: fasta; SWALL: DP3E-ECOLI (SWALL: P03007); Escherichia coli; DNA polymerase

		iii, epsilon chain; dnaQ; length 243 aa; 244 aa overlap; query 2-233 aa; subject 7-241 aa similarity:fasta; SWALL:Q92TE8 (EMBL:AL591782); Rhizobium meliloti; probable DNA polymerase iii, epsilon chain protein; length 242 aa; 240 aa overlap; query 1-240 aa; subject 1-234 aa" /codon-start=1 /transl-table=11 /product="putative DNA polymerase subunit" /protein-id="CAK05493.1" /db-xref="GI:115254419" /db-xref="GOA:Q1MNF2" /db-xref="UniProtKB/TrEMBL:Q1MNF2" /translation="MREIIFDTETTGLDNRADRI IEIGGIELFNHFPTGNTIIHIFINP GDQKVHPDALAVHGITDEFLKDKQPFAEVAEQIL TFFGDAKWIAHNATFDMGFINAEF ARIGLPPILPERVLDTLSMARRKHPMGPNSLDAL CRRYGIDNSHRTKHGALLDSELLA EVYIEMIGGRQAALGLGMVGKSNQAARGEMGMED DVVIAALLERPRPLAPRLSQTEEQ AHEALVAKLGEKSVWAKYANLD" /locus-tag="RL0005" /inference="protein motif: Pfam:PF00929.11" /note="Pfam match to entry PF00929.11 Exonuc-X-T"
misc-feature	3388..3870	
gene	complement(4172..4654)	/gene="secB"
CDS	complement(4172..4654)	/locus-tag="RL0006" /gene="secB" /locus-tag="RL0006" /inference="similar to sequence:INSDC:AE008975" /inference="similar to sequence:UniProtKB:P15040" /note="similarity:fasta; SWALL:SECB-ECOLI (SWALL:P15040); Escherichia coli, Escherichia coli O6, Escherichia coli O157:H7, and Shigella flexneri; protein-export protein SecB; secB; length 155 aa; 151 aa overlap; query 1-151 aa; subject 1-145 aa similarity:fasta; SWALL:Q8UJC2 (EMBL:AE008975); Agrobacterium tumefaciens; protein-export protein; secB; length 160 aa; 160 aa overlap; query 1-160 aa; subject 1-160 aa" /codon-start=1 /transl-table=11 /product="putative SecB protein export protein" /protein-id="CAK05494.1" /db-xref="GI:115254420" /db-xref="GOA:Q1MNF1" /db-xref="UniProtKB/TrEMBL:Q1MNF1" /translation="MADDNNSNGAANPTLSILAQ YTKDLSFENPGAPRSLQARDKAPT

		ININNVNVNANPLSDTDFDVVLSLNAEAKDGDKTV FHAELTYGGVFRVAGFPQEHMLPV LFIECPRMLFPFARQIIADVTRNGGFPPLMIDPI DFTQMFAQRVAEEQARAKVQAVPN
misc-feature	complement(4202..4654)	/gene="secB" /locus-tag="RL0006" /inference="protein motif: Pfam: PF02556.4" /note="Pfam match to entry PF02556.4 SecB"
gene	complement(4756..5271)	/locus-tag="RL0007"
CDS	complement(4756..5271)	/locus-tag="RL0007" /inference="similar to sequence: INSDC: AE007943" /inference="similar to sequence: INSDC: ECUW93" /note="similarity: fasta; with=UniProt: FXSA-ECOLI (EMBL: ECUW93); Escherichia coli.; fxsA; FxsA protein (Suppressor of F exclusion of phage T7).; length=158; id 36.364; 132 aa overlap; query 4-132; subject 1-129 similarity: fasta; with=UniProt: Q8UJC1 (EMBL: AE007943); Agrobacterium tumefaciens (strain C58/ATCC 33970).; fxsA; Hypothetical protein fxsA (AGR-C-11p).; length=178; id 48.521; 169 aa overlap; query 4-167; subject 1-169" /codon-start=1 /transl-table=11 /product="putative transmembrane FxsA-family protein" /protein-id="CAK05495.1" /db-xref="GI:115254421" /db-xref="GOA:Q1MNF0" /db-xref="UniProtKB/TrEMBL:Q1MNF0" /translation="MTDMRFSILPAFILLLPFAE IAGFVVVGQAIGLWLTLLVLMGLF VLGVLLRRQGIGILRRMSSEGRNGVMPGRDLLR PAMNVIASLLLIIPGFLTDIIAIL ILIPPVRDLVWRAIAKRFVVVNAKGGSSSGPQPD FRDRKPNKSVVDLEEEDYHREPDR NSPWSGRHLGD"
misc-feature	complement(4879..5244)	/locus-tag="RL0007" /inference="protein motif: Pfam: PF04186.2" /note="Pfam match to entry PF04186.2 FxsA"
misc-feature	complement(join(4957..5025,5116..5184,5194..5253))	/locus-tag="RL0007"  /inference="protein motif: TMHMM: 2.0" /note="3 probable transmembrane helices predicted at aa 7-26, 30-52 and 83-105"
gene	5394..6098	/locus-tag="RL0008"
CDS	5394..6098	/locus-tag="RL0008"

		/inference="similar to sequence:INSDC:AL591782" /note="similarity:fasta; SWALL:Q92TE6 (EMBL:AL591782); Rhizobium meliloti; putative translocase transmembrane protein; length 233 aa; 234 aa overlap; query 1-233 aa; subject 1-233 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05496.1" /db-xref="GI:115254422" /db-xref="GOA:Q1MNE9" /db-xref="UniProtKB/TrEMBL:Q1MNE9" /translation="MSSNDFITLFFLVAAVLIF QLRSVLGRRTGNEKPPRDLYTPRD AAPAEAADAGKVVTLP RRDATTEDRFAAIDAF AAPGTPLNESLRALNKADPAFSPK EFLNGARMAYEMIVMAYADGDRKTLKNLLSREVY DGFDAAIGEREARGEKVKSTFVGI DKAEITHAETKGSEAQITVRIASQLISATYDKAD VliegDAENVAEVNDVWTFARDTR SRDPNWKLVA TESEHE" /locus-tag="RL0008" /inference="protein motif: Pfam:PF04280.4" /note="Pfam match to entry PF04280.4 Tim44"
misc-feature	5646..6086	
gene	6091..7209	/gene="mltA" /locus-tag="RL0009"
CDS	6091..7209	/gene="mltA" /locus-tag="RL0009" /inference="similar to sequence:INSDC:AL591782" /inference="similar to sequence:UniProtKB:P46885" /note="similarity:fasta; SWALL:MLTA-ECOLI (SWALL:P46885); Escherichia coli, and Escherichia coli O157:H7; membrane-bound lytic murein transglycosylase a precursor; mltA; length 365 aa; 282 aa overlap; query 92-369 aa; subject 112-360 aa similarity:fasta; SWALL:Q92TE5 (EMBL:AL591782); Rhizobium meliloti; putative lytic murein transglycosylase a protein; length 372 aa; 365 aa overlap; query 8-371 aa; subject 3-365 aa" /codon-start=1 /transl-table=11 /product="putative membrane-bound lytic murein transglycosylase a precursor" /protein-id="CAK05497.1" /db-xref="GI:115254423" /db-xref="GOA:Q1MNE8" /db-xref="UniProtKB/TrEMBL:Q1MNE8" /translation="MSDHASDFVLQAISFDTLEG



		WKDDDP SGLFEVMRSCRRQITDVK PYRTGSLGLSSEDLLPLLA AEDFTPSSPASARA FFETHCRPFLIRRNDGNSGFVTAF YEPDIDV SERPDEIFRFPFYRRPDDLIDLDDANR PAGLDKAYAFGRLHEGHVTAYPDR RAIDQGFLEGRGLEIAWAKSKVDVFFVHVQGAAR LRYQDGRIGRITYAAKAGHAFSAI GKLLIERGEIDRAEISMQAIRAWLARNPERVDEV LWHNRSYIFFRDAPVADPQAGPIA AAKVPLLAGRSLAVDRTIHTFGFPFFIRAESLTH LDQGRPFRRMLALDTGSAIVGPA RGDIFTGSGDIAGESAGTVRNQADFVILIPNAAA GRFD"
misc-feature	6310..6936	/gene="mltA" /locus-tag="RL0009" /inference="protein" motif: Pfam: PF03562.4" /note="Pfam match to entry PF03562.4 MltA"
misc-feature	6946..7179	/gene="mltA" /locus-tag="RL0009" /inference="protein" motif: Pfam: PF06725.1" /note="Pfam match to entry PF06725.1 3D"
gene	7209..7775	/locus-tag="RL0010"
CDS	7209..7775	/locus-tag="RL0010" /inference="similar to sequence: INSDC: SME591782" /note="similarity: fasta; with=UniProt: Q92KV6 (EMBL: SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; Hypothetical protein SMC02784.; length=188; id 62.766; 188 aa overlap; query 1-185; subject 1-185" /codon-start=1 /transl-table=11 /product="putative Smr domain protein" /protein-id="CAK05498.1" /db-xref="GI:115254424" /db-xref="UniProtKB/TrEMBL: Q1MNE7" /translation="MARDRKL SADERILWGKVAR STRPMPGKAGALTELD AFLAEAEA AAEREQEKRTPATPTPLQPTAP SMAKPSAGVHHP LEKPVKRKIAKGRLALEARIDLHG LVQSEAHTILLDFLIRAHERSMRHVLVITGKGSS MGSDGALKRAVPLWFSKPEFRYLI SSYESAAQHGGEGALYIRLSRRHGERP"
misc-feature	7500..7751	/locus-tag="RL0010" /inference="protein" motif: Pfam: PF01713.8" /note="Pfam match to entry PF01713.8 Smr"
gene	7772..8149	/locus-tag="RL0011"
CDS	7772..8149	/locus-tag="RL0011" /inference="similar to sequence: INSDC: AE008975" /note="similarity: fasta; SWALL: Q8UJB7 (EMBL: AE008975);

		Agrobacterium tumefaciens; transcriptional regulator; length 121 aa; 121 aa overlap; query 1-121 aa; subject 1-121 aa" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="CAK05499.1" /db-xref="GI:115254425" /db-xref="GOA:Q1MNE6" /db-xref="UniProtKB/TrEMBL:Q1MNE6" /translation="MTPFGEAVRRLRARKGVSQK EMAEALNVSPAYLSALEHGKRG LP TFDLLQRIAGYFNIIWDEAEELFLLARSSDPRVV IDTSGLPPEYTEFANRLARRIRNL DSAEIGRLSALLENGGKGDKAS" /locus-tag="RL0011" /inference="protein motif: Pfam:PF01381.9" /note="Pfam match to entry PF01381.9 HTH-3"
misc-feature	7793..7960	
gene	8285..10720	/gene="gyrB"
CDS	8285..10720	/locus-tag="RL0012" /gene="gyrB" /locus-tag="RL0012" /inference="similar to sequence:INSDC:AE007943" /inference="similar to sequence:INSDC:CEK132C8R" /note="similarity:fasta; with=UniProt:GYRB-ECOLI (EMBL:CEK132C8R); Shigella flexneri.; gyrB; DNA gyrase subunit B (EC 5.99.1.3).; length=EC 5.99.1 ( 803; id 58.612; 807 aa overlap; query 12-811; subject 1-803 similarity:fasta; with=UniProt:Q8UJB6 (EMBL:AE007943); Agrobacterium tumefaciens (strain C58/ATCC 33970).; gyrB; DNA gyrase subunit B (AGR-C-19p).; length=AGR-C-19p; id 86.190; 811 aa overlap; query 1-811; subject 6-816" /codon-start=1 /transl-table=11 /product="putative DNA gyrase subunit B" /protein-id="CAK05500.1" /db-xref="GI:115254426" /db-xref="GOA:Q1MNE5" /db-xref="UniProtKB/TrEMBL:Q1MNE5" /translation="MSDTSATENGVS TEYGADSI KVLKGLDAVRKRPGMYIGDTDDGS GLHHMVYEVVDNAIDEALAGHADIVTVTLNPDGS VTVTDNRGRIPTDIHTGEGVSAAE VIMTQLHAGGKFDQNSYKVS GGLHGVGVSVVNAL SVWLKLIKIRRHDKIHEMSFTHGVA DAPLKVTGDAPNETGTEVSFMPSTDTFTMTEFDY GTLEHRLRELAFLNSGVRILLTDK RHSDIKQEELRYDGGLEAFVAYLDRAKSLVDKP

VAIHGEKDGITVEVAMWWNDSYHE  
 NVLCFTNNIPQRDGGTHMAGFRAALTRQVVSAD  
 SSGITKREKVTLQGEDCREGLTAV  
 LSVKVPDPKFSSQTKDKLVSEVRPVVESLVNEA  
 LNTWFEEHPSEAKILVGKVVEAAA  
 AREAARKARELTRRKGALDIASLPGKLADCSE  
 PTKSEVFLVEGDSAGGSAKQGRSR  
 ENQAILPLRGKILNVERARFDKMLSSQEIGTLIT  
 ALGTGIGKDEFNVEKLRVHKIIIM  
 TDADVDGAHIRTLLLTFFFRQMPQLIERGHLYIA  
 QPPLYKVSRGKSVQYLKDEKALEE  
 YLISQGLEDA SLRLGSGEVVAGQDLREVILDALR  
 MRALLDNLHSRYNRSASVEQAAIAG  
 ALNAELASDPARALALANEVAGRLDIIAEETERG  
 WRGDVTTDGGRLRLERMVRGVREL  
 VLDMALIGSSDARHIDQLTARLKEIYQTPPSLHR  
 REGDIEISGPRALLDAIFASGRKG  
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misc-feature 8405..8839

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 PF02518.9 HATPase-c"

misc-feature 8981..9493

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 PF00204.9 DNA-gyraseB"

misc-feature 9662..9910

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 motif: Pfam: PF01751.7"  
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 PF01751.7 Toprim"

misc-feature 10487..10684

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CDS complement(10828..11427 )

/inference="similar to  
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 /note="similarity: fasta;  
 with=UniProt: Q8UJB5  
 (EMBL: AE007944); Agrobacterium  
 tumefaciens (strain C58/ATCC  
 33970).; NAD(P)H-flavin  
 oxidoreductase (AGR-C-21p).;  
 length=P; id 60.204; 196 aa  
 overlap; query 1-196; subject  
 1-195"  
 /codon-start=1  
 /transl-table=11  
 /product="putative oxidoreductase"

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/misc-feature complement(10936..11379 /locus-tag="RL0013"
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/inference="protein
motif: Pfam: PF00881.10"
/note="Pfam match to entry
PF00881.10 Nitroreductase"

gene complement(11473..11769 /locus-tag="RL0014"
)

CDS complement(11473..11769 /locus-tag="RL0014"
)
/inference="similar to
sequence: INSDC: AP002994"
/note="similarity: fasta;
SWALL: Q98NF3 (EMBL: AP002994);
Rhizobium loti; msl0164 protein;
length 97 aa; 92 aa overlap; query
5-96 aa; subject 1-92 aa"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
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/db-xref="UniProtKB/TrEMBL: Q1MNE3"
/translation="MEFEMHLSKAVVRTEHASRY
LQQLCKHWSHKFSVDFDPLKGRVP
FSETAEVTFAADDAALMTLSVADSSQQERMQHV
IDDHLKRFAFREELDIVWTN"

gene 11922..12887 /locus-tag="RL0015"
CDS 11922..12887 /locus-tag="RL0015"
/inference="similar to
sequence: INSDC: SSD917"
/note="similarity: fasta;
with=UniProt: P74752 (EMBL: SSD917);
Synechocystis sp. (strain PCC
6803).; Slr0605 protein.;
length=319; id 56.013; 316 aa
overlap; query 1-315; subject
1-314"
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/transl-table=11
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glutathione-S-transferase"
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/db-xref="UniProtKB/TrEMBL: Q1MNE2"
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gene	13031..13873	/locus-tag="RL0016"
CDS	13031..13873	/locus-tag="RL0016" /inference="similar to sequence: INSDC: AE007944" /inference="similar to sequence: INSDC: AF169302" /note="similarity: fasta; with=UniProt: Q8VUC7 (EMBL: AF169302); Burkholderia cepacia (Pseudomonas cepacia).; DntG.; length=281; id 38.267; 277 aa overlap; query 5-279; subject 13-279 similarity: fasta; with=UniProt: Q8UJB4 (EMBL: AE007944); Agrobacterium tumefaciens (strain C58/ATCC 33970).; hpcE; 2-hydroxyhepta-2,4-diene-1,7-dioat e isomerase (AGR-C-22p).; length=280; id 87.097; 279 aa overlap; query 1-279; subject 1-279" /codon-start=1 /transl-table=11 /product="putative FAA hydrolase family protein" /protein-id="CAK05504.1" /db-xref="GI:115254430" /db-xref="GOA:Q1MNE1" /db-xref="UniProtKB/TrEMBL:Q1MNE1" /translation="MKLMRVGEAGSEKPALLDAD GKIRDLSGHVADIGGEAIGPAGLA KIAAIDPKSLPELVPGRIGACVAGTGKFCIGLN YSDHAAETGATVPPEPIIFMKATS AIVGPNDNVIIIPRGSEKTDWEVELGVVIGKTAKY VTEAEALDYVAGYCVSNDVSERAF QTERSGQWTKGKSCDTFGPIGPWLVTKDEIPEPQ NLGMWLTVNGQKMONGSSKTMVYG VAFLVSYLSQFMSLHPGDVISTGTPPGVGMGLKP PRYLKSGDVVELGIEGLGTQKQTF VADR"
misc-feature	13286..13783	/locus-tag="RL0016" /inference="protein" motif: Pfam: PF01557.8" /note="Pfam match to entry PF01557.8 FAA-hydrolase"
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CDS	14079..15356	/locus-tag="RL0017" /inference="similar to

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		sequence:INSDC:SME591782"
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		with=UniProt:Q71KW6
		(EMBL:AF474374); Azospirillum
		brasiliense.; phaZ; PHB
		depolymerase.; length=603; id
		57.471; 348 aa overlap; query
		61-406; subject 257-602
		similarity:fasta;
		with=UniProt:Q92TD3
		(EMBL:SME591782); Rhizobium
		meliloti (Sinorhizobium
		meliloti).; Hypothetical protein
		SMc02770.; length=424; id 76.000;
		425 aa overlap; query 1-424;
		subject 1-423 Codons 60 to the
		C-terminus are similar to codons
		255 to the C-terminus of
		Azospirillum brasiliense PHB
		depolymerase phaZ UniProt:Q92TD3
		(EMBL:SME591782) (603 aa), and
		entire protein is similar to
		Rhizobium meliloti (Sinorhizobium
		meliloti) Hypothetical protein
		SMc02770 UniProt:Q92TD3
		(EMBL:SME591782) (424 aa)"
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		DWIDARMVPMTEGTFDFDDYIDYV
		IEMLHFLGHDTHVVAVCQPSVPVLA AAAVMEEAR
		DPLSPASMTLMGGPIDTRINPTAV
		NKLAQERSLQWFSDNVIMNVPWPQPGFVRPVYPG
		FLQLSGFMSMNLDRLVAHKEFFM
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		EEVFIKHSPLPKGELMHRGKRVDP
		AIRNVALLTVEGENDDISGVGTMAAQTCVNIP
		EDMRMHYLPDPVGHYGVFNISRFR
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misc-feature	14694..15299	/locus-tag="RL0017"
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		/note="Pfam match to entry
		PF06850.1 PHB-depo-C"
gene	15502..15936	/locus-tag="RL0018"
CDS	15502..15936	/locus-tag="RL0018"
		/inference="similar to
		sequence:INSDC:AL591782"
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		SWALL:Q92TD2 (EMBL:AL591782);
		Rhizobium meliloti; conserved

		hypothetical transmembrane protein; length 141 aa; 143 aa overlap; query 1-143 aa; subject 1-140 aa" /codon-start=1 /transl-table=11 /product="putative transmembrane protein" /protein-id="CAK05506.1" /db-xref="GI:115254432" /db-xref="GOA:Q1MND9" /db-xref="UniProtKB/TrEMBL:Q1MND9" /translation="MNQSALLRPDWTPATIALMI LGFMVFWPLGLAMLAYIIFGDRLR GFKRDVNEATDGFFASCRRPHGRHRPHFSTGNVA FDDWRKAELDRMEEERRKLDREME EFDSYLRELRRAKDQEEFDRFMRDRRNAKRDDNG PVAEYQTP"
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gene	16044..16802	/locus-tag="RL0019"
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misc-feature	16131..16778	/locus-tag="RL0019" /inference="protein motif:PFam:PF01863.6" /note="Pfam match to entry PF01863.6 DUF45"
gene	16969..17637	/locus-tag="RL0020"
CDS	16969..17637	/locus-tag="RL0020" /inference="similar to sequence:UniProtKB:Q8UJB1" /inference="similar to

		sequence:UniProtKB:Q9X4E3" /note="similarity:fasta; SWALL:TRPF-RHOSH (SWALL:Q9X4E3); Rhodobacter sphaeroides; n-(5'-phosphoribosyl)anthranilate; trpF; length 212 aa; 206 aa overlap; query 5-209 aa; subject 6-210 aa similarity:fasta; SWALL:TRPF-AGRT5 (SWALL:Q8UJB1); Agrobacterium tumefaciens; n-(5'-phosphoribosyl)anthranilate; trpF; length 220 aa; 210 aa overlap; query 1-210 aa; subject 1-210 aa" /codon-start=1 /transl-table=11 /product="putative N-(5'-phosphoribosyl)anthranilate" /protein-id="CAK05508.1" /db-xref="GI:115254434" /db-xref="GOA:Q1MND7" /db-xref="UniProtKB/TrEMBL:Q1MND7" /translation="MRPDIKICGLKTPEAVDRAL KRGATHIGFIFFEKSPRYIEPDLA AKLAEPARGKAKIVAVVVDPTNDELDEIVSLLKP DMLQLHGNEspehVLTIKALYGLP VMKVFSVRTADDLKRVEAYIGIADRFDFDAKAPK GSELPGGNGISFDWSLLSWLDGSV DYMLSGGLNKDNVAEALFVTKAPGIDVSSGVETA PGVKSVAKIDEFFDAVEKANAPMM ASGS" /locus-tag="RL0020" /inference="protein motif:Pfam:PF00697.10" /note="Pfam match to entry PF00697.10 PRAI"
misc-feature	16981..17595	/gene="trpB" /locus-tag="RL0021"
gene	17640..18860	/gene="trpB"
CDS	17640..18860	/locus-tag="RL0021" /EC-number="4.2.1.20" /inference="similar to sequence:UniProtKB:P56929" /inference="similar to sequence:UniProtKB:Q9X4E5" /note="similarity:fasta; SWALL:TRPB-RHOSH (SWALL:Q9X4E5); Rhodobacter sphaeroides; tryptophan synthase beta chain; trpB; length 409 aa; 401 aa overlap; query 8-406 aa; subject 7-407 aa similarity:fasta; SWALL:TRPB-RHIET (SWALL:P56929); Rhizobium etli; tryptophan synthase beta chain; trpB; length 406 aa; 406 aa overlap; query 1-406 aa; subject 1-406 aa" /codon-start=1 /transl-table=11 /product="putative tryptophan synthase beta chain" /protein-id="CAK05509.1" /db-xref="GI:115254435"



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misc-feature	17820..18809	/gene="trpB" /locus-tag="RL0021" /inference="protein motif: Pfam:PF00291.10" /note="Pfam match to entry PF00291.10 PALP"
gene	18864..19703	/gene="trpA" /locus-tag="RL0022"
CDS	18864..19703	/gene="trpA" /locus-tag="RL0022" /inference="similar to sequence: INSDC:AE007944" /inference="similar to sequence: INSDC:AF107094" /note="similarity:fasta; with=UniProt:TRPA-RHOSH (EMBL:AF107094); Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).; trpA; Tryptophan synthase alpha chain (EC 4.2.1.20).; length=263; id 62.214; 262 aa overlap; query 4-265; subject 3-259 similarity:fasta; with=UniProt:TRPA-AGRT5 (EMBL:AE007944); Agrobacterium tumefaciens (strain C58/ATCC 33970).; trpA; Tryptophan synthase alpha chain (EC 4.2.1.20).; length=279; id 84.229; 279 aa overlap; query 1-279; subject 1-279; putative tryptophan synthase, alpha subunit" /codon-start=1 /transl-table=11 /product="Tryptophan synthase alpha chain." /protein-id="CAK05510.1" /db-xref="GI:115254436" /db-xref="GOA:Q1MND5" /db-xref="UniProtKB/TrEMBL:Q1MND5" /translation="MTARMDKRFAELKAEGRPAL VTYFMGGDPDYDTSLGIMKALPEA GSDIIELGMPFSDPMADGPAIQLAGQRALKGGQT LKKTLLQLAADFRKTNDATPIVMMG YYNPIYIYGVEKFLDDALLAGIDGLIVVDLPPEM

		DDELCPAIRKGINFIRLATPTTD EKRLPKVLKNTSGFVYYVSMNGITGSALPDPSLV SGAVERIKQHTKLPVCVGFVVKTA EHAKVIGGSADGVVVGTAIVNQVATSLTHDGKAT ADTVQAVATLVRGLSTGTRSARLV AAE"
misc-feature	18888..19676	/gene="trpA" /locus-tag="RL0022" /inference="protein motif: Pfam: PF00290.9" /note="Pfam match to entry PF00290.9 Trp-syntA"
gene	19845..20750	/locus-tag="RL0023"
CDS	19845..20750	/locus-tag="RL0023" /inference="similar to sequence: INSDC: HS028244" /inference="similar to sequence: INSDC: SME591782" /note="similarity: fasta; with=UniProt: ACCD-ECOLI (EMBL: HS028244); Escherichia coli O157: H7.; accD; Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta (EC 6.4.1.2) (ACCcase beta chain).; length=304; id 46.831; 284 aa overlap; query 1-283; subject 1-281 similarity: fasta; with=UniProt: Q92TC7 (EMBL: SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PROBABLE ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA PROTEIN (EC 6.4.1.2).; length=304; id 85.526; 304 aa overlap; query 1-301; subject 1-304; putative acetyl-coenzyme A carboxylase carboxyl transferase subunit" /codon-start=1 /transl-table=11 /product="Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta (ACCcase beta chain)." /protein-id="CAK05511.1" /db-xref="GI: 115254437" /db-xref="GOA: Q1MND4" /db-xref="UniProtKB/TrEMBL: Q1MND4" /translation="MNWITNYVRPRINSMLGRRE VPENLWIKPETGEMVFHKDLEGN KWVIPASGYHMKMPAKARLADLFDNGEFESLPQP KVAQDPLKFRDSKKYSDRLRDSRL KTEQEDTILAGVGKVQGLKLVAVVHEFNFIGGSL GMAAGEAIVKAFERATAEKCPLVM FPASGGARMQEGILSLMQLPRTTVAVDMLKESGQ PYIVVLTNPTTGGVTASYAMLGDI HLAEPGAEIGFAGKRVIEQTLREKLPEGFQTA EY LLEHGMVDMVVKRHDIPETLARLL KILTKKPVSAANDMNGGAIALAASA"
misc-feature	20172..20372	/locus-tag="RL0023" /inference="protein motif: Pfam: PF01039.9" /note="Pfam match to entry

gene	20778..22130	PF01039.9 Carboxyl-trans"
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		/locus-tag="RL0024"
CDS	20778..22130	/gene="folC"
		/locus-tag="RL0024"
		/inference="similar to
		sequence:INSDC:ECD862"
		/inference="similar to
		sequence:INSDC:SME591782"
		/note="similarity:fasta;
		with=UniProt:FOLC-ECOLI
		(EMBL:ECD862); Escherichia coli.;
		folC; FolC bifunctional protein
		[Includes: Folylpolyglutamate
		synthase (EC 6.3.2.17)
		(Folylpoly-gamma-glutamate
		synthetase) (FPGS); Dihydrofolate
		synthase (EC 6.3.2.12)].;
		length=422; id 31.757; 444 aa
		overlap; query 1-442; subject
		2-411 similarity:fasta;
		with=UniProt:Q92TC6
		(EMBL:SME591782); Rhizobium
		meliloti (Sinorhizobium
		meliloti).; PROBABLE FOLC
		BIFUNCTIONAL PROTEIN INCLUDES:
		FOLYLPOLYGLUTAMATE SYNTHASE AND
		DIHYDROFOLATE SYNTHASE (EC
		6.3.2.17) (EC 6.3.2.12).;
		length=447; id 75.901; 444 aa
		overlap; query 7-450; subject
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		(Folylpoly-gamma-glutamate
		synthetase) (FPGS); Dihydrofolate
		synthase]."
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		/db-xref="UniProtKB/TrEMBL:Q1MND3"
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		QLVDDAVFAEAVRRVADANAGQHITVFEILTAVT
		FILFSEHPADAAIIEVGLGGRFDA
		TNVISDPAVSVIMPISLDHQPYLGDRVELIAAEK
		AGIMKPGFPVVIHQEYDAALDVL
		MSTAERLHCPSAVFGQDFMAHEEYGRVYQDEFG
		LADLPLPRLPGRHQYANAAAAIRA
		VKAAGFTVTETMMEKAMSSVEWPGRLQRLSEGRL
		LSHAPAGAEIWIIDGGHNP GAGEVI
		AEAMANFEERQSRPLFLIIGMINTKDPVG YFKAF
		AGLVEKVFCVPIRGSEAMIDPVIL
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misc-feature	20877..21641	/gene="folC"

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/inference="similar to
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with=UniProt:THIO-RHOSH
(EMBL:A35135); Rhodobacter
sphaeroides (Rhodopseudomonas
sphaeroides).; trxA; Thioredoxin
(TRX).; length=TRX; id 57.692; 104
aa overlap; query 2-105; subject
1-104 similarity:fasta;
with=UniProt:Q8UJA6
(EMBL:AE008976); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; trxA; Thioredoxin C-1.;
length=133; id 91.509; 106 aa
overlap; query 1-106; subject
28-133 Similar to entire protein
of Rhodobacter sphaeroides
(Rhodopseudomonas sphaeroides)
Thioredoxin (TRX) trxA (104 aa),
and similar, but truncated at the
N-terminus,to Agrobacterium
tumefaciens (strain C58/ATCC
33970) Thioredoxin C-1 trxA (133
aa)"
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misc-feature complement(22206..22520 /locus-tag="RL0025"
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CDS       complement(22599..26150 /locus-tag="RL0026"
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TIQQAIASDPLRSAWVSANAGSGK  
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HAFCEALLHQFPLEANVAGHFSVL  
DDRAAVALLSDARRALLTATAPDEDSALAEAFAY  
VLNLGDESGLENLLGDIVANRNAI  
RRFTAAAEQQGGVEMVLKRLGLAVGDTEDRIEA  
QYWPLPELSGSVLELYLSLADQKG  
GAKAQEVAYGLRLAGRERDDARRAQFLEKIFLTV  
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LNHDYEELKKQRSQDLDFEDLITRT  
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IQWSVIQSLAEDFFSGESARPIVR  
TLFAVGDEKQSIYSFQGARPERFSEESDRTRRRV  
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FAIAALRGDNESFWSHLRSFAADGTSELFRAAVER  
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GGRRQFLARLGTEVSDILDEFLLTLDHESGLP  
GLQSFISTLELEAPVMKREQDKGR  
NEVRIMTVHASKGLEAPIVFLVDGGSKAFTHTHL  
PKLRLIETRPDEPPMPVWVPVSDL  
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HDDHPHVEATTFSGSDGEWPGIKWRVPRVERSFE  
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EHSDRSLEKGRLIHRMLQALPEIP  
LAERPDAASRYAERAARFWPEVERRKLVDVSVLKL  
LDEEGLQAVLGAQAQPEVSIMGTL  
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KTK"

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gene      complement(29338..30069 /locus-tag="RL0028"
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CDS      complement(29338..30069 /locus-tag="RL0028"
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mallei (Pseudomonas mallei).;
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aa overlap; query 3-236; subject
1-225 similarity:fasta;
with=UniProt:Q92TC3
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE NUCLEOTIDYL
TRANSFERASE PROTEIN (EC 2.7.7.-).;
length=243; id 72.500; 240 aa
overlap; query 1-240; subject
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/inference="protein
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/note="Pfam match to entry
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CDS             complement(30083..31600 /locus-tag="RL0029"
)
/inference="similar to
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/note="similarity:fasta;
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(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; Hypothetical protein
SMc02757.; length=504; id 64.113;
496 aa overlap; query 10-505;
subject 7-501"
/codon-start=1
/transl-table=11
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gene	complement(31597..34182)	/locus-tag="RL0030"
CDS	complement(31597..34182)	/locus-tag="RL0030"  /inference="similar to sequence:INSDC:B87681" /inference="similar to sequence:INSDC:C97362" /note="similarity:fasta; with=UniProt:DIVL-CAUCR (EMBL:B87681); Caulobacter crescentus.; divL; Sensor protein divL (EC 2.7.3.-).; length=769; id 31.950; 795 aa overlap; query 81-861; subject 2-766 similarity:fasta; with=UniProt:Q8UJA1 (EMBL:C97362); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Two component sensor kinase (AGR-C-44p).; length=881; id 70.905; 818 aa overlap; query 46-861; subject 67-881 Similar, but truncated at the N-terminus, to Caulobacter crescentus Sensor protein divL (769 aa), and entire protein is similar to Agrobacterium tumefaciens (strain C58/ATCC 33970) Two component sensor kinase (AGR-C-44p) (881 aa)" /codon-start=1 /transl-table=11 /product="putative two-component sensor histidine kinase transcriptional regulatory protein" /protein-id="CAK05518.1" /db-xref="GI:115254444"



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/db-xref="UniProtKB/TrEMBL:Q1MNC7"
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IADKNRRIVIWDGNARPELLGQLP
PETGAPQDGEFLAFGLWLKSRASASELEKAIDRLR
DEAQSFDMVVETIRDEILEAQGRV
SGGRAFVRFVALNNLRAELAELRIERDRLMTSIS
AFQTMLDAIDMPAWQRDPVGRLTW
VNQAYGEAVEARSPPQAINEGREMLTTVARERIR
ATTTPESPFHDKISTVVRGNRTFF
DVVDVRVPGGSAGIAIDVSDIEAVRAELERTLKS
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DLWHLPNGQTLRVFATAHPQGGATWVFENLTEQV
DLETRYNTLVKVQGETIDHLSEGV
AVFGPDGRIRLSNPAFRALWGITETEAKEPGTHIR
ALGEACTPSYDRPDGWKTFAELIT
SFDDERRSGQGTLELFSGLVLDYAVIPLPNAQTM
LTFVNMTDSVRAERALTEKNEALR
KADELKNDFVQHVSIELRSPLTNIIGFTDLLRTP
GVGPLTERQAEYIDHISTSSSVLL
TLVNDILDLATVDAGIMRLNYADIDLNDLLDDVS
MQIADRLHESGVALEITAPAYLGS
IVADPQRLKQILLKLLSNAANFSPEGTSISLECH
REGTDFVFAVSDRGPGISPDMIAT
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VTIDSEPGKGTTVVCRIPSVDVPH SAAAE"
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CDS             complement(34386..35786 /locus-tag="RL0031"
)
                /inference="similar to
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                /inference="similar to
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                with=UniProt:SAHH-RHOSH
                (EMBL:U76671); Rhodobacter
                sphaeroides (Rhodopseudomonas
                sphaeroides).; ahcY;
                Adenosylhomocysteinase (EC
                3.3.1.1)
                (S-adenosyl-L-homocysteine
                hydrolase) (AdoHcyase).;
                length=463; id 82.251; 462 aa

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overlap; query 6-466; subject  
 3-463 similarity:fasta;  
 with=UniProt:SAHH-RHIME  
 (EMBL:SME591782); Rhizobium  
 meliloti (Sinorhizobium  
 meliloti).; ahcY;  
 Adenosylhomocysteinase (EC  
 3.3.1.1)  
 (S-adenosyl-L-homocysteine  
 hydrolase) (AdoHcyase).;  
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 overlap; query 1-466; subject  
 1-466"  
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 S-adenosyl-L-homocysteine  
 hydrolase"  
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 KGESLEDYWVYTDKIFQWADGGLSNMILDDGGDA  
 TMYILLGARAEAGEDVLSHPHSEE  
 EEILFAQIKKRLAASPGWFTKQRDAIKGVTEETT  
 TGVNRLYQLSQKGLLPFPAINVND  
 SVTKSKFDNKYGCKESLVDGIRRGTDVMMAGKVA  
 VVCGYGDVGKGSAAASLSGAGARVK  
 VTEADPICALQAAMDGYEVVLLLEDVVSSADIFIT  
 TTGNKDVIRIDHMRAMKDMAIVGN  
 IGHFDNEIEVAALRNKWTNVKPQVDLIEFPKGN  
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 motif: Pfam: PF00670.10"  
 /note="Pfam match to entry  
 PF00670.10 AdoHcyase-NAD"  
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 sequence: INSDC: SME591782"  
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 (EMBL: A38120); Alcaligenes

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misc-feature complement(34629..35108  
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gene complement(35943..36218  
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CDS complement(35943..36218  
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eutrophus (Ralstonia eutropha).;
phbH; Phosphocarrier protein HPr
(Histidine-containing protein)
(Protein H).; length=His ( 89; id
51.163; 86 aa overlap; query 4-89;
subject 2-87 similarity:fasta;
with=UniProt:Q92TC0
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE
PHOSPHOCARRIER HPR TRANSMEMBRANE
PROTEIN.; length=96; id 83.333; 90
aa overlap; query 2-91; subject
7-96"
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protein HPr"
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/db-xref="UniProtKB/TrEMBL:Q1MNC5"
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LDQLIQNRFGEEM"
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                /inference="protein
motif: Pfam:PF00381.8"
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PF00381.8 PTS-HPr"
gene            complement(36228..36629 /locus-tag="RL0033"
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CDS             complement(36228..36629 /locus-tag="RL0033"
)
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sequence:INSDC:AE005404"
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sequence:INSDC:AE007946"
                /note="similarity:fasta;
with=UniProt:PTNA-ECOLI
(EMBL:AE005404); Escherichia
coli.; manX; PTS
system, mannose-specific IIAB
component (EIIAB-Man)
(Mannose-permease IIAB component)
(Phosphotransferase enzyme II, AB
component) (EC 2.7.1.69)
(EIII-Man).; length=322; id
30.645; 124 aa overlap; query
2-123; subject 2-125
similarity:fasta;
with=UniProt:Q8UJ97
(EMBL:AE007946); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; PTS system, IIA component
(AGR-C-50p).; length=AGR-C-50 (
133; id 85.714; 133 aa overlap;
query 1-133; subject 1-133 Similar
to the N-terminus to codon 135 of
Escherichia coli mannose-specific

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IIAB component, manX,PTS system
(322 aa), and similar to entire
protein of Agrobacterium
tumefaciens (strain C58/ATCC 33970
PTS system, IIA component (133
aa); putative phosphotransferase
system component"
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mannose-specific IIAB component
(EIIAB-Man) (Mannose-permease IIAB
component) (Phosphotransferase
enzyme II, AB component)
(EIII-Man)."
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/db-xref="UniProtKB/TrEMBL:Q1MNC4"
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EHVVGPKKFIETVCIGPEDDMDQR
RQDILEAVSGADDGHGVVILTDMFGGTPSNLAIS
VMSSGHTTEVIAGVNLPLIKLAGV
RGENNMEKALVEASEAGRKYINVASRVLSGK"
misc-feature    complement(36279..36626 /locus-tag="RL0033"
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/inference="protein
motif: Pfam:PF03610.4"
/note="Pfam match to entry
PF03610.4 EIIA-man"
gene            complement(36780..37232 /locus-tag="RL0034"
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CDS             complement(36780..37232 /locus-tag="RL0034"
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/note="similarity:fasta;
with=UniProt:Q92KV2
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; Hypothetical protein
SMc02752.; length=148; id 48.951;
143 aa overlap; query 7-148;
subject 7-148"
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protein"
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SATGENRIPPEGEMVSLAADFSLPALRLLTGVCS
PLAILMAKVDPDGR"
gene            complement(37229..39019 /locus-tag="RL0035"
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CDS             complement(37229..39019 /locus-tag="RL0035"
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sequence:INSDC:HS362250"
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with=UniProt:CHVG-RHIME
(EMBL:AF027298); Rhizobium
meliloti (Sinorhizobium
meliloti).; chvG; Sensor protein
chvG (EC 2.7.3.-) (Histidine
kinase sensory protein exoS).;
length=EC 2.7.3.- ( 577; id
82.087; 575 aa overlap; query
21-593; subject 1-574
similarity:fasta;
with=UniProt:CHVG-AGRT5
(EMBL:HS362250); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; chvG; Sensor protein chvG
(EC 2.7.3.-).; length=EC 2.7.3.- (
596; id 81.475; 583 aa overlap;
query 9-591; subject 11-589;
putative two-component regulator
sensor histidine kinase
transcriptional regulator"
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(Histidine kinase sensory protein
exoS)."
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/db-xref="UniProtKB/TrEMBL:Q1MNC2"
/translation="MAQLVQERDLDDAEGVSTRR
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SITIDPQKLELQAGQSITPVPNDEDLEFPIDPE
KVAPVLRRLISPTRTRARIFDADA
NLLLSRHLYSRGQVLRFDLPPVEEEKQTWSEWF
ATLFNKALQPGNLPPLYKEAPGGDG
SIYPEVMNALTGVRGAVVRTTEKGELIVSVAVPI
QRFRAVLGVLLLSTQAGDIDNIVH
AERLAIMRVFGVATLVNVLLSLVLSSTIANPLRR
LSAAAIRVRRGAKTREEIPDFSAR
QDEIGNLSIALREMTTALYDRIDAIESFAADVSH
ELKNPLTSLRSVETLPLARSDDS
KKRLMDVIQHDVRRDLRLISDISDASRLDAELAR
VDAGSVDMEVLLRDLIEVSRQVRS
TKKQVEIEYAIERKPNVKTRFVVNGHDLRIGQII
ANLIENARSFVPEKGGKITVRLVR
TRSRCVTTIEDNGPGIQAENIDRIFERFYTDPRPE
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misc-feature    complement(37241..37597
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PF02518.9 HATPase-c"

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misc-feature    complement(37751..37948
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misc-feature	complement(38816..38875)	
		/inference="protein motif: TMHMM: 2.0" /note="1 probable transmembrane helix predicted at aa 49-68" /locus-tag="RL0036"
gene	complement(39204..39938)	
CDS	complement(39204..39938)	/locus-tag="RL0036"  /inference="similar to sequence: INSDC: B49902" /inference="similar to sequence: INSDC: SME591782" /note="similarity: fasta; with=UniProt: CHVI-RHIME (EMBL: SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; chvI; Transcriptional regulatory protein chvI.; length=240; id 90.574; 244 aa overlap; query 1-244; subject 1-240 similarity: fasta; with=UniProt: Q8UJ95 (EMBL: B49902); Agrobacterium tumefaciens (strain C58/ATCC 33970).; chvI; Two component response regulator.; length=265; id 91.393; 244 aa overlap; query 1-244; subject 25-265" /codon-start=1 /transl-table=11 /product="putative two-component response regulator transcriptional regulatory protein" /protein-id="CAK05524.1" /db-xref="GI:115254450" /db-xref="GOA: Q1MNG3" /db-xref="UniProtKB/TrEMBL: Q1MNG3" /translation="MPTIALVDDDRNILTSVSIA LEAEGYKVETYTDGASALDGLLAR PPQLAIFDIKMPRMDGMELLRRLRQKSDIPVIFL TSKDEEIDELFGLKMGADDFITKP FSQRLIVERVRAVLRRASSREAAAAGTSPTGAPK NGAVQQARSLERGLVMDQERHTC TWKGEAVTLTVTEFLILHSLAQRPVVKSRDALM DAAYDEQVYVDDRTIDSHIKRLRK KFKMVDITDFDMIETLYGVGYRFREAA" /locus-tag="RL0036"
misc-feature	complement(39219..39449)	
		/inference="protein motif: Pfam: PF00486.11"

		/note="Pfam match to entry PF00486.11 Trans-reg-C"
misc-feature	complement(39579..39935 )	/locus-tag="RL0036"
		/inference="protein motif: Pfam: PF00072.9"
gene	40276..41886	/note="Pfam match to entry PF00072.9 Response-reg"
CDS	40276..41886	/gene="pckA" /locus-tag="RL0037"
		/gene="pckA" /locus-tag="RL0037"
		/EC-number="4.1.1.49"
		/inference="similar to sequence: INSDC: AE007946"
		/inference="similar to sequence: INSDC: SME591782"
		/note="similarity: fasta; with=UniProt: PPCK-RHIME (EMBL: SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; pckA; Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) (PEP carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK).; length=536; id 80.224; 536 aa overlap; query 1-536; subject 1-536 similarity: fasta; with=UniProt: PPCK-AGRT5 (EMBL: AE007946); Agrobacterium tumefaciens (strain C58/ATCC 33970).; pckA; Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) (PEP carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK).; length=536; id 81.716; 536 aa overlap; query 1-536; subject 1-536; putative phosphoenolpyruvate carboxykinase"
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		/transl-table=11
		/product="Phosphoenolpyruvate carboxykinase [ATP] (PEP carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK)."
		/protein-id="CAK05525.1"
		/db-xref="GI:115254451"
		/db-xref="GOA:Q1MNG2"
		/db-xref="UniProtKB/TrEMBL:Q1MNG2"
		/translation="MEMFGVHNPAIELATVGLGG AASVRYNFSAAALYEEAIRRGEAE LTAQGALRAITGQHTGRSPRDKFVVRDINTDGEI WWDNNKPISPEHFAVLRDDMLAHA AGKELFVQDLVGGAEEGHALPTRVVTEFAWHSLF IRNLLIRPDTAALSSFVPKLTIID LPSFKADPARHGCRSETVIACDLTNGLVLIGGTS YAGEMKKSFTVLNLYLLPAKGVM MHCSANVGPDGDAAVFFGLSGTGKTTLSADPART LIGDDEHGWSENGIFNFEGGCYAK TIRLSAEAEPEIYATTQRFGTVLENVVLNESREP"

		DFNDGSLTENTRCAYPMDFI PNAS KTGRAGHPKTIIMLTADAFGVMPPIARLTPDQAM YHFLSGYTAKVAGTEKGVVEPEAT FSTCFGAPFMPRHPAEYGNLLKELIGRHGVQCWL VNTGWTGGAYGTGKRMP IKATRAL LAAALSGELGQVEFRADTNFGFAVPVSVHGVVDGS ILDPRSTWADKAAAYDAQAEKLVSM FIANFAKFENHVDGGVRDAAPGVKVAEE"
misc-feature	40339..41730	/gene="pckA" /locus-tag="RL0037" /inference="protein motif: Pfam: PF01293.8" /note="Pfam match to entry PF01293.8 PEPCK-ATP"
gene	41993..42436	/locus-tag="RL0038"
CDS	41993..42436	/locus-tag="RL0038" /inference="similar to sequence: INSDC: C97363" /note="similarity: fasta; with=UniProt: Q8UJ93 (EMBL: C97363); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0036.; length=156; id 84.615; 143 aa overlap; query 1-143; subject 13-155" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05526.1" /db-xref="GI: 115254452" /db-xref="GOA: Q1MNF8" /db-xref="UniProtKB/TrEMBL: Q1MNF8" /translation="MASDALYIDDRITIAGWELT EQFVLAGGPGGQNVNKVSTAVQLF FNIANSPSLNDRVKTNAIKLAGRRLSKDGVLMIE ASRFRSQDRNREDARDRLKELILE AAKPPPPPRKKTRPTKGSVERRLKEKSGRSEVKK MRGRPGGGSGE"
misc-feature	42011..42406	/locus-tag="RL0038" /inference="protein motif: Pfam: PF00472.8" /note="Pfam match to entry PF00472.8 RF-1"
gene	42438..43049	/locus-tag="RL0039"
CDS	42438..43049	/locus-tag="RL0039" /inference="similar to sequence: INSDC: A87250" /inference="similar to sequence: INSDC: SME591782" /note="similarity: fasta; with=UniProt: ALKB-CAUCR (EMBL: A87250); Caulobacter crescentus.; alkB; Alkylated DNA repair protein alkB homolog.; length=220; id 54.315; 197 aa overlap; query 4-200; subject 22-216 similarity: fasta; with=UniProt: Q92TB6 (EMBL: SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PROBABLE DNA REPAIR



		SYSTEM SPECIFIC FOR ALKYLATED DNA PROTEIN.; length=206; id 73.786; 206 aa overlap; query 1-203; subject 1-206" /codon-start=1 /transl-table=11 /product="putative alkylated DNA repair protein" /protein-id="CAK05527.1" /db-xref="GI:115254453" /db-xref="UniProtKB/TrEMBL:Q1MNG1" /translation="MPELLSGIRHLPGYLDRARQ EALVEVIRTVVAEAPLYVPAMPGT GKPM SVRMTNCGPLGWVTDKERGYRYQPTHPATG RPWPDMPQQLLDIWNDVSGYDKPP EACLNVNFYSDEARMGLHQDKDEQDLKAPVVSISL GNSCLFRVGGLSRNDRTLSFKLSS GDLVVLGGEGRLCFHGVDRIHDPATSTLLKNGGRI NLT LRRVNP"
misc-feature	42738..43043	/locus-tag="RL0039" /inference="protein motif: Pfam: PF03171.7" /note="Pfam match to entry PF03171.7 2OG-FeII-Oxy"
gene	complement(43056..44051 )	/gene="coaA" /locus-tag="RL0040"
CDS	complement(43056..44051 )	/gene="coaA" /locus-tag="RL0040" /inference="similar to sequence: INSDC: A45727" /inference="similar to sequence: INSDC: AE007946" /note="similarity: fasta; with=UniProt: COAA-ECOLI (EMBL: A45727); Escherichia coli O157: H7.; coaA; Pantothenate kinase (EC 2.7.1.33) (Pantothenic acid kinase) (Rts protein).; length=EC 2.7.1.3 ( 316; id 53.526; 312 aa overlap; query 23-330; subject 10-316 similarity: fasta; with=UniProt: COAA-AGRT5 (EMBL: AE007946); Agrobacterium tumefaciens (strain C58/ATCC 33970).; coaA; Pantothenate kinase (EC 2.7.1.33) (Pantothenic acid kinase).; length=EC 2.7.1.3 ( 322; id 81.988; 322 aa overlap; query 10-331; subject 1-322; putative pantothenate kinase" /codon-start=1 /transl-table=11 /product="Pantothenate kinase (Pantothenic acid kinase) (Rts protein)." /protein-id="CAK05528.1" /db-xref="GI:115254454" /db-xref="GOA: Q1MNG0" /db-xref="UniProtKB/TrEMBL: Q1MNG0"

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                                VESSQMLFEQRNRFLSLSDVTKTP
                                FVIGIAGSVAVGKSTTARILKELLGRWPSSPKVD
                                LVTTDGFLLHPNAVLQREKLMQRKG
                                FPESYDTGAILRFLSAIKAGRPDVKAPSYSHLVY
                                DVLDPDEYKIVDRPDILIFEGINVL
                                QSRDLPAGGKIVPMVSDFFDFSIIYIDAAEDEIHN
                                WYVTRFMRLRETAFRDPNSYFHRY
                                ASISDAEAEIAEDLWANINLKNLRQNILPTRPR
                                ADLILKKGKDHLIEQVALRKL"
misc-feature    complement(43080..43742 /gene="coaA"
                                )
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                                /inference="protein
                                motif: Pfam: PF00485.7"
                                /note="Pfam match to entry
                                PF00485.7 PRK"
gene            complement(44048..44371 /locus-tag="RL0041"
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CDS             complement(44048..44371 /locus-tag="RL0041"
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                                /inference="similar to
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                                sequence: INSDC: ECRFBM"
                                /note="similarity: fasta;
                                with=UniProt: HIS2-ECOLI
                                (EMBL: ECRFBM); Escherichia coli.;
                                hisI; Histidine biosynthesis
                                bifunctional protein hisIE
                                [Includes: Phosphoribosyl-AMP
                                cyclohydrolase (EC 3.5.4.19)
                                (PRA-CH); Phosphoribosyl-ATP
                                pyrophosphatase (EC 3.6.1.31)
                                (PRA-PH)].; length=203; id 47.126;
                                87 aa overlap; query 6-92; subject
                                115-201 similarity: fasta;
                                with=UniProt: HIS2-AGRT5
                                (EMBL: AE007946); Agrobacterium
                                tumefaciens (strain C58/ATCC
                                33970).; hisE; Phosphoribosyl-ATP
                                pyrophosphatase (EC 3.6.1.31)
                                (PRA-PH).; length=107; id 71.698;
                                106 aa overlap; query 1-106;
                                subject 1-106"
                                /codon-start=1
                                /transl-table=11
                                /product="putative histidine
                                biosynthesis bifunctional protein"
                                /protein-id="CAK05529.1"
                                /db-xref="GI:115254455"
                                /db-xref="GOA:Q1MNF9"
                                /db-xref="UniProtKB/TrEMBL:Q1MNF9"
                                /translation="MSGFSLSDLESIVAERSKAP
                                PEQSWTAKLVAGGQPKAAKKLGEE
                                AIEAVMAAVTGDRDNLTYEAADVLYHLLVVLKIA
                                EIPLENVMAELERRTAQSGLKEKA SRQSS"
misc-feature    complement(44090..44356 /locus-tag="RL0041"
                                )
                                /inference="protein

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motif: Pfam:PF01503.6"
/feature="Pfam match to entry
PF01503.6 PRA-PH"
gene complement(44389..45177 /gene="hisF"
)
/locus-tag="RL0042"
CDS complement(44389..45177 /gene="hisF"
)
/locus-tag="RL0042"
/inference="similar to
sequence:INSDC:ABHISHAFE"
/inference="similar to
sequence:INSDC:AE007946"
/note="similarity:fasta;
with=UniProt:HIS6-AZOBR
(EMBL:ABHISHAFE); Azospirillum
brasiliense.; hisF; Imidazole
glycerol phosphate synthase
subunit hisF (EC 4.1.3.-) (IGP
synthase cyclase subunit) (IGP
synthase subunit hisF) (ImGP
synthase subunit hisF) (IGPS
subunit hisF).; length=261; id
69.767; 258 aa overlap; query
3-260; subject 2-251
similarity:fasta;
with=UniProt:HIS6-AGRT5
(EMBL:AE007946); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; hisF; Imidazole glycerol
phosphate synthase subunit hisF
(EC 4.1.3.-) (IGP synthase cyclase
subunit) (IGP synthase subunit
hisF) (ImGP synthase subunit hisF)
(IGPS subunit hisF).; length=258;
id 82.129; 263 aa overlap; query
1-262; subject 1-258"
/codon-start=1
/transl-table=11
/product="putative imadazole
glycerol phosphate synthase
sununit"
/protein-id="CAK05530.1"
/db-xref="GI:115254456"
/db-xref="GOA:Q1MNF7"
/db-xref="UniProtKB/TrEMBL:Q1MNF7"
/translation="MTLKARVIPCLDVKDGRVVK
GVNFLNLVDAGDPVEAAKAYDAAG
ADELCFLDITASSDNRETIFDVVSRTADQCFMPL
TVGGGVRTIADIRKLLLCGADKVS
INSAAVSNPDFVTEAADKFGDQCIVVSIDAKRRR
TQAVGGDNLSAWEIYTHGGRNATG
IDAVEFAQKMVARGAGELLVTSMDRDGTVKGYDL
ELTRAIAAVRVPVIASGGVGDLD
DLVAGVKEGHANAVLAASIFHFGTYSVSEAKHYM
SKCGIDMRLD"
misc-feature complement(44446..45162 /gene="hisF"
)
/locus-tag="RL0042"
/inference="protein
motif: Pfam:PF00977.8"
/note="Pfam match to entry

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gene      complement(45178..45924 /gene="hisA"
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CDS       complement(45178..45924 /gene="hisA"
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          /locus-tag="RL0043"
          /inference="similar to
sequence:INSDC:ECD840"
          /inference="similar to
sequence:INSDC:SME591782"
          /note="similarity:fasta;
with=UniProt:HIS4-ECOLI
(EMBL:ECD840); Escherichia coli.;
hisA;
1-(5-phosphoribosyl)-5-[(5-phospho
ribosylamino)methylidene amino]
imidazole-4-carboxamide isomerase
(EC 5.3.1.16)
(Phosphoribosylformimino-5-aminoim
idazole carboxamide ribotide
isomerase).;
length=5-phosphoribosyl; id
35.081; 248 aa overlap; query
2-242; subject 1-245
similarity:fasta;
with=UniProt:HIS4-RHIME
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; hisA;
1-(5-phosphoribosyl)-5-[(5-phospho
ribosylamino)methylidene amino]
imidazole-4-carboxamide isomerase
(EC 5.3.1.16)
(Phosphoribosylformimino-5-aminoim
idazole carboxamide ribotide
isomerase).;
length=5-phosphoribosyl; id
88.066; 243 aa overlap; query
1-243; subject 1-243"
          /codon-start=1
          /transl-table=11
          /product="putative
imidazole-4-carboxamide isomerase"
          /protein-id="CAK05531.1"
          /db-xref="GI:115254457"
          /db-xref="GOA:Q1MNC1"
          /db-xref="UniProtKB/TrEMBL:Q1MNC1"
          /translation="MILFPAIDLKGGQCVRLKLG
DMQQATVYNTDPAAQARSFEDQGF
EWLHVVDLDGAFAGHSANGDAVEAILKATDNPVQ
LGGGIRTLDHIEAWLSRGLRRVIL
GTVAVRNPDLVIEACRKFPDHVAVGIDAKGGKVA
VEGWAEASELGIIELARKFEGAGV
AIIYTDIDRDGILAGINWSSTLELADAVSIPVI
ASGGLASLDDIRRMLEPDARKLEG
AISGRALYDGRIDPKEALALIKAAARAKETA"
misc-feature complement(45232..45921 /gene="hisA"
)
          /locus-tag="RL0043"
          /inference="protein
motif: Pfam:PF00977.8"

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gene                complement(45931..46488 /note="Pfam match to entry
                    )                  PF00977.8 His-biosynth"
CDS                 complement(45931..46488 /locus-tag="RL0044"
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                                /note="no significant database
                                hits"
                                /codon-start=1
                                /transl-table=11
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                                /protein-id="CAK05532.1"
                                /db-xref="GI:115254458"
                                /db-xref="UniProtKB/TrEMBL:Q1MNC0"
                                /translation="MIHDSFPANDGSSRRQNGVS
AGDIAEAVLEFYIEGEDDLIGLLA
YALYERQKRDFVLSHRKRNAGRSPDEAEELAAVNS
NYLSTDLRNTLRDRASQILSSYAE
TYVEAMEPQIRLTAVNSDALRQVRSIEKSIKRRL
GFWRQVRAGFAVTLLLLLLLFGAAA
IAAVFFQSDIVDAWNALMVPTTLRM"
misc-feature        complement(45991..46059 /locus-tag="RL0044"
                    )
                                /inference="protein
motif:TMHMM:2.0"
                                /note="1 probable transmembrane
helix predicted at aa 144-166"
gene                complement(46485..46676 /locus-tag="RL0045"
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CDS                 complement(46485..46676 /locus-tag="RL0045"
                    )
                                /note="no significant database
                                hits"
                                /codon-start=1
                                /transl-table=11
                                /product="hypothetical protein"
                                /protein-id="CAK05533.1"
                                /db-xref="GI:115254459"
                                /db-xref="UniProtKB/TrEMBL:Q1MNB9"
                                /translation="MRSMPASRKSGKV FYTLRPS
REGLPPFSDIKLPGGTVIRR VDEA
IHRKALSNAAKALKERLDR"
gene                complement(46921..47571 /gene="hisH"
                    )
                                /locus-tag="RL0046"
CDS                 complement(46921..47571 /gene="hisH"
                    )
                                /locus-tag="RL0046"
                                /inference="similar to
sequence:INSDC:ECD840"
                                /inference="similar to
sequence:INSDC:SME591782"
                                /note="similarity:fasta;
with=UniProt:HIS5-ECOLI
(EMBL:ECD840); Escherichia coli.;
hisH; Imidazole glycerol phosphate
synthase subunit hisH (EC 2.4.2.-)
(IGP synthase glutamine
amidotransferase subunit) (IGP
synthase subunit hisH) (ImGP
synthase subunit hisH) (IGPS
subunit hisH).; length=196; id

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36.792; 212 aa overlap; query
1-212; subject 1-194
similarity:fasta;
with=UniProt:HIS5-RHIME
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; hisH; Imidazole
glycerol phosphate synthase
subunit hisH (EC 2.4.2.-) (IGP
synthase glutamine
amidotransferase subunit) (IGP
synthase subunit hisH) (ImGP
synthase subunit hisH) (IGPS
subunit hisH).; length=216; id
81.944; 216 aa overlap; query
1-216; subject 1-216"
/codon-start=1
/transl-table=11
/product="putative imadazole
glycerol phosphate synthase
subunit"
/protein-id="CAK05534.1"
/db-xref="GI:115254460"
/db-xref="GOA:Q1MNB8"
/db-xref="UniProtKB/TrEMBL:Q1MNB8"
/translation="MRVAIIDYGGNLRSATKAF
ERAAHEAGIDAHIDLTDR AEDVAA
ADRIVLPGVGAYADCRRGLDAVPDMAEVLIEAVE
KKARPFLGICVGMQLMSSRGLEKT
VTHGFGWIPGNVEMTPDDPALKIPQIGWNTLDL
KRQHPLFEGIPTGSQGLHAYFVHS
YHLAAENTEDVIATADYGGPMTAFVGRDNMVGAQ
FHPEKSQKLGLALIANFLRWNP"
misc-feature    complement(46927..47562 /gene="hisH"
)
                /locus-tag="RL0046"
                /inference="protein
motif: Pfam:PF00117.10"
                /note="Pfam match to entry
PF00117.10 GATase"
gene            complement(47574..48059 /locus-tag="RL0047"
)
CDS             complement(47574..48059 /locus-tag="RL0047"
)
                /inference="similar to
sequence:INSDC:A97364"
                /note="similarity:fasta;
with=UniProt:Q8U5P8 (EMBL:A97364);
Agrobacterium tumefaciens (strain
C58/ATCC 33970).; AGR-C-67p.;
length=164; id 32.099; 162 aa
overlap; query 3-161; subject
2-163"
                /codon-start=1
                /transl-table=11
                /product="putative transmembrane
protein"
                /protein-id="CAK05535.1"
                /db-xref="GI:115254461"
                /db-xref="GOA:Q1MNB7"
                /db-xref="UniProtKB/TrEMBL:Q1MNB7"
                /translation="MTSSYIFLTPPGGTSATADE

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LWLHAAAFLQLQGIGGALMDEPGLGPAGAAILLG
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DALIAADTIGTAEQVYFSDRAAIAASDDAAAPDW
QNKARPNGQHGNATSLGLFGFDGG R"
misc-feature    complement(join(47805.. /locus-tag="RL0047"
47864,47922..47981))
                /inference="protein
                motif:TMHMM:2.0"
                /note="2 probable transmembrane
                helices predicted at aa 27-46 and
                66-85"
sig-peptide     complement(48002..48059 /locus-tag="RL0047"
                )
                /inference="protein
                motif:SignalP-HMM:2.0"
                /note="Signal peptide predicted
                for RL0047 by SignalP 2.0 HMM
                (Signal peptide probability 0.696)
                with cleavage site probability
                0.687 between residues 18 and 19"
gene            complement(48082..48690 /gene="hisB"
                )
                /locus-tag="RL0048"
CDS             complement(48082..48690 /gene="hisB"
                )
                /locus-tag="RL0048"
                /EC-number="4.2.1.19"
                /inference="similar to
                sequence:INSDC:AB091436"
                /inference="similar to
                sequence:INSDC:AE007946"
                /inference="similar to
                sequence:INSDC:E64967"
                /note="Similar to C-terminus from
                codon 160 of Escherichia coli.
                hisB HIS7-ECOLI (EMBL:E64967) (
                Histidine biosynthesis
                bifunctional protein hisB
                [Includes: Histidinol-phosphatase
                (EC 3.1.3.15)) ehydratase (EC
                4.2.1.19) (IGPD)]., and to entire
                protein of Agrobacterium
                tumefaciens (strain C58/ATCC
                33970). hisB HIS7-AGRT5
                (EMBL:AE007946) (
                Imidazoleglycerol-phosphate
                dehydratase (EC 4.2.1.19)
                (IGPD).), and to entire protein of
                Burkholderia multivorans. hisB
                HIS7-BURML (EMBL:AB091436) (
                Imidazoleglycerol-phosphate
                dehydratase (EC 4.2.1.19) (IGPD).)
                similarity:fasta;
                with=UniProt:HIS7-ECOLI
                (EMBL:E64967); Escherichia coli.;
                hisB; Histidine biosynthesis
                bifunctional protein hisB
                [Includes: Histidinol-phosphatase
                (EC 3.1.3.15);
                Imidazoleglycerol-phosphate
                dehydratase (EC 4.2.1.19)

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(IGPD)].; length=355; id 48.990;
198 aa overlap; query 4-201;
subject 163-355 similarity:fasta;
with=UniProt:HIS7-AGRT5
(EMBL:AE007946); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; hisB;
Imidazoleglycerol-phosphate
dehydratase (EC 4.2.1.19) (IGPD).;
length=198; id 89.286; 196 aa
overlap; query 6-201; subject
2-197 similarity:fasta;
with=UniProt:HIS7-BURML
(EMBL:AB091436); Burkholderia
multivorans.; hisB;
Imidazoleglycerol-phosphate
dehydratase (EC 4.2.1.19) (IGPD).;
length=195; id 54.124; 194 aa
overlap; query 8-201; subject
2-195"
/codon-start=1
/transl-table=11
/product="putative histidine
biosynthesis bifunctional protein
hisB"
/protein-id="CAK05536.1"
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/db-xref="GOA:Q1MNB6"
/db-xref="UniProtKB/TrEMBL:Q1MNB6"
/translation="MAETAASRTGVSVRKTNETS
ISVSVNLDGTGKSTISTGVGFFDH
MLDQLSRHSLIDMEIDAKGDLHIDDHHTVEDTGI
AIGQAISKALGDRRGITRYASIDL
AMDETMTKAAVDLSGRPFLVWNVAFSAPKIGTFD
TELVREFFHALAQNAGITLHILNH
YGANNHHIAETCFKAVARALRTATEIDPRQAGRV
PSTKGTLV"
misc-feature    complement(48148..48582 /gene="hisB"
)

/locus-tag="RL0048"
/inference="protein
motif: Pfam:PF00475.7"
/note="Pfam match to entry
PF00475.7 IGPD"
gene            48847..49374 /gene="hslV"
/locus-tag="RL0049"
CDS             48847..49374 /gene="hslV"
/locus-tag="RL0049"
/inference="similar to
sequence:INSDC:AE007946"
/inference="similar to
sequence:INSDC:C91236"
/note="similarity:fasta;
with=UniProt:HSLV-ECOLI
(EMBL:C91236); Shigella flexneri.;
hslV; ATP-dependent protease hslV
(EC 3.4.25.-) (Heat shock protein
hslV).; length=175; id 62.573; 171
aa overlap; query 2-171; subject
1-171 similarity:fasta;
with=UniProt:HSLV-AGRT5
(EMBL:AE007946); Agrobacterium

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		tumeefaciens (strain C58/ATCC 33970).; hslV; ATP-dependent protease hslV (EC 3.4.25.-).; length=173; id 91.908; 173 aa overlap; query 2-174; subject 1-173; putative heat-shock ATP-dependent protease" /codon-start=1 /transl-table=11 /product="ATP-dependent protease hslV (Heat shock protein hslV)." /protein-id="CAK05537.1" /db-xref="GI:115254463" /db-xref="GOA:Q1MNB5" /db-xref="UniProtKB/TrEMBL:Q1MNB5" /translation="MTTIIITVRKGGKVVMAGDGQ VSLGQTVMKGNARKVRRIGKGEVV AGFAGATADAFTLLERLEKKLEQYPGQLMRAAVE LAKDWRTDKYLRNLEAMMLVADKS ITLAITGNGDVLEPEHGTTAIGSGGNFALAAALA LMDTDKSAEEIARRALDIAADICV YTNHNVVVVELLDAEG" /gene="hslV" /locus-tag="RL0049" /inference="protein motif: Pfam:PF00227.11" /note="Pfam match to entry PF00227.11 Proteasome" /locus-tag="RL0050" /locus-tag="RL0050" /inference="similar to sequence:INSDC:AF360385" /inference="similar to sequence:INSDC:AP003005" /note="similarity:fasta; with=UniProt:Q93TB3 (EMBL:AF360385); Klebsiella pneumoniae.; Mutant AAC6'-IbY166A 6'-N-acetyltransferase.; length=201; id 31.325; 166 aa overlap; query 9-165; subject 27-192 similarity:fasta; with=UniProt:Q98CT9 (EMBL:AP003005); Rhizobium loti (Mesorhizobium loti).; Aminoglycoside 6'-N-acetyltransferase.; length=173; id 44.186; 172 aa overlap; query 1-170; subject 1-170; putative acetyltransferase" /codon-start=1 /transl-table=11 /product="putative Mutant AAC6'-IbY166A 6'-N-acetyltransferase." /protein-id="CAK05538.1" /db-xref="GI:115254464" /db-xref="GOA:Q1MNB4" /db-xref="UniProtKB/TrEMBL:Q1MNB4" /translation="MPKAEPYAFRPLAVADLPLL AEWLESRHVRRWWSDBAKALASME KHIDAASVSCFMVTLSGKDFAFIQAADLDEVDDDE
misc-feature	48847..49359	
gene	49361..49873	
CDS	49361..49873	

		ALAGQPKGTYGIDQFIGIEELAGK GHGPAFMIGFCNMLFAKGAQRILVDPHPDNAFAI RAYTKAGFQGLGETTTNYGRALLM ALDRQENDTQ"
misc-feature	49523..49795	/locus-tag="RL0050" /inference="protein motif: Pfam: PF00583.9" /note="Pfam match to entry PF00583.9 Acetyltransf-1"
gene	49870..51177	/gene="hslU" /locus-tag="RL0051"
CDS	49870..51177	/gene="hslU" /locus-tag="RL0051" /inference="similar to sequence: INSDC: AE007947" /inference="similar to sequence: INSDC: B86083" /note="similarity: fasta; with=UniProt: HSLU-ECOLI (EMBL: B86083); Shigella flexneri.; hslU; ATP-dependent hsl protease ATP-binding subunit hslU (Heat shock protein hslU).; length=443; id 57.942; 447 aa overlap; query 1-435; subject 1-443 similarity: fasta; with=UniProt: HSLU-AGRT5 (EMBL: AE007947); Agrobacterium tumefaciens (strain C58/ATCC 33970).; hslU; ATP-dependent hsl protease ATP-binding subunit hslU.; length=435; id 91.264; 435 aa overlap; query 1-435; subject 1-435" /codon-start=1 /transl-table=11 /product="putative ATP-dependent heat shock protease component" /protein-id="CAK05539.1" /db-xref="GI: 115254465" /db-xref="GOA: Q1MNB3" /db-xref="UniProtKB/TrEMBL: Q1MNB3" /translation="MTTFSPREIVSELDRIYIGQ HDAKRAVAIALRNRWRRQQLDPSL RDEVMPKNILMIGPTGVGKTEISRRLAKLAGAPF IKVEATKFTVEGYVGRDVEQIIRD LVEVGIGLVREKKRAEVQAKAHVSAEERVLDALV GTTASPATRENFRKKLRDGELEDDK EIDIEVADAGSGMGGFEIPGMPGANIGVLNLSEM FGKAMGGRTKKVRTTVKASYSDLI RDESKLIDNEVIQREAVRSTENDGIVFLDEIDK IAARDGGMGAGVSREGVQRDLLPL VEGTTVSTKYGPVKTDHILFIASGAFHVSKPSDL LPELQGRLP IRVELRPLNKDDFRR ILTETEASLIRQYRALMETESLSLEFTDDAIDAL ADVAVHLNSSVENIGARRLQTVME RVLDDISYNAPDRGGTAVTIDAAYVREHVGDLAQ NTDLSRFIL"
misc-feature	50023..51003	/gene="hslU" /locus-tag="RL0051" /inference="protein motif: Pfam: PF00004.12"

gene	51470..52417	/note="Pfam match to entry PF00004.12 AAA"
CDS	51470..52417	/locus-tag="RL0052" /locus-tag="RL0052" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:Q92TA6 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; CONSERVED HYPOTHETICAL TRANSMEMBRANE PROTEIN.; length=316; id 70.032; 317 aa overlap; query 1-315; subject 1-316" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05540.1" /db-xref="GI:115254466" /db-xref="UniProtKB/TrEMBL:Q1MNB2" /translation="MRLLTSLMIAVALVNSAPA FAMQTVPAGNRHAEQPDIPGASIR RTKGTKSSFDLKYEKVHELLATDRELMSKIRKVS SAYGINPIHVVGAIIVGEHTYNVDA YDRLQAYYVKAASYAGESFRFAYDGESVDEFVAR PQFAECKSKSDSYTLWSCREDVWE TDFRGKTVGGTSFPNNRFSVFFQPFYAGQTFGL GQVNPLTALMLSDLVTRVSGYPKL NEKNAGAVYRAIMDPDISLAFVAASIRRSIDYK EIAGMDISGNPGLTATLYNVGNSR QRAAALAANKRGAGATVWPEENYYGWLINDKLDE LKGLL"
sig-peptide	51470..51533	/locus-tag="RL0052" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0052 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.991 between residues 22 and 23"
misc-feature	51503..52414	/locus-tag="RL0052" /inference="protein motif:Pfam:PF07182.1" /note="Pfam match to entry PF07182.1 DUF1402"
gene	52466..53878	/locus-tag="RL0053"
CDS	52466..53878	/locus-tag="RL0053" /inference="similar to sequence:INSDC:A32966" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:CP43-RAT (EMBL:A32966); Rattus norvegicus (Rat).; Cyp4a3; Cytochrome P450 4A3 precursor (EC 1.14.15.3) (CYP4A3) (Lauric acid omega-hydroxylase) (P450-LA-omega 3).; length=EC ( 507; id 27.902; 448 aa overlap; query 37-461;

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subject 75-503 similarity:fasta;
with=UniProt:Q92TA5
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE CYTOCHROME
P450 MONOOXYGENASE PROTEIN (EC
1.14.-.-).; length=466; id 71.828;
465 aa overlap; query 1-465;
subject 1-465; putative cytochrome
P450 protein"
/codon-start=1
/transl-table=11
/product="Cytochrome P450 4A3
precursor (CYP1VA3) (Lauric acid
omega-hydroxylase) (P450-LA-omega
3)."
/protein-id="CAK05541.1"
/db-xref="GI:115254467"
/db-xref="GOA:Q1MNB1"
/db-xref="UniProtKB/TrEMBL:Q1MNB1"
/translation="MDMRPDPFVPPAPLPRTVPP
SRLEIIRIILRNPLELWGEPSYTL
PWIRTNFFGQRTLIVNDPGLIKHVLVDNANNYRM
SDVRQLVLRPILRDGLLTAEGPVW
KRSRKAVAPIFTPRHAQGFAGQMLRQSEDYARKY
EGAGEAGAIFDISTDMEITFAIL
ADTLFSGEIVTSSGHFADDVNELLHRMGRVDPMD
LMRAPSWVPRVTRIGGQKVLEKFR
AIVRNTMDMRLAKMKADRSSAPEDFLTLLLEQAG
PDGLTKEEIEDNILTFIGAGHETT
ARALAWTLYCVSNSPHIREGMEEEIDAVLATGAK
PVEWLDMMMPQTRAAFEELRLYP
APSINRAAISDDFWTSPKGERVELEAGVTVLVMP
WTLHRHELHWDPRAYMPERFLPE
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misc-feature      52493..53845
/locus-tag="RL0053"
/inference="protein
motif: Pfam:PF00067.9"
/note="Pfam match to entry
PF00067.9 p450"
gene              53965..56136
/gene="glcB"
/locus-tag="RL0054"
CDS               53965..56136
/gene="glcB"
/locus-tag="RL0054"
/inference="similar to
sequence:INSDC:AY059637"
/inference="similar to
sequence:INSDC:U00096"
/note="similarity:fasta;
with=UniProt:MASZ-ECOLI
(EMBL:U00096); Escherichia coli.;
glcB; Malate synthase G (EC
2.3.3.9) (MSG).; length=EC
2.3.3.9; id 60.083; 724 aa
overlap; query 4-721; subject
4-722 similarity:fasta;
with=UniProt:MASZ-RHILV
(EMBL:AY059637); Rhizobium
leguminosarum (biovar viciae).;
glcB; Malate synthase G (EC

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2.3.3.9).; length=EC 2.3.3.9; id
99.170; 723 aa overlap; query
1-723; subject 1-723; putative
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(MSG)."
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VDPEIASIAGPQLVVPVMNARYALNAANARWGSL
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DGALVVRSIDGEQAMLTGKHAFAG
YRGDAAAPTHILLKNNGIHIEIVIDAATTIGKAD
PAHISDVWLESAITTIMDCEDSIA
AVDAEDKVVVYRNWLGLMKGDLQEEVAKGGTSFI
RTLNPDLQYAGPDGAAFEVHRRSL
MLVRNVGHLMI SPAILDRDGNEVPEGIMDAAITG
LIALYDIGPSGRRKNSRTGSMYVV
KPKMHGPPEEVAFAVEIFSRVEDALGLPRNTIKMG
IMDEERRTTVNLKECIRAARERVV
FINTGFLDRTGDEIHTSMEAGPMIRKGDMRQAAW
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ARAKLSDILSVPVAVRPNWTPEEIQRELDNNAQG
ILGYVVRWVDQGVGCSKVPDINN
GLMEDRATLRISAQHMANWLHHKVVTEAQIIETM
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                    /note="Pfam match to entry
PF01274.10 Malate-synthase"
gene              complement(56207..56890
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CDS               complement(56207..56890
)
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sequence: INSDC: AF228577"
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with=UniProt: Q9KIP0
(EMBL: AF228577); Rhizobium
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Hypothetical protein.; length=227;
id 100.000; 227 aa overlap; query
1-227; subject 1-227"
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protein"
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misc-feature	complement(56216..56647)	/locus-tag="RL0055"  /inference="protein motif: Pfam: PF03734.4" /note="Pfam match to entry PF03734.4 ErfK-YbiS-YhnG"
sig-peptide	complement(56803..56890)	/locus-tag="RL0055"  /inference="protein motif: SignalP-HMM: 2.0" /note="Signal peptide predicted for RL0055 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.438 between residues 28 and 29"
gene	57070..57564	/locus-tag="RL0056"
CDS	57070..57564	/locus-tag="RL0056" /inference="similar to sequence: INSDC: AF228577" /note="similarity: fasta; with=UniProt: Q9KIP1 (EMBL: AF228577); Rhizobium leguminosarum (biovar viciae).; Hypothetical protein.; length=164; id 98.780; 164 aa overlap; query 1-164; subject 1-164" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05544.1" /db-xref="GI:115254470" /db-xref="UniProtKB/TrEMBL:Q1MNA8" /translation="MTILSVYNNNPLIDGRQSDR AMMVRRGTQILLHEMRHAVLP LASGRRADLITLSEKGEIWIIEIKTSIEDFRVDR KWPEYRLHCDRLFFATHQDVPLEI FPEECGLFLSDGYGAHMIREAPEHRMAPATRKSV TLNFSRAAAQRLMMAEWANGKPFT VDDV"
misc-feature	57070..57543	/locus-tag="RL0056" /inference="protein motif: Pfam: PF06319.1" /note="Pfam match to entry PF06319.1 DUF1052"
gene	complement(57585..58163)	/locus-tag="RL0057"
CDS	complement(57585..58163)	/locus-tag="RL0057"  /inference="similar to sequence: INSDC: AF228577" /note="similarity: fasta;

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actR; ActR.; length=192; id
99.479; 192 aa overlap; query
1-192; subject 1-192"
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response regulator transcriptional
regulatory protein"
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GEKAELPENPMSADRVVRWEHIQRV
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gene            complement(58232..59560 /locus-tag="RL0058"
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CDS             complement(58232..59560 /locus-tag="RL0058"
)
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sequence: INSDC:AF228577"
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with=UniProt:Q9KIP3
(EMBL:AF228577); Rhizobium
leguminosarum (biovar viciae).;
actS; Sensor histidine protein
kinase.; length=436; id 98.624;
436 aa overlap; query 7-442;
subject 1-436"
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regulator sensor histidine kinase
transcriptional regulator"
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ALLFITGGLANPFAALVCVPVVIISFASQPIRYST
ALIGVAMVCITVLAFFSPFPLPWF
GVEINVHNMVQFGVWCSIASTMAFAAFYAYRVSM
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TLSSEGEAHMRLPLSSMIEEIVAPHREFGIRLE

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LIEKCPRKGEPTVDRNAGIMYGLG
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GYAPDILTRIGEPYVTKRQKEDTA
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misc-feature    complement(58709..58909 /locus-tag="RL0058"
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59056,59084..59152,
59186..59254,
59405..59473))
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                motif: TMHMM: 2.0"
                /note="4 probable transmembrane
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gene            complement(59583..62048 /locus-tag="RL0059"
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CDS             complement(59583..62048 /locus-tag="RL0059"
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                length=821; id 74.908; 817 aa
                overlap; query 6-820; subject
                4-820 similarity: fasta;
                with=UniProt: Q92TA0
                (EMBL: SME591782); Rhizobium
                meliloti (Sinorhizobium
                meliloti).; ATP-DEPENDENT HELICASE
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                IEVVTEGVFARMILDDPELTGVSVVIFDEFHERS
                LDADFGLALALDVQSALREDLRIL

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VMSATLDVERVAALLDHPPVIESLGRSFPIDIRY  
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 LATSIAETSITIDGVRIVIDSGLQRLPVFEASTG  
 ITRLETVRVSRASADQRAGRAGRT  
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 LDLAHWGVQDPASLAFVDQPPETT  
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 TRLGAIVFEETPLPRPSGAAVTQA  
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misc-feature	complement (61527..62024 )	/locus-tag="RL0059"  /inference="protein motif: Pfam: PF00270.12" /note="Pfam match to entry PF00270.12 DEAD"
gene	complement (62045..62992 )	/locus-tag="RL0060"
CDS	complement (62045..62992 )	/locus-tag="RL0060"  /inference="similar to sequence: INSDC: AE007928" /inference="similar to sequence: INSDC: AP003001" /note="similarity: fasta; with=UniProt: OCD-AGRT5 (EMBL: AE007928); Agrobacterium tumefaciens (strain C58/ATCC 33970).; arcB; Ornithine cyclodeaminase (EC 4.3.1.12) (OCD).; length=354; id 30.882; 272 aa overlap; query 44-313; subject 57-320 similarity: fasta; with=UniProt: Q98GR8 (EMBL: AP003001); Rhizobium loti (Mesorhizobium loti).; Ornithine cyclodeaminase; Ocd2.; length=321;

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(OCD). "
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QAAEKIAAEARALGLNAEAVADAEAAARTADIIS
CATLSSAPLISGEWLKPGAHLDLV
GAFKPSMRESDDAAIRRASVYVDTRAGIAEAGD
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VTGQK"
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/note="Pfam match to entry
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gene 63649..65093 /gene="16S rRNA"
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/note="anticodon GAT"
gene 65632..65707 /gene="tRNA-Ala"
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/note="anticodon TGC"
gene 66549..69209 /gene="23S rRNA"
rRNA 66549..69209 /gene="23S rRNA"
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gene 69432..69551 /gene="5S rRNA"
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gene 69764..69840 /gene="tRNA-Met"
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CDS complement(70180..71670 /locus-tag="RL0061"
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/inference="similar to
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(EMBL: AP006577); Gloeobacter
violaceus.; Glr2801 protein.;
length=453; id 44.892; 372 aa
overlap; query 5-374; subject
1-355"

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family protein"
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RNDPASFATVGSKVFARGRDPFFPAWPDVLQLNT
FSPALRETVVETIAEIIAGQCEGVR
CDMAMLVNLTIFERTWGDHAGAKPDDDYWSTIIP
TIKSRYPEFKFIAEAYWDLEWELQ
QQGFDYCYDKKLYDRMEHGDAESVRQHLLADSTY
QEKMVRFIENHDEPRAAAAFPLEK
ARAAVAMLTLTGAKLLHEGQFEGATTRLPIFLG
RRPVASVDCDLASFYARLLTAIHG
DVFKNGEWRLCETSGWSDNQSCRNILSWCWAKGE
ARCLIVINFSETASQALVHVPWDE
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PWKSSLFELRAR"
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motif: Pfam: PF00128.11"
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gene            complement(71667..74426 /locus-tag="RL0062"
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CDS             complement(71667..74426 /locus-tag="RL0062"
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5-916; subject 1-908"
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YPQAVFPYADLVETNGRRSRNEFE
YELLDTGVFDDDRYFDVFVEYAKAAPEDILVKIT
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CDS       complement(74746..76002 /locus-tag="RL0063"
)

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meliloti).; Putative membrane
protein.; length=420; id 76.667;
420 aa overlap; query 1-418;
subject 1-420"
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misc-feature complement(75478..75765 /locus-tag="RL0063"
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/inference="protein
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gene      complement(76906..78225 /locus-tag="RL0064"
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        (Mesorhizobium loti).; M115242
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        LTVATYFDRDTADEAEIRGLATAL
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        DEGLLLYIIIGLGSPHPLPPESYA
        AYTSEYEWARNIYGRELLYSGPLFTHQLSHMWIDF
        RGIRDAFMREHDTDYFENTRHATY
        VQQEYAIRNPMNFAGYGEHCWGFTACDGPWGGR
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        TIAPWVAVASLPFAPEIVVPTVRNFARMNLGMTR
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gene      complement(78231..82121 /locus-tag="RL0065"
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        meliloti).; ndvB; Protein ndvB.;
        length=2832; id 40.078; 1290 aa
        overlap; query 17-1282; subject
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        with=UniProt:Q7X325
        (EMBL:AY281354); uncultured
        Acidobacteria bacterium.; Putative
        cyclic beta 1'-2' glucan
        synthetase.; length=2714; id
        44.648; 1308 aa overlap; query
        2-1296; subject 1418-2711 Similar
        to codons 1550 to the C-terminus
        of Rhizobium meliloti
        (Sinorhizobium meliloti) Protein
        ndvB (2832 aa), and similar to
        codons 1420 to the C-terminus of

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uncultured Acidobacteria bacterium  
 Putative cyclic beta 1'-2' glucan  
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 SCHAGDIEIASKICVAPDVDVEVRMLTVTNHGTR  
 ERTLELTSYAEVCLYNRSADMAHP  
 GFAKL FVETQFDEATGALFARRRPRAAGEKATWA  
 VHVSSSNLQPAQAAQYETDRLRFL  
 GRGRTTANPVAFDAGASLSGTTGPVLDPIFCLRR  
 TVRLAPGADARIAFVTGAADDQSA  
 VQLIAKRYAEIDAVEQAFSDASRRYESELQTLGL  
 KPGDISL FNRLAGSVIFANPAMRQ  
 ATDLQRDRWDRAALWAHGISGDLPIVLVRANSR  
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 ILVDEGGSASAKRLAEKLQSGPQAEMIGKPGGIF  
 ILSEPDGTGNDHLATIAAAARVLL  
 GSGGELGDQLNRLSPARSPLSPTFTTRLNEQPAA  
 PLPKPAEDLQYWNLGGFTADGHE  
 YVVRVDALKPQAPTLPPAPWTNVIANPHFGCLTT  
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 VTDAPGEVLYLRDEETGDIWTPTPLPLGPGAVVT  
 VRHGQGYSTRYTSFSRHLSQELTVS  
 VAPNDPVKIMRLRLSNEDTRVRHVTAIYFAEWVL  
 GTQREQTAARVVCERDARSGAIVA  
 RNPWAGDFAGRLAFAAASQPARSTTSDRTEFLGQ  
 YGSVFQPAALGRTDLAERFGPLLD  
 PCAALMVDISLRPNESREIVFVLGQAADLDEVSR  
 LVHEHTDLERAAASLSAVCRQWDD  
 ILNSIQVSTPDTGVNLMNRLVYQVLACRMWAR  
 TSNYQSGGAYGFRDQLQDVMALVY  
 SVPSEARSHILRSAARQFEEDVQHHWHPPSGVG  
 VRTRITDDL YFLPLVHHYVSTTG  
 DVQLLDETVPFITSPLVRDDQEEDFNQPATSEQS  
 GTVYEHCVRAL EHG YRLGSHGLPL  
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 RIALEANAWDGGWYRRAYFDDGTPLGSSLNDECQ  
 IDAIPQAWAVISGEADAERASQAM  
 RAVHDRLVRQEDRLIKLFDPPFDDGVLQPGYIKG  
 YVPGIRENGGQYTHAATWVWATA  
 LQGDGDLALKLWNLINPIYHGATKDQVERYKVEP  
 YAVAADIYGAPPHTGRGGWTWYTG  
 SASWLYRVALEAILGFRQEGRFLRFEPV PAGWP  
 AYEIAYRYGSATYRIHFDNSKGIG  
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misc-feature      complement(79809..80078 /locus-tag="RL0065"  
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/inference="protein  
 motif: Pfam:PF06205.1"  
 /note="Pfam match to entry

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misc-feature      complement(80091..80417 /locus-tag="RL0065"
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motif: Pfam: PF06165.1"
                  /note="Pfam match to entry
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                  /inference="protein
motif: Pfam: PF06204.1"
                  /note="Pfam match to entry
misc-feature      complement(81294..81566 /locus-tag="RL0065"
)
                  /inference="protein
motif: Pfam: PF06205.1"
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)
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motif: Pfam: PF06165.1"
                  /note="Pfam match to entry
misc-feature      complement(81948..82121 /locus-tag="RL0065"
)
                  /inference="protein
motif: Pfam: PF06204.1"
                  /note="Pfam match to entry
gene              complement(82152..84617 /locus-tag="RL0066"
)
CDS               complement(82152..84617 /locus-tag="RL0066"
)
                  /EC-number="4.1.2.9"
                  /inference="similar to
sequence: INSDC: LPE309011"
                  /inference="similar to
sequence: INSDC: SME591782"
                  /note="similarity: fasta;
with=UniProt: XPKA-LACPE
(EMBL: LPE309011); Lactobacillus
pentosus.; xpkA;
Xylulose-5-phosphate
phosphoketolase (EC 4.1.2.9).;
length=787; id 51.216; 781 aa
overlap; query 25-802; subject
6-783 similarity: fasta;
with=UniProt: PHK1-RHIME
(EMBL: SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; Probable
phosphoketolase 1 (EC 4.1.2.-).;
length=EC ( 789; id 87.959; 789 aa
overlap; query 32-820; subject
1-788"
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xylulose-5-phosphate
phosphoketolase"

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FKQFSFPGGIPSHVAPETPGSIHE
GGELGYALSHAYGAAFDNPNIIVACVVGDEAET
GPLATGWHGNKFLNPARDGCVLP
LHLNGYKIANPCFLARIPRDELRKFFEGMGYTPY
FVEGSDPENVHQQLAGVLDTAVAD
IQEIWATARTKGKIKRPMWPMIIFRTPKGWTCPP
EIDGKKCEDYWRAHQVPMGDMDKP
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DFRDYAVSVSPGQTHTEAARVMGKFLRDIMKMN
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DSMFNQHAKWLKVCNDIPWRRSVASLNYFLSSHV
WRQDHNGFSHQDPGFIDHVVNKKA
DVVRIYLPDANTLLSVTDHCLRSRNYVNVVVG
KQPAPQWLTMQAIKHCSEGLGIW
EWASNDKGSEPDVVMACCGDVPTLETAAVELIR
EHLPELKVRVINNVNLMKLQPPSE
HPHGLPDRDFDALFTKNKPIIFAFHGYPWLIHRL
TYRRTNHGNLHVRGYKEEGTTTTTP
FDMVVLNEMDRFHLVEDVIDRLPQLGARAAYFKQ
AIREKLVEHRQYIEKYGDDMPAIS
GWKWGSKAQPKTRQRTSTEGDNA"
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                /inference="protein
                motif:Pfam:PF03894.3"
                /note="Pfam match to entry
                PF03894.3 XFP"
gene            complement(84994..85662 /locus-tag="RL0067"
)
CDS             complement(84994..85662 /locus-tag="RL0067"
)
                /inference="similar to
                sequence:INSDC:AE007225"
                /note="similarity:fasta;
                with=UniProt:Q92ZW4
                (EMBL:AE007225); Rhizobium
                meliloti (Sinorhizobium
                meliloti).; Hypothetical protein.;
                length=217; id 57.746; 213 aa
                overlap; query 7-219; subject
                1-213"
                /codon-start=1
                /transl-table=11
                /product="putative CBS domain
                protein"
                /protein-id="CAK05555.1"
                /db-xref="GI:115254481"
                /db-xref="UniProtKB/TrEMBL:Q1MN97"
                /translation="MLVKDVMITKVVGSPDNSV
                RRAAEIMLANHVSQVVIDDAGRL

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TAYVRSNAWRVADVMSCDPIVVEG
DTSLARVSALMQEHHIKRLPVMRDGVLVGIVSRA
DLLKAIVTADQDETASGDEAIRRS
IATRLSENADLLGKDTTIVTVTDGVAHLWGTIDTE
ECKKAARVAAESVRGVRRVVEHFS  EDRR"
misc-feature    complement(85021..85191 /locus-tag="RL0067"
)
                /inference="protein
                motif: Pfam: PF04972.3"
                /note="Pfam match to entry
                PF04972.3 BON"
misc-feature    complement(85234..85392 /locus-tag="RL0067"
)
                /inference="protein
                motif: Pfam: PF00571.13"
                /note="Pfam match to entry
                PF00571.13 CBS"
misc-feature    complement(85489..85650 /locus-tag="RL0067"
)
                /inference="protein
                motif: Pfam: PF00571.13"
                /note="Pfam match to entry
                PF00571.13 CBS"
gene            complement(85775..87463 /locus-tag="RL0068"
)
CDS             complement(85775..87463 /locus-tag="RL0068"
)
                /inference="similar to
                sequence: INSDC: AP005369"
                /note="similarity: fasta;
                with=UniProt: Q8DM98
                (EMBL: AP005369); Synechococcus
                elongatus (Thermosynechococcus
                elongatus).; ATP-binding protein
                of ABC transporter.; length=616;
                id 38.973; 526 aa overlap; query
                30-555; subject 84-608"
                /codon-start=1
                /transl-table=11
                /product="putative component of
                ABC transporter"
                /protein-id="CAK05556.1"
                /db-xref="GI:115254482"
                /db-xref="GOA: Q1MN96"
                /db-xref="UniProtKB/TrEMBL: Q1MN96"
                /translation="MDTQQIPFKVTAVRFVRAVK
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                IGVFAAFTIVAVVSRFIEERLALL
                WREFLTRRAVSLYLADRAYYHLDVSGQLTHPDQR
                IAEDMRVFTVTTLSFILMILNSSL
                TIIAFSGVLWSISPLLFAVAVVYAACGSYLTIAL
                GRPLIKLNYDQLDKEASFRLSLIQ
                VRENAEGIMLAHCEEQQGFRLRLRDDAVANFRK
                VTAINRNVGFFTTGYNWLIQIIPA
                LIIAPAYIRGNIDFGVITQSGAAFAMLVGAFSLV
                ITQFQSISTFAAVVARLSSLMEAI
                ERAGTPADAGIEVVEGKERLAYEQLTLLHATNSV
                PIVKDVSISIPLGTRVLITGPARD
                AQAALFRATAGISFKGSGRIIRPAADDILFLPQR
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RIVQFLRELNLEHVLEQAGGLNTEQNWEILLSPQ
EQQLLAFINILIAAPQFAFLDRLD
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misc-feature    complement(join(86528.. /locus-tag="RL0068"
86596,86615..86683,
86882..86950,
86969..87037,
87179..87238,
87299..87367))
                /inference="protein
                motif:TMHMM:2.0"
                /note="6 probable transmembrane
                helices predicted at aa 33-55,
                76-95, 143-165, 172-194,261-283
                and 290-312"
misc-feature    complement(86543..87376 /locus-tag="RL0068"
                )
                /inference="protein
                motif:PFam:PF00664.9"
                /note="Pfam match to entry
                PF00664.9 ABC-membrane"
gene            complement(87586..89265 /locus-tag="RL0069"
                )
CDS             complement(87586..89265 /locus-tag="RL0069"
                )
                /inference="similar to
                sequence:INSDC:AE009260"
                /inference="similar to
                sequence:INSDC:I39710"
                /note="similarity:fasta;
                with=UniProt:Q59152 (EMBL:I39710);
                Agrobacterium tumefaciens.; celd;
                CelD protein.; length=584; id
                64.159; 452 aa overlap; query
                10-460; subject 1-452
                similarity:fasta;
                with=UniProt:Q8UAR8
                (EMBL:AE009260); Agrobacterium
                tumefaciens (strain C58/ATCC
                33970).; celd; Cellulose
                biosynthesis protein.; length=553;
                id 62.202; 545 aa overlap; query
                7-545; subject 3-547"
                /codon-start=1
                /transl-table=11
                /product="putative cellulose
                biosynthesis protein"
                /protein-id="CAK05557.1"
                /db-xref="GI:115254483"
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                DYTGFIVRPDYEHHAIAAGFASFLKHQNWTDLKLE
                YFSGPAGRREKMI EALQGPEVMFR
                DSSPKNSENIDNTICPIVPLPASFDDYLEQRMSS
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                TAETIDRDL DILFNLWRIKWSARKGTERTERLII
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QPLGALANIIDRQKKAILFYITGRDENWKTPSPG
LILHGYCIRRAIEHGFKTYDFLRG
NEPYKYMFGVEERRISCTLFRTNRGQNLHGVLNP
RSIRFVYEQALDMYRNGARSKAEI
AFNQVLQSAPGHTGAIEFGLANLLFDRGKLTEAQA
AYKVLVEQAPDPTPIQMRLGDTQL
ALHQYDQAAETFRQIGEIGPHLIQAHYKRGIALA
ASKRLAEAEAVFAAIQEVHSDPT
ALDYVAKASAAALERIRVSAEPAPCKTDAVPETIA
RWNRRGRQLSERRRRLH"
misc-feature    complement(87748..87849 /locus-tag="RL0069"
)
                /inference="protein
                motif: Pfam: PF00515.11"
                /note="Pfam match to entry
                PF00515.11 TPR"
misc-feature    complement(87850..87951 /locus-tag="RL0069"
)
                /inference="protein
                motif: Pfam: PF00515.11"
                /note="Pfam match to entry
                PF00515.11 TPR8"
misc-feature    complement(87952..88053 /locus-tag="RL0069"
)
                /inference="protein
                motif: Pfam: PF00515.11"
                /note="Pfam match to entry
                PF00515.11 TPR8"
gene            complement(89508..89999 /locus-tag="RL0070"
)
CDS             complement(89508..89999 /locus-tag="RL0070"
)
                /inference="similar to
                sequence: INSDC: B98318"
                /note="similarity: fasta;
                with=UniProt: Q8UAP9 (EMBL: B98318);
                Agrobacterium tumefaciens (strain
                C58/ATCC 33970).; Hypothetical
                protein Atu3324.; length=170; id
                77.160; 162 aa overlap; query
                1-162; subject 7-168"
                /codon-start=1
                /transl-table=11
                /product="conserved hypothetical
                protein"
                /protein-id="CAK05558.1"
                /db-xref="GI:115254484"
                /db-xref="UniProtKB/TrEMBL: Q1MN94"
                /translation="MAAMSDVLLRVGRLNYVWTN
                TESLLIYIIAHLLRVEKDAAIVVF
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                SRLKKESKTRNKYNHCIYSFDEKG
                DISSTQLMRLVEDDKQIRYGKIEQMDAREIEHLE
                KSIAEIVAISRTLWAFIHASPQIS GEL"
gene            complement(90117..91466 /locus-tag="RL0071"
)
CDS             complement(90117..91466 /locus-tag="RL0071"
)
                /inference="similar to
                sequence: INSDC: C95953"
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                sequence: INSDC: C98318"

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  Rhizobium meliloti (Sinorhizobium
  meliloti).; Hypothetical protein
  expD2.; length=Hypothetical
  protein; id 32.710; 428 aa
  overlap; query 24-448; subject
  52-472 similarity:fasta;
  with=UniProt:Q8UAQ0 (EMBL:C98318);
  Agrobacterium tumefaciens (strain
  C58/ATCC 33970).; Secretion
  protein, HlyD family.; length=497;
  id 80.778; 437 aa overlap; query
  13-449; subject 61-497; putative
  HlyD family secretion protein"
  /codon-start=1
  /transl-table=11
  /product="Hypothetical protein
  expD2."
  /protein-id="CAK05559.1"
  /db-xref="GI:115254485"
  /db-xref="GOA:Q1MN93"
  /db-xref="UniProtKB/TrEMBL:Q1MN93"
  /translation="MGRKNRETTGPVQLEWYSDV
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  KEMRVSEGDITVKEGDILLTLDPTA
  SRSNERMLQLRRLRLEAVVARLRAEAQGLRQFQL
  PDIVTKEAGDPDINAI IQSQNVVF
  HSKQIKLEEQLNLIGKNIASLEFRFVGYRGQRES
  FERQLSLLTEERDSKARLVKVGYM
  RKTDLLAIERAIADAMGDIARLNGELNESEAEIA
  KFRQEAVIAVNSNKQAALDALETA
  ETDLDSVREQMREAAGVLERTTIRSPVSGTVVRS
  YFHTAGGVITTGKPI MEILPSHVP
  LILEAKVLRTSIDQLHEGETASIRLTALNRRTP
  VLQGVFYVSADSI EENAGASVKD
  VYIVRVGIPDSEIARVHNFHPVPGMPAEVLIQTS
  ERTFFEYLSKPITDSMSRAFKER"
  /locus-tag="RL0071"
  /inference="protein
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  /note="Pfam match to entry
  PF00529.8 HlyD"
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  motif: TMHMM:2.0"
  /note="1 probable transmembrane
  helix predicted at aa 26-48"
}

/feature "gene" complement(91472..93769)
{
  /locus-tag="RL0072"
}

/feature "CDS" complement(91472..93769)
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  /locus-tag="RL0072"
  /inference="similar to
  sequence: INSDC:AE009262"
  /note="similarity:fasta;
  with=UniProt:Q8UAQ1
  (EMBL:AE009262); Agrobacterium
  tumefaciens (strain C58/ATCC
  33970).; ABC transporter,

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nucleotide binding/ATPase  
protein.; length=690; id 82.138;  
683 aa overlap; query 88-765;  
subject 9-690 Similar, but  
truncated at the N-terminus to  
Agrobacterium tumefaciens (strain  
C58/ATCC 33970) ABC transporter,  
nucleotide binding/ATPase protein  
(690 aa)"  
/codon-start=1  
/transl-table=11  
/product="putative ATP-binding  
component of ABC transporter"  
/protein-id="CAK05560.1"  
/db-xref="GI:115254486"  
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/db-xref="UniProtKB/TrEMBL:Q1MN92"  
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AVAQGLATAKTPEAPARPQIEARVSPEQPKEKIE  
LKSSPTMPFAKTIEGESGPISENN  
RRMRAGGGGNGKSDPGGGGGGGGGSGGGFHKRS  
EPVNFAASLSRGMAAVRHNMVVVM  
MFTIAINVLLLAIPLYLFQISDRVLTSSVDTLV  
MLSIAVIGAVLLQAFMDSVRRFIL  
MRTAVELEVQLGAPILSAAARASLHGSGKDYQTL  
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PFFVVVYFVHPHLGIIIMVCCAVLFVIAYLNQK  
FTARQFAESNGYLSRANFHLDSMS  
RNSQIINAMAMIPEAVKMWGRETAGSLKSQVEAQ  
DRNIIIFSGISKACRMITQVTLLGW  
GAHLSLSGELTGGMVIAASIIISGRALAPIEGAIE  
GWNQFNRSAAAYSRIKGLLLNSPL  
NFPRLRLPNPEGRDLVERILFVPPPQKKVILNGI  
SFSLRKGESLAIIGNSGSGKTTLG  
KMLVGSIVPTSGNVRLDLMDLRNWDQRQFGESIG  
YLPQDVQLFPGTIKANICMRDDV  
DDHQIYDAAVLADVHELIAGFPQGYETIVAADGA  
PLSGGQKQRIALARAFFGNPKFVV  
LDEPNSNLDTQGEAALAKALIHAKKQGITTVTIT  
QRPALLQCVDKILVLKDGTVAMFG  
ERIEVLQALSKNNGNNGQQAPRIEG"

misc-feature complement(91568..92125  
)

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/inference="protein  
motif: Pfam:PF00005.11"  
/note="Pfam match to entry  
PF00005.11 ABC-tran"

misc-feature complement(92333..93130  
)

/locus-tag="RL0072"  
  
/inference="protein  
motif: Pfam:PF00664.9"  
/note="Pfam match to entry  
PF00664.9 ABC-membrane"

misc-feature complement(join(92363..  
92431,92675..92743,  
92756..92824,  
92966..93019,  
93062..93130))

/locus-tag="RL0072"  
  
/inference="protein"

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motif:TMHMM:2.0"
/note="5 probable transmembrane
helices predicted at aa 214-236,
251-268, 316-338,343-365 and
447-469"
gene      complement(93795..95831 /locus-tag="RL0073"
)
CDS       complement(93795..95831 /locus-tag="RL0073"
)

/inference="similar to
sequence:INSDC:AE009262"
/note="similarity:fasta;
SWALL:Q8UAQ2 (EMBL:AE009262);
Agrobacterium tumefaciens;
hypothetical protein atu3321;
length 680 aa; 687 aa overlap;
query 1-678 aa; subject 8-680 aa"
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protein"
/protein-id="CAK05561.1"
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VNALYDDDYLDMTDGVHAPRDTSF
VIERLADFSTKAEIFTPFASLHRTDTYDGALKVA
EDLEVYIQNAQNTEDSGTTS LGTD
ATHEFVRLDPGVNDTVYINGKAETDIPVLDDFLP
DRGLAKLPEEPDDSNTSVEQDDPS
GTSLEVTAGANLVVNVASVINTGVITSVTAVMGN
YHQVDAISQAFVYSDNDEIASTLH
SSDRSGEAAETIAKNIALFEHSTFEASSHADTDA
TEPTFPNSWRVSVIDGDVSVFVQWI
EQYQFVTDNDTMTVITSGSETTVLTGGNTSINF
SFFGMGMQYDLVIIGGNVLDINSI
TQISLLYDNDWVRAEDGVDPGADIQTGDNLIWNF
ASIHNVTGTDSPFAAMPDYMAATQK
AIEDRDPNMPEGLSFDVNFQGYAGLNVLYITGNL
YDMTIIKQVSILGDSDDVTLAAS
ILENNPDATVTIDTGSNAVVNIAEIVDYDSFGQT
TYLAGQLYSDAILIQGLVEHDTT
QPQPADDRLANEVIAFFDNDPAGGDCADGVINA
GNDFSWSSTHPADVMQAMVA"
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)
CDS       complement(95973..96929 /locus-tag="RL0074"
)

/inference="similar to
sequence:INSDC:AE008350"
/note="similarity:fasta;
with=UniProt:Q8UAQ3
(EMBL:AE008350); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; Fibrinogen binding
protein (AGR-L-3004p).;
length=321; id 65.109; 321 aa
overlap; query 6-317; subject

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11-321"
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/transl-table=11
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protein"
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DNTDNSVDVDVKAIDVATNNGDNRDNEYDWSYK
SDDDTSTKTTTITDIDTKTDYDWS
YDSKTYSDNDTDTKTITDIDTKTVDTDIKTVTE
TETDTKTVDSDNNTSDSFNKTDTD
FAVIEDVKDSNLGVAGHDLTFNLGDDFSFTLDVD
SILNNSLTGAGNDSGFSAVQANHL
ADQDSAWNTKMENEGAQNHLNANGGTANSAEGME
MDGKSWDLKAGDDANGASTADASA
ILANSGFHLELVQGANLLSNTVDSSVIGGNSHTS
DVGEDTST"
repeat-unit complement(96580..96593 /locus-tag="RL0074"
)
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repeat-unit complement(96640..96653 /rpt-unit-seq="tagctccagtc"
) /locus-tag="RL0074"
repeat-unit 96700..96710 /note="accgacaccaagac"
repeat-unit 96767..96780 /rpt-unit-seq="tagctccagtc"
repeat-unit complement(96767..96780 /note="cgctcgacgtcgacg"
) /locus-tag="RL0074"
gene 97773..98555 /note="cgctcgacgtcgacg"
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/locus-tag="RL0075"
/inference="similar to
sequence:INSDC:BM3181"
/inference="similar to
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/note="similarity:fasta;
with=UniProt:DEGU-BACBR
(EMBL:I39835); Bacillus brevis
(Brevibacillus brevis).; degU;
Transcriptional regulatory protein
degU.; length=236; id 28.821; 229
aa overlap; query 24-239; subject
12-223 similarity:fasta;
with=UniProt:Q8UAQ5 (EMBL:BM3181);
Agrobacterium tumefaciens (strain
C58/ATCC 33970).; Transcriptional
regulator, LuxR family
(AGR-L-3006p).; length=265; id
59.231; 260 aa overlap; query
1-260; subject 10-265"
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/product="putative GerE family
transcriptional regulator"
/protein-id="CAK05563.1"
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/translation="MFMTGSGMENADQGRKLGS

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gene	complement(98571..98891	/locus-tag="RL0076"
	)	
CDS	complement(98571..98891	/locus-tag="RL0076"
	)	
		/inference="similar to sequence: INSDC:A98319" /note="similarity: fasta; with=UniProt:Q8UAQ6 (EMBL:A98319); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu3317 (AGR-L-3007p).; length=116; id 37.864; 103 aa overlap; query 13-104; subject 15-116" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05564.1" /db-xref="GI:115254490" /db-xref="UniProtKB/TrEMBL:Q1MN88" /translation="MVKKQDAAQLKGRIRISAMF AWGTALLAIGPTACTVDDHIAVV AKKNIPVVEAPRVSKAYAYPANRVGRPAAATVRT VAYHGSAPYICSPSGFGQKSRCA RPPI"
misc-feature	complement(98781..98849	/locus-tag="RL0076"
	)	
		/inference="protein motif: TMHMM:2.0" /note="1 probable transmembrane helix predicted at aa 15-37"
gene	99276..100301	/locus-tag="RL0077"
CDS	99276..100301	/locus-tag="RL0077"
		/inference="similar to sequence: INSDC:AT8927" /inference="similar to sequence: INSDC:B98319" /note="similarity: fasta; with=UniProt:Q9LFG7 (EMBL:AT8927); Arabidopsis thaliana (Mouse-ear cress).; F4P12-220; DTDG-glucose 4-6-dehydratase-like protein (UDP-glucuronic acid decarboxylase).; length=433; id 50.303; 330 aa overlap; query 2-328; subject 96-420 similarity: fasta; with=UniProt:Q8UAQ7 (EMBL:B98319);



		Agrobacterium tumefaciens (strain C58/ATCC 33970).; DTD-glucose 4-6-dehydratase (AGR-L-3008p).; length=340; id 72.093; 344 aa overlap; query 1-341; subject 1-340" /codon-start=1 /transl-table=11 /product="putative dTDP-glucose 4-6-dehydratase-like protein (UDP-glucuronic acid decarboxylase)" /protein-id="CAK05565.1" /db-xref="GI:115254491" /db-xref="GOA:Q1MN87" /db-xref="UniProtKB/TrEMBL:Q1MN87" /translation="MRSFVPSEGYSEVSSGIPVA QALRTVLVNGGGGFLGSHLCERLL QHGHRVICLDNFSTGRRANVDHLASNTRFHIVEH DVRQPFIDIEASLIFNFASPASPPD YQRDPVGTLTNTVLGAVNTLDCARKTGAIVVQSS TSEVYGDPIHSPQHESYCGNVNQI GPRGICYDEGKRSAETLFFDYHRTYGVDVKVGRIF NTYGPRMRLDDGRVVSNFIVQALR NADLTIYGDGQQTRSFCYVDDLIIEGFLRFSTAGS ACNGPINLGNPTEMTVRRRLAEIIR DLTNSRSRIVHLPVATDDPRQRRPDISRMAELD WQPRIGLETGLARTVDYFDGLLAG TEKAEVV" /locus-tag="RL0077" /inference="protein motif: Pfam: PF01370.8" /note="Pfam match to entry PF01370.8 Epimerase"
misc-feature	99351..100271	
gene	100303..101286	/gene="exoB" /locus-tag="RL0078"
CDS	100303..101286	/gene="exoB" /locus-tag="RL0078" /inference="similar to sequence: INSDC: C98319" /inference="similar to sequence: INSDC: RLEXOBGEN" /note="similarity: fasta; with=UniProt: EXOB-RHILT (EMBL: RLEXOBGEN); Rhizobium leguminosarum (biovar trifolii).; exoB; UDP-glucose 4-epimerase (EC 5.1.3.2) (UDP-galactose 4-epimerase) (Galactowaldenase).; length=EC 5.1 ( 327; id 51.757; 313 aa overlap; query 5-317; subject 6-317 similarity: fasta; with=UniProt: Q8UAQ8 (EMBL: C98319); Agrobacterium tumefaciens (strain C58/ATCC 33970).; galE; UDP-glucose 4-epimerase.; length=356; id 74.695; 328 aa overlap; query 1-327; subject 30-356" /codon-start=1 /transl-table=11 /product="putative UDP-glucose 4-epimerase (UDP-galactose

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		/db-xref="GOA:Q1MN86"
		/db-xref="UniProtKB/TrEMBL:Q1MN86"
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		YVGESVEMPRKYYRNNVVGSLTLL
		EACLDQDIDRIVFSSSCATYGVPASLPiREESpQ
		HPVNPYGRTKLIFEMALEDFAAAY
		GIRFAALRYFNAAGADPDGELAERHQPETHLIPR
		ALLAAAGRLERLDIFGTDYATEDG
		TCVRDYIHVSDLAQAHLAAVNHLLADGGSLSVNL
		GSGRGTSVREILEAIHRASGREVP
		VRYSRRVGDPPILFANTARAKAELGFAPAFSDI
		DTIIRTAGPTFGLEMRA"
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		/locus-tag="RL0078"
		/inference="protein
		motif: Pfam: PF01370.8"
		/note="Pfam match to entry
		PF01370.8 Epimerase"
gene	101283..103151	/gene="acsAB"
		/locus-tag="RL0079"
CDS	101283..103151	/gene="acsAB"
		/locus-tag="RL0079"
		/EC-number="2.4.1.12"
		/inference="similar to
		sequence: INSDC: AE008351"
		/inference="similar to
		sequence: INSDC: AXCCPENG"
		/note="similarity: fasta;
		with=UniProt: ACS1-ACEXY
		(EMBL: AXCCPENG); Acetobacter
		xylinus.; acsAB; Cellulose
		synthase 1 [Includes: Cellulose
		synthase catalytic domain
		[UDP-forming] (EC 2.4.1.12);
		Cyclic di-GMP binding domain
		(Cellulose synthase 1 regulatory
		domain)].; length=1550; id 24.421;
		561 aa overlap; query 38-567;
		subject 80-606 similarity: fasta;
		with=UniProt: Q8UAQ9
		(EMBL: AE008351); Agrobacterium
		tumefaciens (strain C58/ATCC
		33970).; Cellulose synthase
		(AGR-L-3012p).;
		length=AGR-L-3012p; id 65.772; 596
		aa overlap; query 14-608; subject
		14-607"
		/codon-start=1
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		LGYFWIWWCQSAHIIISWATEFVLVTLVLVWITLVP AYFILIFLDARTVSPRAGLPEGRV AMVVTKAPSEPFVVRITTLQAMLDQIGVDFDVWL ADEDPSEETRRWCEEHGVLISTRK GVAEYHRTTWPRRTRCKEKNLAYFYDHFYARYD FVAQFDADHVPTPTYLREILRPFA DPEIGYVSAPSICDANAGTSWAARGRLYAEASLH GSLQTGYNNGWAPLCIGSHYAVRT SALRQIGGLGPELAEDHSTTLMMNSGGWGRGVHAV DAIAHGDPANFTDLVVQEFQWSR SLVTILLQHSRRHIMHLPWRLRFQVFVSQLWYPL FSVFMAMMFLLPVAALLTGRVFN VTYPDFLLHFVPMVMVLTLFAFFWRTTATFRPHD AKLLGWEGLAFIFLRWPWSLAGSL AAVRDYICGSFVDFRITPKGRQQQSLPLRVIAP YIGLAGLSAAAMMFATDAAAQGF YVFAMMNLSVYLALTVLIVVRHAVENDLPLLPQS RGLWLATATGLAIFVAGGTQAGSH GLRGLEALSHGQTFVSFTETQFAVAGAGLGGGKT RIVKFHLRWNGFGRTGRDEQGA"
misc-feature	order(101376..101435, 101472..101540, 102369..102437, 102474..102542, 102585..102653, 102711..102779, 102807..102875, 102912..102980)	/gene="acsAB"  /locus-tag="RL0079" /inference="protein" motif:TMHMM:2.0" /note="8 probable transmembrane helices predicted at aa 32-51, 64-86, 363-385, 398-420,435-457, 477-499, 509-531 and 544-566"
misc-feature	101586..102131	/gene="acsAB" /locus-tag="RL0079" /inference="protein" motif:Pfam:PF00535.10" /note="Pfam match to entry PF00535.10 Glycos-transf-2"
gene	103148..103711	/locus-tag="RL0080"
CDS	103148..103711	/locus-tag="RL0080" /inference="similar to sequence:INSDC:AE009261" /note="similarity:fasta; with=UniProt:Q8UAR0 (EMBL:AE009261); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu3313.; length=173; id 50.000; 152 aa overlap; query 26-177; subject 21-169" /codon-start=1 /transl-table=11 /product="conserved hypothetical exported protein" /protein-id="CAK05568.1" /db-xref="GI:115254494" /db-xref="UniProtKB/TrEMBL:Q1MN84" /translation="MSRRNRQVSSMEDVMSIGSR LWGAALALSLCLPVATHGAEVAKT

		KAPTPLSAYELYRIYGDKTWTWNTGGGRFFYDGR RFVAWSNDKGKPSFAEGRWVVDL GQLCMRATWTNAEGAARASTCFGHRKIGNTIYQR RQPNGEWYVFRHASVRQGDEFQKL VPTDTVSAKASEVKQILLSQEVARKGG"
sig-peptide	103148..103259	/locus-tag="RL0080" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0080 by SignalP 2.0 HMM (Signal peptide probability 0.995) with cleavage site probability 0.977 between residues 38 and 39"
misc-feature	103202..103648	/locus-tag="RL0080" /inference="protein motif:Pfam:PF06191.1" /note="Pfam match to entry PF06191.1 DUF995"
gene	103715..104686	/locus-tag="RL0081"
CDS	103715..104686	/locus-tag="RL0081" /inference="similar to sequence:INSDC:AB039953" /inference="similar to sequence:INSDC:AE008351" /note="similarity:fasta; with=UniProt:Q8RS40 (EMBL:AB039953); Alcaligenes sp. XY-234.; 3xynAlc; Beta-1,3-xylanase.; length=469; id 28.105; 153 aa overlap; query 87-229; subject 65-209 similarity:fasta; with=UniProt:Q7CS49 (EMBL:AE008351); Agrobacterium tumefaciens (strain C58/ATCC 33970).; AGR-L-3016p.; length=320; id 66.901; 284 aa overlap; query 34-317; subject 32-315 Codons 85 to 235 are similar to codons 65 to 215 of Alcaligenes sp. XY-234 Beta-1,3-xylanase (469 aa), and entire protein is similar to Agrobacterium tumefaciens (strain C58/ATCC 33970) AGR-L-3016p (320 aa)" /codon-start=1 /transl-table=11 /product="putative polysaccharide degradation protein" /protein-id="CAK05569.1" /db-xref="GI:115254495" /db-xref="UniProtKB/TrEMBL:Q1MN83" /translation="MKKLMKKNLSTAAIALLLLC VADLPGRSEVQYAGIAPNPAAAVR TIIDKRPVLHADGIKFGAYDPHGDFGAQASVATE ALFLPWEDVDLETLRVADAYAQAR GRNLLITVEPWSWDVDWRLTSAELRAKVLRGDYG VNMRAIAQMISELKSPVIVRWGQE MEDKSGRFSWSGWSPQDYITAYKRMMDIVRQEAP GTELMWSPKGEPGLQAYYPGDDYV DLVGLSVFGLQRYDELAYNGHRTFSEALKQGYDL VAGYGKPIWVAELGYGGDAYMKP

		WIETVALKQSAFPNLQEVVYFNDRDVHAWPFDLG RPDWRVVESLANR"
sig-peptide	103715..103778	/locus-tag="RL0081" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0081 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.849 between residues 22 and 23"
gene	complement(104748..106034)	/locus-tag="RL0082"
CDS	complement(104748..106034)	/inference="similar to sequence:INSDC:RME591985" /note="similarity:fasta; with=UniProt:Q92W28 (EMBL:RME591985); Rhizobium meliloti (Sinorhizobium meliloti).; Putative solute-binding protein.; length=428; id 72.326; 430 aa overlap; query 1-427; subject 1-426" /codon-start=1 /transl-table=11 /product="putative solute-binding component of ABC transporter" /protein-id="CAK05570.1" /db-xref="GI:115254496" /db-xref="GOA:Q1MN82" /db-xref="UniProtKB/TrEMBL:Q1MN82" /translation="MQVNRRSFLMGSAGAAAGLA FGAGSAIPAFEDAQLRAMWWGSN DRAKRTLDVAKLYQSKTPGVTIVGESLSGDGYWT KLATQMAGRSIADIFQLEPGTISD YSKRGACMPLDEFVPSTLQVDSFGADMLKLTTID GKLYGVGLGLNSFSMFFDTVEFEK AGIPVPTPDLTWDEYAKLAVELAKSSGKSGGPYA ARYAYVFDawLRQRGKSLFARESV GLGFTADDAREWFDYWEKLRKAGGTVAADVQTLD QNTIDTNALGLGKSVIGMAYSNQM IGYQLIIKNKLGITMLPREKKGGPSGHYYRPALI WSVGATTKNGEAAAKFIDFFVNDI EAGKILGVERGVPMSPVTVREAILPQLNPTEQETV KYVNLLKDQVGEYPPPVPMGATQF DQRVLRPICDELAFERVSPADAATRLIEEGKATI KG"
misc-feature	complement(105024..106010)	/locus-tag="RL0082"  /inference="protein motif:Pfam:PF01547.11" /note="Pfam match to entry PF01547.11 SBP-bac-1"
sig-peptide	complement(105938..106034)	/locus-tag="RL0082"  /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0082 by SignalP 2.0 HMM (Signal peptide probability 1.000)

		with cleavage site probability 0.981 between residues 31 and 32"
misc-feature	complement(105948..106016)	/locus-tag="RL0082"
		/inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted at aa 7-29"
gene	106182..107201	/locus-tag="RL0083"
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sig-peptide	106182..106269	/locus-tag="RL0083" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0083 by SignalP 2.0 HMM (Signal peptide probability 0.906) with cleavage site probability 0.895 between residues 30 and 31"
misc-feature	106206..106283	/locus-tag="RL0083" /inference="protein motif:Pfam:PF00356.8" /note="Pfam match to entry PF00356.8 LacI"
misc-feature	106365..107198	/locus-tag="RL0083" /inference="protein motif:Pfam:PF00532.8" /note="Pfam match to entry PF00532.8 Peripla-BP-1"
gene	107329..109185	/locus-tag="RL0084"
CDS	107329..109185	/locus-tag="RL0084" /inference="similar to

gene  
CDS

109182..110192  
109182..110192

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Rhizobium meliloti (Sinorhizobium
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619 aa overlap; query 1-618;
subject 1-617"
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ALAFSDDGLHYRVRETNEEAKIAG
EVLFAKWSPFADVDVETWLVPAAPWHIRLHRI
SRPLRIAEGGFAIGRRDFELDTLS
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sequence:INSDC:B95906"
/inference="similar to
sequence:INSDC:MESERCYC"
/note="Codon 70 to the C-terminus
are similar to codons 60 to the
C-terminus of Methylobacterium
extorquens. HprA DHGY-METEX
(EMBL:MESERCYC) ( Glycerate
dehydrogenase (EC 1.1.1.29)
(NADH-dependent hydroxypyruvate
reductase) (HPR) (GDH)
(Hydroxypyruvate dehydrogenase)
(Glyoxylate reductase) (HPR-A).),
and to entire protein of Rhizobium
meliloti (Sinorhizobium meliloti).
Putative dehydrogenase protein.
Q92W31 (EMBL:B95906) (336)
similarity:fasta;
with=UniProt:DHGY-METEX
(EMBL:MESERCYC); Methylobacterium
extorquens.; hprA; Glycerate
dehydrogenase (EC 1.1.1.29)
```

		(NADH-dependent hydroxypyruvate reductase) (HPR) (GDH) (Hydroxypyruvate dehydrogenase) (Glyoxylate reductase) (HPR-A).; length=313; id 36.047; 258 aa overlap; query 75-322; subject 63-307 similarity:fasta; with=UniProt:Q92W31 (EMBL:B95906); Rhizobium meliloti (Sinorhizobium meliloti).; Putative dehydrogenase protein.; length=336; id 64.881; 336 aa overlap; query 1-336; subject 1-336" /codon-start=1 /transl-table=11 /product="putative glycerate dehydrogenase" /protein-id="CAK05573.1" /db-xref="GI:115254499" /db-xref="GOA:Q1MN79" /db-xref="UniProtKB/TrEMBL:Q1MN79" /translation="MSQPAIILAMQPSRTQHVLPEVLRRLGGIGRLLDSKPLQRFDDERARRLLAEAEILITGWGGPYVGPEIPTAAPHLKFIVHAAGTVKGVIDDAIFEAGIPVSHSAEANAVPVAEFTLAAIIFAGKRVFRFRDLYVADNRNRNRTHLMQREAIIGNYRRTVGIVGASRIGRRVIELLKPFDYRLLLSDPITLDAAEAAGLGTEKIDLDLMRQSDIVSLHAPSLPSTQHMIDARRLSLMKDGATLINTARGILIDEAALLSVLKTGRIDAVLDVTDPEIPEAGSAFYDLPNVFLTPHIAGAIGLERARLGEMAVDEIERFVTGQPLLYQIHQANLAN IA" /locus-tag="RL0085" /inference="protein motif: Pfam: PF02826.5" /note="Pfam match to entry PF02826.5 2-Hacid-dh-C"
misc-feature	109518..110063	/locus-tag="RL0086" /inference="similar to sequence: INSDC: B95991" /inference="similar to sequence: INSDC: SME591782" /note="similarity: fasta; with=UniProt: MI2D- RHIME (EMBL: B95991); Rhizobium meliloti (Sinorhizobium meliloti).; idhA; Inositol 2-dehydrogenase (EC 1.1.1.18).; length=330; id 26.471; 204 aa overlap; query 22-225; subject 4-194 similarity: fasta; with=UniProt: Q92T57 (EMBL: SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE OXIDOREDUCTASE PROTEIN.; length=433; id 82.892; 415 aa overlap; query 20-434; subject 5-419 N-terminus to codon 230 is
gene	complement(110281..111609)	
CDS	complement(110281..111609)	



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similar to the N-terminus to codon
200 of Rhizobium meliloti
(Sinorhizobium meliloti) Inositol
2-dehydrogenase (330 aa), and
entire protein is similar to
Rhizobium meliloti (Sinorhizobium
meliloti) PUTATIVE OXIDOREDUCTASE
PROTEIN. (433 aa)"
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/db-xref="GI:115254500"
/db-xref="GOA:Q1MN78"
/db-xref="UniProtKB/TrEMBL:Q1MN78"
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DSMLAEQKPDLVIVCTPDHTHDDI
VVRALSGIDVITEKPMTTSVEKIRRILDAEKRT
GRRVDVSFNRYRYAPTAARIKELLN
AGEIGRVTSVDFHWYLNTHGADYFRRWHAYKEN
SGSLFVHKATHHFDLLNWYLDSDP
EAVTSFADLQNYGRKGPFGRCKLCPHTECDY
YLDLEADPFLDSLYEDPSKIDGYF
RDGCVFREDIDIPDTMVVSLRYRNNVHVSYSLNT
FQPIEGHHLAFNGTKGRIELRQYE
AQPWEEPQDITILLIRNFPDGKEAVERIVVPHT
GGHYGGDDMRNMIFKPDTEDLA
QRAGTRAGAMSVLCGIAALESRTGKVVDIADLM
PELANDGSPNSLRTSR"
misc-feature      complement(110833..1111 /locus-tag="RL0086"
44)
/inference="protein
motif: Pfam: PF02894.4"
/note="Pfam match to entry
PF02894.4 GFO-IDH-MocA-C"
misc-feature      complement(111178..1115 /locus-tag="RL0086"
49)
/inference="protein
motif: Pfam: PF01408.8"
/note="Pfam match to entry
PF01408.8 GFO-IDH-MocA"
gene              complement(111710..1125 /locus-tag="RL0087"
34)
CDS               complement(111710..1125 /locus-tag="RL0087"
34)
/inference="similar to
sequence: INSDC: A69646"
/inference="similar to
sequence: INSDC: AY316746"
/note="similarity: fasta;
with=UniProt: IOLI-BACSU
(EMBL: A69646); Bacillus subtilis.;
iolI; IolI protein.; length=278;
id 26.429; 280 aa overlap; query
6-265; subject 3-263
similarity: fasta;
with=UniProt: Q6W2E1
(EMBL: AY316746); Rhizobium sp.
(strain NGR234).;

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3-dehydroshikimate dehydratase (EC 4.2.1.-).; length=EC ( 274; id 85.766; 274 aa overlap; query 1-274; subject 1-274"  
/codon-start=1  
/transl-table=11  
/product="conserved hypothetical protein"  
/protein-id="CAK05575.1"  
/db-xref="GI:115254501"  
/db-xref="UniProtKB/TrEMBL:Q1MN77"  
/translation="MQVEGLSINLATIREQCGFA  
EAVDICLKHGITAIPWRDQVAKV  
GLDEAVRIVKSNGIKLTGLCRGGFFPAANDADWQ  
KNLDDNRRRAIDEEAAFSADCLVLV  
VGGLPGSSKDIVAARRMVFDGIAAVLPHAQAAGV  
KLAIEPLHPMYAADRACVNTLGQA  
LDLCEQLGEDVGVAVDVYHVWDPDLANQIARAG  
RMKRIFAHHCIDWLVPTKDMLLDR  
GMMGDGVIDLKGIRRMVEAAGFFGAQEVEIFSAE  
NWWKRPAAEEVIATCVERFRSCC"

gene complement (112672..1138 /locus-tag="RL0088"  
35)

CDS complement (112672..1138 /locus-tag="RL0088"  
35)

/inference="similar to  
sequence:INSDC:SME591782"  
/note="similarity:fasta;  
with=UniProt:Q92T60  
(EMBL:SME591782); Rhizobium  
meliloti (Sinorhizobium  
meliloti).; Hypothetical protein  
SMc04132.; length=387; id 84.197;  
386 aa overlap; query 1-386;  
subject 1-386"  
/codon-start=1  
/transl-table=11  
/product="conserved hypothetical  
protein"  
/protein-id="CAK05576.1"  
/db-xref="GI:115254502"  
/db-xref="UniProtKB/TrEMBL:Q1MN76"  
/translation="MTTINLPLDGKIVPYTLTGT  
PIALAKRDAKAFPRIAFAAAHVVA  
DPLADNDPWLTPAIDWERTLAFRHRLWDLGLGVA  
EAMDTAQRGMGLGWPEARDLIRRA  
LSEAAGRKDAL IACGAGTDHLTPGPDVTVDTILS  
AYEEQIETVEAAGGRIILMASRAL  
AAAAKGPDDYIRVYDRILRQVKEPVIIHWLGEMF  
DPALEGYWNGDHIQAMSTCLEVI  
EAHADKVDGIKISLLSKEKEVAMRRRLPKGVRMY  
TGDDFNAYAELIAGDEEGHSDALLG  
IFDAIAPAASAALEALGRKSNHEFFDLLEPTVPL  
SRHIFKAPTRFYKTGVVFLAYLNG  
LQDHFVMVGGQQSTRSLTHLAELFRLADKARVLA  
DPELATARMKQVLAVHGVN"

misc-feature complement (112678..1138 /locus-tag="RL0088"  
32)

/inference="protein  
motif: Pfam:PF06187.1"  
/note="Pfam match to entry  
PF06187.1 DUF993"

gene complement(113839..1149 /locus-tag="RL0089"  
87)

CDS complement(113839..1149 /locus-tag="RL0089"  
87)

/inference="similar to  
sequence:INSDC:AY316746"  
/note="similarity:fasta;  
with=UniProt:Q6W2E4  
(EMBL:AY316746); Rhizobium sp.  
(strain NGR234).; Oxidoreductase  
(EC 1.1.1.-).; length=382; id  
91.099; 382 aa overlap; query  
1-382; subject 1-382"  
/codon-start=1  
/transl-table=11  
/product="putative oxidoreductase"  
/protein-id="CAK05577.1"  
/db-xref="GI:115254503"  
/db-xref="GOA:Q1MN75"  
/db-xref="UniProtKB/TrEMBL:Q1MN75"  
/translation="MARLGIILHGVTGRMGYNQH  
LVR SILAFRDQGGITLKS GEKLEI  
DPIIVGRNGAKMEELAKKHNIKRWSTDLDAALAN  
PDDTIFFDAGTTLMRAELLSKALD  
AGKHVYCEKPI SDDLQVALDLARKARRSGLKHGV  
VQDKLFLPGLRKLALLRDSGFFGK  
ILSVRGEFGYWVFEGDWGVPAQRP SWNYRKGDGG  
GIILDM LCHWRYVLDNLFGEVKAV  
SCLGATHIPRRIDEQGKPYDCDTDDAAYATFELE  
GGAIAQVNSSWAVRVRRDDLVTFQ  
VDGTHGSAVAGLTKCWSQHRVNTPKPVWNPDPQ  
TIDFYKTWDEVPDTQAFDNGFKAQ  
WEMFIRHVVEDAPWPYGLEAGAKGVQLAELGLKS  
WAERRWLDVPALEF"

misc-feature complement(114166..1145 /locus-tag="RL0089"  
10)

/inference="protein  
motif: Pfam:PF02894.4"  
/note="Pfam match to entry  
PF02894.4 GFO-IDH-MocA-C"

misc-feature complement(114574..1149 /locus-tag="RL0089"  
84)

/inference="protein  
motif: Pfam:PF01408.8"  
/note="Pfam match to entry  
PF01408.8 GFO-IDH-MocA"

gene complement(115119..1157 /locus-tag="RL0090"  
96)

CDS complement(115119..1157 /locus-tag="RL0090"  
96)

/inference="similar to  
sequence:INSDC:SME591782"  
/note="similarity:fasta;  
with=UniProt:Q92T62  
(EMBL:SME591782); Rhizobium  
meliloti (Sinorhizobium  
meliloti).; PUTATIVE TRANSCRIPTION  
REGULATOR PROTEIN.; length=225; id  
75.111; 225 aa overlap; query  
1-225; subject 4-225"  
/codon-start=1  
/transl-table=11

		/product="putative TetR family transcriptional regulator" /protein-id="CAK05578.1" /db-xref="GI:115254504" /db-xref="GOA:Q1MN74" /db-xref="UniProtKB/TrEMBL:Q1MN74" /translation="MNDSGGNGEKKRSRRPSAER TAQRDPERTRAAILDAATREFAEN GMGGARVDAIAERAGTNKRMLYHYFGDKEQLYLR VLEEAYVGIRTAERALHIGDRSPE EGISELALFTWRYFLQHPEFLSLLGTENLHRARW LRQSVRLKELHSHLIGELSDVLEQ GKKQGVFIETADPLHVYLTIASLGYFYLSNQYTL STIFGRDLMEPTHLNAWERHIVHV TLASIKR" /locus-tag="RL0090"
misc-feature	complement(115560..115700)	
gene	115995..117281	/inference="protein motif:Pfam:PF00440.8" /note="Pfam match to entry PF00440.8 TetR-N" /locus-tag="RL0091"
CDS	115995..117281	/locus-tag="RL0091" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:Q92T63 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE PERIPLASMIC BINDING ABC TRANSPORTER PROTEIN.; length=427; id 69.159; 428 aa overlap; query 1-428; subject 1-427" /codon-start=1 /transl-table=11 /product="putative ATP-binding component of ABC transporter" /protein-id="CAK05579.1" /db-xref="GI:115254505" /db-xref="GOA:Q1MN73" /db-xref="UniProtKB/TrEMBL:Q1MN73" /translation="MTFRVSRNRFVAGGATLLSL SALGTSALAQETRLRLLLWWGSQPR ADRTNKVSQLYQSKKPGTSITGEFLGWGDYWPRL ATQVAGRNPADVIQMDYRYIVQYA RRGALAPLESYMPAKLNLDDFDKAQIEGGSVDGH LYGVSLGANSAAATVLNTTAFKEAG VDLPTQATTWEEFGRIGAEITKAGKRKGMFGIAD GSGGEPLFENWLRQRGKALYTADG KIAFDVDDASEWYDMWAKFREAGACVPADIQALD KNDIETNTVSLGKSAAGFAHSNQF VAYQAMNKDKLALTNYMRIKPESKGGHYRKPSMF FSVSAQSKAVDLAVDYVNFFVKNP EAALLLDVERGIPESAMREVVAAKLDENGKVAL AYVSLGLDLAGKLPPPPAGAGEG ELMLRNIAEQVGFQQLSPSDGGKQLVAEITQILAR" /locus-tag="RL0091" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0091 by SignalP 2.0 HMM
sig-peptide	115995..116079	

[illegible]

		sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:Q92T65 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE TRANSPORT SYSTEM PERMEASE ABC TRANSPORTER PROTEIN.; length=295; id 85.567; 291 aa overlap; query 2-292; subject 5-295" /codon-start=1 /transl-table=11 /product="putative transmembrane component of ABC transporter" /protein-id="CAK05581.1" /db-xref="GI:115254507" /db-xref="GOA:Q1MN71" /db-xref="UniProtKB/TreMBL:Q1MN71" /translation="MTASVTAARPPSDITKRSLP ASLIIHALLIAASLLMLYPLLWMV SASVRPETEIFSSTSLIPSSIDFSSYARGWVGDL VSFGRFFWNSLVISLLVVTGNVIA CSLTAFAFARLRFAGRNFWFAIMLGTLMIPIYHVT LIPQYVLFDLGWVNTILPLVVPK FLASDAFFIFLMVQFFRGIPRELDEAAMMDGCSA WRIYWKIMLPLSLPVLATAAIFSF IWTWDDFFGPLIYLNDMNTYTIQLGLRTFVDSTS ASDWGGLFAMSTLTLPVVFVFFFLF FQRLLEIEGIATTGMKR" /locus-tag="RL0093"
misc-feature	order(118309..118377, 118510..118578, 118612..118680, 118708..118776, 118837..118905, 119026..119094)	/inference="protein motif:TMHMM:2.0" /note="6 probable transmembrane helices predicted at aa 21-43, 88-110, 122-144, 154-176,197-219 and 260-282" /locus-tag="RL0093" /inference="protein motif:Pfam:PF00528.10" /note="Pfam match to entry PF00528.10 BPD-transp-1" /locus-tag="RL0094" /locus-tag="RL0094" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:Q92T67 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE OXIDOREDUCTASE PROTEIN.; length=357; id 82.913; 357 aa overlap; query 1-357; subject 1-357" /codon-start=1 /transl-table=11 /product="putative GFO/IDH/MocA
misc-feature	118489..119109	
gene	119151..120224	
CDS	119151..120224	

		family oxidoreductase"
		/protein-id="CAK05582.1"
		/db-xref="GI:115254508"
		/db-xref="GOA:Q1MN70"
		/db-xref="UniProtKB/TrEMBL:Q1MN70"
		/translation="MSIRTVAIVGCGIGRSHIVE GYLPHSDKFKVVAICDLNEQRMAA VGDEFGIERRTTSFAELLADDTIDIIDICTPPGI HLEQVVAALAAGKHVVCEKPLTGS LAAVDTIMAAEKTAKGVLMPIFYQRYGDGIQKAK RIIDAGIAGKPYTASVETFWLRKP EYYAVPWRGKWATELGGLVTHALHLHMLMHL GPAARVFGRVATRVNDIEVEDCAS ASLLMESGAFVSLCTLGSQEQISRLRLHFENV FESSHEPYTPGKDPWKIIAANDDV REQIDRVVGDWQPVAPRFTTQMGQFHAFLSGHAP LPVTTKDARRALELVTAIYQSSDS GADVPLPVGPDSPKYADWRARTK"
misc-feature	119160..119522	/locus-tag="RL0094" /inference="protein motif: Pfam: PF01408.8" /note="Pfam match to entry PF01408.8 GFO-IDH-MocA"
misc-feature	119556..119888	/locus-tag="RL0094" /inference="protein motif: Pfam: PF02894.4" /note="Pfam match to entry PF02894.4 GFO-IDH-MocA-C"
gene	120256..121332	/locus-tag="RL0095"
CDS	120256..121332	/locus-tag="RL0095" /inference="similar to sequence: INSDC: SME591782" /note="similarity: fasta; with=UniProt: Q92T68 (EMBL: SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE ATP-BINDING ABC TRANSPORTER PROTEIN.; length=360; id 84.680; 359 aa overlap; query 1-358; subject 1-359" /codon-start=1 /transl-table=11 /product="putative ATP-binding component of ABC transporter protein" /protein-id="CAK05583.1" /db-xref="GI:115254509" /db-xref="GOA:Q1MN69" /db-xref="UniProtKB/TrEMBL:Q1MN69" /translation="MATSVVLQKVEKRYGAMDVI HGIDLTIIDPGEFVVFVGPSCGKS TLLRMIAGLEEITGGGLLLDNERMNEVAPAKRGI AMVFQSYALYPHMSVYKNLAFGLE TAGYKKAIEIEPKVKRAAEILQIEKLLERKPKALS GGQRQ RVAIGRAIVREPRIFLFDE PLSNLDAELRVQMRVEISRLHRS LGNTMIYVTHD QVEAMTMADKIVVLNSGRIEQVGA PLDLYNNPANRFVAGFIGSPKMNFLKARIEQAGE TETSIHVCGNSVRLPRRLKGGAGE EVTFGIRPEHL SLAEGAITLSTINVDLVENLGGA TMLYTTTPDNQLLTVALDGGQKVE

misc-feature	120343..120888	RGANVKASFDPARCHVFDAAGKTI" /locus-tag="RL0095" /inference="protein motif: Pfam: PF00005.11" /note="Pfam match to entry PF00005.11 ABC-tran"
misc-feature	121156..121305	/locus-tag="RL0095" /inference="protein motif: Pfam: PF03459.4" /note="Pfam match to entry PF03459.4 TOBE"
gene	121601..122494	/locus-tag="RL0096"
CDS	121601..122494	/locus-tag="RL0096" /inference="similar to sequence: INSDC: AP003006" /inference="similar to sequence: INSDC: HILICL" /note="similarity: fasta; with=UniProt: LIA2-HAEIN (EMBL: HILICL); Haemophilus influenzae.; licA; LicA protein.; length=339; id 28.333; 300 aa overlap; query 9-295; subject 53-337 similarity: fasta; with=UniProt: Q98BZ0 (EMBL: AP003006); Rhizobium loti (Mesorhizobium loti).; M115370 protein.; length=414; id 49.123; 285 aa overlap; query 10-293; subject 123-405 Similar, but truncated at the N-terminus, to Haemophilus influenzae LicA protein (339 aa), and similar, but truncated at the N-terminus to Rhizobium loti (Mesorhizobium loti) M115370 protein. (414 aa)" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05584.1" /db-xref="GI:115254510" /db-xref="UniProtKB/TrEMBL: Q1MN68" /translation="MLWGVSMTPEDRIHALGIWQ GPIAISPIAGGITNRNYLVSDAVA RCVVRLGTDIPIHHINRQNELAASRAAHAAGISP AVIHHSPGVLVLEYIEARALSPED IRTPQMLARVPLVLRACHRDIAHFRGQAMIFWV FHVIRDYAANLKASESAYLPLLPG LVGRAETLEEAAGPFEIAFGHNDLLAANFLDDGK RLWLIDWDYAGFNTPLFDLGGLAS NNELSEATERTMLETYFDRPLTDDLNRRTAMKC ASLLRETLWSMISEIHSSIDFDYA GYTAENLARFDRAVQAFEQDQ"
misc-feature	121724..122464	/locus-tag="RL0096" /inference="protein motif: Pfam: PF01633.7" /note="Pfam match to entry PF01633.7 Choline-kinase"
gene	122495..124945	/locus-tag="RL0097"
CDS	122495..124945	/locus-tag="RL0097" /inference="similar to



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sequence:INSDC:AF026954"
/inference="similar to
sequence:INSDC:AP003006"
/note="similarity:fasta;
with=UniProt:O46504
(EMBL:AF026954); Bos taurus
(Bovine).; Pyruvate dehydrogenase
phosphatase regulatory subunit.;
length=878; id 37.772; 826 aa
overlap; query 5-806; subject
38-857 similarity:fasta;
with=UniProt:Q98BZ1
(EMBL:AP003006); Rhizobium loti
(Mesorhizobium loti).; Sarcosine
dehydrogenase.; length=869; id
63.171; 820 aa overlap; query
2-816; subject 52-869; putative
dehydrogenase"
/codon-start=1
/transl-table=11
/product="Pyruvate dehydrogenase
phosphatase regulatory subunit."
/protein-id="CAK05585.1"
/db-xref="GI:115254511"
/db-xref="GOA:Q1MN67"
/db-xref="UniProtKB/TrEMBL:Q1MN67"
/translation="MTKELPKTAKAVVIGGGIIG
CSTAYHLGKLGWTDITVLLERKKLT
SGTTFHAAGLVGQLRTSANITQLLGYSVDLYKRL
EEETGLGTGWKMNGGLRVACNEER
WTEVRRQATTAQSFGLEMQLLTPQEAFDLWPLMA
VDDLVGAAFLPTDGQANPSDITQA
LAKGARMSGVS IFEDTEVLDLEIDKGRIRAVITA
QGRIECERVVVCAGQWTRAFARF
GVNVPLVSVEHQYIITESFGVPSNLPTLRDPDL
TYYKEEVGGIVMGGYEPNIPWAA
NGIPDGFHYTLDSNFDHFEQIMEQALGRVPALE
NVGVKQLLNGPESFTPDGNFILGE
APELKNFFVVGAGFNAFGIASAGGAGMALAEWVTK
GEPPYDLWPVDIRRFGRPHFDTDW
VRTRTLEAYGKHYTMAWPFEHSSGRPCRKSPLY
DRLKAQGACFGEKLGWERPNWFAD
LFANEKPKDVYSYTRQNWFDVGREHKAVREAAA
IFDQTSFAKFVLKGRDAEAALSWI
ASNDVARPVGSLVYTQMLNDKGGIECDVTVARIA
ENEYYIVTGTGFATHDFDWIARNI
PAEMHAELVDVTSAYSVLSLMGPNSRAVLEKVTG
SDVSNAAFPFGKVRTIGIAGCPVR
ALRITYVGELGYELHIPVEYATTYDVLMAAGGE
LGLVNAGYRAIESCRLEKGYRAWG
SDIGPDHTPVEAGLGWAVKMRKSIPFRGREAIER
QLSGGVKKRLACFVPEDADTVLLG
RETIYRDGKRVGWLSSGGFGYTLGKPIGYGYVRN
PDGVTEDFVLSGTYELDVARERIP
CKVSLSPLYDPDMARVKA"
misc-feature      122519..123595
/locus-tag="RL0097"
/inference="protein
motif: Pfam:PF01266.8"
/note="Pfam match to entry
PF01266.8 DAO"
misc-feature      123947..124921
/locus-tag="RL0097"
/inference="protein

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		motif: Pfam: PF01571.8"
		/note="Pfam match to entry PF01571.8 GCV-T"
gene	complement(125075..126532)	/locus-tag="RL0098"
CDS	complement(125075..126532)	/locus-tag="RL0098"
		/inference="similar to sequence: INSDC: AF007800" /inference="similar to sequence: INSDC: RME591985" /note="similarity: fasta; with=UniProt: O08355 (EMBL: AF007800); Pseudomonas fluorescens.; mtlD; Mannitol dehydrogenase (EC 1.1.1.67).; length=493; id 40.959; 459 aa overlap; query 6-459; subject 6-459 similarity: fasta; with=UniProt: Q92TQ9 (EMBL: RME591985); Rhizobium meliloti (Sinorhizobium meliloti).; Putative D-mannonate oxidoreductase protein (EC 1.1.1.57).; length=487; id 47.468; 474 aa overlap; query 6-478; subject 6-475" /codon-start=1 /transl-table=11 /product="putative mannitol dehydrogenase" /protein-id="CAK05586.1" /db-xref="GI:115254512" /db-xref="GOA:Q1MN66" /db-xref="UniProtKB/TrEMBL:Q1MN66" /translation="MTERLQTLSDLAPTAKLPAY DRNQLKSGILHLGPGAFFRAHFAP FTDAALAAEGGDWGIEVASLRTADVADNLSAQNG LYTTLIRDSSGTTAEVIGSILKAH VAPRDPAGLLARLEDPAIRIVSMTVTEKAYGFDP ATGGLDLKHPDIVADLVSRHTPRG VIGYLVEGLARRRQKGIAPFTPLSCDNLPNGAV LKRLVLEFASRIDPDLHRWIEASV PFPSTMVDRITPASTEATYADAERLTGRDMAAV ETEPFTQWVIEDHFANGRPWEKV RGALMVEEV SAYEKMKLRLNGAHSLLAYLGYIG GYEFIRDVMDDAALAYRHMHA AARTLDPVPGIDLDDYASELIARFANKAIAHRTY QIAMDGTQKLPQRLLEPASEALAH GDRAETYAIAVAAMRYAIGE HNGERYELRDPR AGEIAALIADIPRTGLAISALFT LPGLFPAALTGHRAWTQDVADKLEILIQDDRLPL F"
misc-feature	complement(125159..126454)	/locus-tag="RL0098"
		/inference="protein motif: Pfam: PF01232.10" /note="Pfam match to entry PF01232.10 Mannitol-dh"
gene	complement(126529..127944)	/locus-tag="RL0099"
CDS	complement(126529..127944)	/locus-tag="RL0099"

44)

		/inference="similar to sequence:INSDC:A65098" /inference="similar to sequence:INSDC:B95958" /note="similarity:fasta; with=UniProt:UXAC-ECOLI (EMBL:A65098); Shigella flexneri.; uxaC; Uronate isomerase (EC 5.3.1.12) (Glucuronate isomerase) (Uronic isomerase).; length=EC 5.3.1.12; id 28.670; 436 aa overlap; query 24-445; subject 16-441 similarity:fasta; with=UniProt:UXAC-RHIME (EMBL:B95958); Rhizobium meliloti (Sinorhizobium meliloti).; uxaC; Uronate isomerase (EC 5.3.1.12) (Glucuronate isomerase) (Uronic isomerase).; length=EC 5.3.1.12; id 56.103; 467 aa overlap; query 6-471; subject 3-469" /codon-start=1 /transl-table=11 /product="putative uronate isomerase (glucuronate isomerase)" /protein-id="CAK05587.1" /db-xref="GI:115254513" /db-xref="GOA:Q1MN65" /db-xref="UniProtKB/TrEMBL:Q1MN65" /translation="MDAGNGFLHPDRLFPADPAT RTVARDLYETVRNLPVSPHGHT PSWFADDKPFEDAASLLVIPDHYLFRMLHSGVGT LDELGVPRLDGKPVASGRAIWRTF AAHYHLFRGTPSSLWVDHMSAVLGCTEPLTPDN ADALYDHINAQLALPEFRPRALHQ RFGIETIATTDGALDPLAHHQKMAADGWIGKVRT TYRPDSVTDPAVGFRDNLVKFGE ITGTEVTRWDGLIEAHHRRRRAYFRQFGATATDHG VPTAFTADLPLTEKQALLDKALKG PLSAEDAELFRGQMMTEMAGLSAEDGMVMQIHAG SRRNTDSGLFATRGPNMGADIPTS TDWVGGLNALLSKYGHAPGLRVLLFTLDETTYAR ELAPMVGHWPCLMIGPPWWFHDSP LGIRRYLDQVVETAGFANMAGFNDDTRALLSIPA RHDVWRREVCRFLAQLAGEHRLSK REAEIVAGELSYGNAKKAYKL" /locus-tag="RL0099"
misc-feature	complement(126532..1279 32)	
gene	128125..128334	/inference="protein motif:Pfam:PF02614.4" /note="Pfam match to entry PF02614.4 UxaC" /locus-tag="RL0100"
CDS	128125..128334	/locus-tag="RL0100" /inference="similar to sequence:INSDC:B97373" /inference="similar to sequence:INSDC:C85999" /note="similarity:fasta; with=UniProt:SLYX-ECOLI (EMBL:C85999); Escherichia coli

		O157:H7.; slyX; Protein slyX.; length=72; id 33.333; 63 aa overlap; query 8-69; subject 10-72 similarity:fasta; with=UniProt:SLYX-AGRT5 (EMBL:B97373); Agrobacterium tumefaciens (strain C58/ATCC 33970).; slyX; Protein slyX homolog.; length=70; id 82.857; 70 aa overlap; query 1-69; subject 1-70" /codon-start=1 /transl-table=11 /product="putative slyX protein" /protein-id="CAK05588.1" /db-xref="GI:115254514" /db-xref="UniProtKB/TrEMBL:Q1MN64" /translation="MSDETNNHITRLEEMLAHQAK TIEELSDQLAEQWKTVEQMRTKLD RLTERFLSLEEQSLDAPAITRPPHY" /locus-tag="RL0100" /inference="protein motif: Pfam:PF04102.2" /note="Pfam match to entry PF04102.2 SlyX"
misc-feature	128146..128331	/gene="gabD"
gene	complement(128390..129871)	/locus-tag="RL0101"
CDS	complement(128390..129871)	/gene="gabD" /locus-tag="RL0101" /EC-number="1.2.1.16" /inference="similar to sequence:INSDC:C95948" /inference="similar to sequence:INSDC:ECD890" /note="similarity:fasta; with=UniProt:GABD-ECOLI (EMBL:ECD890); Escherichia coli.; gabD; Succinate-semialdehyde dehydrogenase [NADP+] (EC 1.2.1.16) (SSDH).; length=482; id 65.409; 477 aa overlap; query 15-491; subject 6-481 similarity:fasta; with=UniProt:Q92V65 (EMBL:C95948); Rhizobium meliloti (Sinorhizobium meliloti).; Putative succinate-semialdehyde dehydrogenase (NAD(P)+) protein (EC 1.2.1.16).; length=491; id 67.814; 494 aa overlap; query 1-493; subject 1-491; putative succinate-semialdehyde dehydrogenase [NAD(P)+]" /codon-start=1 /transl-table=11 /product="Succinate-semialdehyde dehydrogenase [NADP+] (SSDH)." /protein-id="CAK05589.1" /db-xref="GI:115254515" /db-xref="GOA:Q1MN63"

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LTAEMGKPFPEARGEILYAAAYIEWYAEAEAKRIY
GETIPAPSDDKRMIVIRQPVGVVG
TITPWNFPAAMITRKIAPALAVGCTVVSKEPAEQT
PLTAIALAVLAEQAGIPAGVFNV
VGVDGPAIGRELCGNEKVRKISFTGSTEVGRILM
RQCADQIKKVSLELGGNAPFIVFD
DADLDAAVEGAIASKYRNAGQTCVCANRLYVQSN
VYDAFAAKLAAKVAEMSVGDGFEP
GVVIGPLIDEQGLAKVEDHVSDALAKGAKLLTGG
KRIDGAGTFFTPTVLTGVARGMKV
AREETFGPVAPLFRFDTVEDVINQANDTEFGLAA
YFYAGDLKKVWRVAEAELEYGMIGI
NTGLMSSETAPFGGIKQSGLGREGSRHGADDYLE
MKYLCIGGV"

misc-feature    complement(128396..1297 /gene="gabD"
90)

/locus-tag="RL0101"
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motif: Pfam: PF00171.9"
/note="Pfam match to entry
PF00171.9 Aldedh"

gene            complement(130039..1313 /gene="gabT"
19)

/locus-tag="RL0102"
/note="synonym: goaG"

CDS             complement(130039..1313 /gene="gabT"
19)

/locus-tag="RL0102"
/inference="similar to
sequence: INSDC: A64879"
/inference="similar to
sequence: INSDC: AF335502"
/note="similarity: fasta;
with=UniProt: GOAG-ECOLI
(EMBL: A64879); Escherichia coli.;
goaG; 4-aminobutyrate
aminotransferase (EC 2.6.1.19)
(Gamma-amino-N-butyrate
transaminase) (GABA transaminase)
(Glutamate:succinic semialdehyde
transaminase) (GABA
aminotransferase) (GABA-AT).;
length=421; id 61.575; 419 aa
overlap; query 1-419; subject
1-419 similarity: fasta;
with=UniProt: Q9AGD3
(EMBL: AF335502); Rhizobium
leguminosarum.; gabT;
4-aminobutyrate aminotransferase
(EC 2.6.1.19).; length=E ( 426; id
100.000; 426 aa overlap; query
1-426; subject 1-426"
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aminotransferase"
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misc-feature	complement(130051..131283)	/gene="gabT"  /locus-tag="RL0102" /inference="protein motif: Pfam: PF00202.8" /note="Pfam match to entry PF00202.8 Aminotran-3"
gene	131486..132295	/locus-tag="RL0103"
CDS	131486..132295	/locus-tag="RL0103" /inference="similar to sequence: INSDC: RME591985" /note="similarity: fasta; with=UniProt: Q92V63 (EMBL: RME591985); Rhizobium meliloti (Sinorhizobium meliloti).; Hypothetical protein SMb21187.; length=276; id 75.362; 276 aa overlap; query 1-269; subject 1-276" /codon-start=1 /transl-table=11 /product="putative MerR family transcriptional regulator" /protein-id="CAK05591.1" /db-xref="GI:115254517" /db-xref="GOA:Q1MN61" /db-xref="UniProtKB/TrEMBL:Q1MN61" /translation="MNDNGPVRYKVAEAAARLAGV SASTLRLWESQGLVVPGRSETGHR QYSADDVARLKRISWYRVERGLNPAAIREALESE EPSADGAEASQDTGLGRKLRLRH ANGKTLDQVAGDIGVTSSTLSTLERTSQGVSFKT LHDLAEYYGTTVSRLSGEESGDVP VLVORAGEWRKWPETTPGVTVQLLAEGRRMMDCHR FVLAPGAASEGAYRHEGEFFMHVL SGRLELVLDGDQFFDLGPGDSLYFESRRDHWRN RHDGETVLLWINTPPTF"
misc-feature	131513..131623	/locus-tag="RL0103" /inference="protein motif: Pfam: PF00376.9" /note="Pfam match to entry PF00376.9 MerR"
misc-feature	131774..131938	/locus-tag="RL0103"

		/inference="protein motif: Pfam: PF01381.9" /note="Pfam match to entry PF01381.9 HTH-3" /locus-tag="RL0104" /locus-tag="RL0104" /inference="similar to sequence: INSDC: AE008273" /inference="similar to sequence: INSDC: ECD823" /note="similarity: fasta; with=UniProt: RND-ECOLI (EMBL: ECD823); Escherichia coli.; rnd; Ribonuclease D (EC 3.1.26.3) (RNase D).; length=375; id 31.847; 157 aa overlap; query 13-168; subject 14-166 similarity: fasta; with=UniProt: Q8U8I4 (EMBL: AE008273); Agrobacterium tumefaciens (strain C58/ATCC 33970).; rnd; Ribonuclease D (AGR-L-1490p).; length=AGR-L-1490p; id 88.942; 208 aa overlap; query 1-208; subject 1-208 Similar to the N-terminus to codon 170 of Escherichia coli Ribonuclease D (375 aa), and entire protein is similar to Agrobacterium tumefaciens (strain C58/ATCC 33970) Ribonuclease D (208 aa)" /codon-start=1 /transl-table=11 /product="putative ribonuclease" /protein-id="CAK05592.1" /db-xref="GI:115254518" /db-xref="GOA:Q1MN60" /db-xref="UniProtKB/TrEMBL:Q1MN60" /translation="MAATIRYHEGDISAADVARY TGAIAIDTETLGLVPRDRRLCVVQ LSPGDGTADIIRIAAGQKEAPNLVALLEDPTHQK IFHYGRFDIAVLFTFSVTTTPVF CTKIASRLIRTYTDRHGLKDNLKEMLDVDVSKAQ QSSDWAAERLSPAQLEYAASDVLY LHALRDKLTERLIRDGRYDHATACFEFLPTRAKL DLLGWEEADIFAHS" /locus-tag="RL0104" /inference="protein motif: Pfam: PF01612.10" /note="Pfam match to entry PF01612.10 3-5-exonuc" /locus-tag="RL0105" /locus-tag="RL0105" /inference="similar to sequence: INSDC: AE008273" /note="similarity: fasta; with=UniProt: Q8U8I7 (EMBL: AE008273); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu4105 (AGR-L-1495p).; length=513; id 26.449; 552 aa
gene	132535..133161	
CDS	132535..133161	
misc-feature	132547..133053	
gene	133393..134958	
CDS	133393..134958	

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overlap; query 1-519; subject
1-511"
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protein"
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PEAARIVAYLEIVRYKDRDLAARA
VVRSYRQNDASPMRTEARPEIQLHEDNRPAAATR
QLAEKVPVLVAPLTEAAALLTAAE
PLIAETVEAADPETPQPEEAPAPVAAAEVAA
EESLPQELEAQQLLSTDLDKIEDT
QEAVEQSAVQPRIVSDKADPVI PRNWAGIVASMT
EEASEMIATLIREQEIETVLEDVP
VEAAVEIDTILDEAVISEATGSLTKQPMELAAPD
VRQTAALRPSQPDIPPLVVETRQP
REVSAQAEMIPVPETIESPYVPLAARMPEGLAYT
QLPYQFAKDILSNEKAGETHHQHQ
HHRDGAPQDQNDQEQQAQSGGEDAEPDGEETDAA
PARRTPRMIDAEPVAHQPAGAAAD
PVYALYQRMVGWE"
gene      complement(135131..1368 /gene="rpsA"
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CDS      complement(135131..1368 /gene="rpsA"
34)
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/inference="similar to
sequence:INSDC:AE009341"
/inference="similar to
sequence:INSDC:SME591783"
/note="similarity:fasta;
with=UniProt:RS1-RHIME
(EMBL:SME591783); Rhizobium
meliloti (Sinorhizobium
meliloti).; rpsA; 30S ribosomal
protein S1.; length=568; id
92.908; 564 aa overlap; query
1-564; subject 1-564
similarity:fasta;
with=UniProt:Q8U8I8
(EMBL:AE009341); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; rpsA; 30S ribosomal
protein S1.; length=572; id
95.398; 565 aa overlap; query
1-565; subject 7-571"
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/product="putative 30S ribosomal
protein S1"
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 ERIENALGEAVLSREKARREESWV  
 KLEAKFEAGERVEGVIFNQVKGFFTVDLDGAIAF  
 LPRSQVDIRPIRDVTPLMHNPQPF  
 EILKMDKRRGNIVVSRRTVLEESRAEQRSEIVQN  
 LEEGQVVDGVVKNITDYGAFVDLG  
 GIDGLLHVTDMAWRRVNHPSIILNIGQQVKVQII  
 RINQETHRISLGMKQLESDPWDGI  
 QAKYPEGKKISGTVTNITDYGAFVELEPGIEGLI  
 HISEMSWTKKNVHPGKILSTSQEV  
 EVVVLEVDPSKRRISLGLKQTLENPWAAFARSHP  
 AGTEVEGEVKNKTEFGLFIGLDGD  
 VDGMVHLSDLTDWNRPGEQVIEEFNKGDVVKAVVL  
 DVDVEKERISLGIKQLGKDAVGDA  
 AASGDLRKNAVVSCEVIAVNDGGVEVKLVNHEDI  
 TSFIRRADLARDRDEQRPERFSVG  
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misc-feature complement(135245..1354  
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 motif: Pfam: PF00575.9"  
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misc-feature complement(135515..1357  
 39)

/locus-tag="RL0106"  
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 motif: Pfam: PF00575.9"  
 /note="Pfam match to entry  
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misc-feature complement(135776..1360  
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/locus-tag="RL0106"  
 /inference="protein  
 motif: Pfam: PF00575.9"  
 /note="Pfam match to entry  
 PF00575.9 S1"

misc-feature complement(136037..1362  
 55)

/locus-tag="RL0106"  
 /inference="protein  
 motif: Pfam: PF00575.9"  
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 PF00575.9 S1"

misc-feature complement(136304..1365  
 16)

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 motif: Pfam: PF00575.9"  
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 PF00575.9 S1"

misc-feature complement(136556..1367  
 68)

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58)
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58)
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          (EMBL:A04448); Escherichia coli
          0157:H7.; cmk; Cytidylate kinase
          (EC 2.7.4.14) (CK) (Cytidine
          monophosphate kinase) (CMP kinase)
          (MssA protein) (P25).; length=EC
          2.7.4.14; id 41.475; 217 aa
          overlap; query 1-203; subject
          1-216 similarity:fasta;
          with=UniProt:KCY-RHIME
          (EMBL:SME591783); Rhizobium
          meliloti (Sinorhizobium
          meliloti).; cmk; Cytidylate kinase
          (EC 2.7.4.14) (CK) (Cytidine
          monophosphate kinase) (CMP
          kinase).; length=EC 2.7.4.14; id
          83.092; 207 aa overlap; query
          5-211; subject 2-208"
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          /product="putative cytidylate
          kinase"
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          /db-xref="GOA:Q1MN57"
          /db-xref="UniProtKB/TrEMBL:Q1MN57"
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          KHEIGEAAASRIAVMPAVRRALVEA
          QRRFSTKAPGTVLDGRDIGTVVCPNAAVKFYVTA
          SPEVRARRRYDEILGKGLTADFDA
          IFEDVKRRDERDMGRADSPLKPADDAHLLDTSEM
          SIEAAFQAAQSIIDAVLSRNA"
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81)
          /inference="protein
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          /note="Pfam match to entry
          PF02224.5 Cytidylate-kin"
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31)
          /inference="protein
          motif:PFam:PF00406.10"
          /note="Pfam match to entry
          PF00406.10 ADK"
gene      complement(137731..1390 /gene="aroA"
89)
          /locus-tag="RL0108"
CDS       complement(137731..1390 /gene="aroA"
89)
          /locus-tag="RL0108"
          /EC-number="2.5.1.19"

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		<pre> /inference="similar to sequence:INSDC:AF326475" /note="similarity:fasta; with=UniProt:AROAB-BRUAB (EMBL:AF326475); Brucella abortus.; aroA; 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5- enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).; length=450; id 79.418; 447 aa overlap; query 1-447; subject 1-444 similarity:fasta; with=UniProt:AAL67577; length=455; id 86.637; 449 aa overlap; query 1-449; subject 1-449" /codon-start=1 /transl-table=11 /product="putative 3-phosphoshikimate 1-carboxyvinyltransferase (5-enolpyruvylshikimate-3-phosphat e synthase) (EPSP synthase)" /protein-id="CAK05596.1" /db-xref="GI:115254522" /db-xref="GOA:Q1MN56" /db-xref="UniProtKB/TrEMBL:Q1MN56" /translation="MLNGSASKPATARKSAGLTG SVRIPGDKSISHRSFMIGGLASGE TRITGLLEGEDVINTGRAMQAMGARIRKEGAQWV IEGTGNGALLAPDAPLDFGNAGTG VRLTMGLVGTYDFHSTFIGDASLSKRPMGRVLNP LREMGVQVSASEGDRLPVTLRGPG TPSPIRYRVPMASAVKSAVLLAGLNTPGVTTVI EPVMTRDHTEKMLQGFGAALSJET DGDGVRTIRLEGRGKLAGQVIDVPGDPSSTAFPL VAALIVPGSDITIVNVLNPNTRTG LILTLQEMGADIEVVNARLAGGEDVADLRVRHSE LKGVTVPEDRAPSMIDEYPILAVA ACFAEGATVMKGLEELRVKESDRLSAVADGLKLN GVDCDEGEDFLIVRGRPDGKGLGN AADGRVSTHLDHRIAMSFLVLGLASEHAVTIDDA AMIATSFPEFMQLMTGLGAKIELV AE" </pre>
misc-feature	complement(137770..139050)	<pre> /gene="aroA" </pre>
gene	139366..139749	<pre> /locus-tag="RL0108" /inference="protein motif: Pfam:PF00275.8" /note="Pfam match to entry PF00275.8 EPSP-synthase" </pre>
CDS	139366..139749	<pre> /locus-tag="RL0109" /inference="similar to sequence:INSDC:AE008273" /note="similarity:fasta; with=UniProt:Q8U4Y6 (EMBL:AE008273); Agrobacterium tumefaciens (strain C58/ATCC 33970).; AGR-L-1500p.; length=129; id 77.344; 128 aa overlap; query 1-126; subject 1-128" /codon-start=1 </pre>

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gene	139901..139976	/gene="tRNA-Ala"
tRNA	139901..139976	/gene="tRNA-Ala"
		/product="tRNA-Ala"
		/note="anticodon GGC"
gene	140098..140430	/locus-tag="RL0110"
CDS	140098..140430	/locus-tag="RL0110"
		/inference="similar to sequence:INSDC:AE010061" /note="similarity:fasta; with=UniProt:YE20-STRP8 (EMBL:AE010061); Streptococcus pyogenes (serotype M18).; Hypothetical UPF0213 protein spyM18-1420.; length=92; id 39.726; 73 aa overlap; query 3-73; subject 7-76"
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		/transl-table=11
		/product="conserved hypothetical protein"
		/protein-id="CAK05598.1"
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		/db-xref="GOA:Q1MN54"
		/db-xref="UniProtKB/TrEMBL:Q1MN54"
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misc-feature	140098..140340	/locus-tag="RL0110"
		/inference="protein motif: Pfam:PF01541.11" /note="Pfam match to entry PF01541.11 GIY-YIG"
gene	140531..141253	/locus-tag="RL0111"
CDS	140531..141253	/locus-tag="RL0111"
		/inference="similar to sequence:INSDC:HS377250" /note="similarity:fasta; with=UniProt:Q8UIY5 (EMBL:HS377250); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0156.; length=236; id 61.572; 229 aa overlap; query 1-229; subject 1-229"
		/codon-start=1
		/transl-table=11
		/product="putative transmembrane protein"
		/protein-id="CAK05599.1"
		/db-xref="GI:115254525"

		/db-xref="GOA:Q1MN53" /db-xref="UniProtKB/TrEMBL:Q1MN53" /translation="MTRSRRRRIIRTRTLTGLA LVGSISFLAGMTDATGLLLTGDFV SFMTGNTTTRAAALALSEGNLYHAAVLICAIVFVL GNAAGIVISHISQRRIFVVLGCVG LVLALASMMTVQNMLFARFYMIVFSMGMVNAAVE HIEGLPIGLTYVTGALSRFGRGIG RWIIGDRRVEWTIQIVPWGGMVLGAIAGAVLTRL TGAHALWLVSFLFAMVLALAAMLIP RPLQRRFNQKVAPSGSAITRAK" /locus-tag="RL0111"
misc-feature	order(140573..140641, 140723..140791, 140810..140869, 140927..140995, 141053..141106, 141116..141184)	/inference="protein motif:TMHMM:2.0" /note="6 probable transmembrane helices predicted at aa 31-53, 81-103, 110-129, 149-171,191-208 and 212-234" /locus-tag="RL0111"
misc-feature	140585..141175	/inference="protein motif:Pfam:PF06912.1" /note="Pfam match to entry PF06912.1 DUF1275" /locus-tag="RL0112"
gene	141322..142110	/locus-tag="RL0112" /inference="similar to sequence:INSDC:SME591783" /note="similarity:fasta; with=UniProt:Q92KS9 (EMBL:SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; HYPOTHETICAL TRANSMEMBRANE PROTEIN.; length=335; id 60.377; 265 aa overlap; query 1-261; subject 74-334" /codon-start=1 /transl-table=11 /product="putative transmembrane protein" /protein-id="CAK05600.1" /db-xref="GI:115254526" /db-xref="GOA:Q1MN52" /db-xref="UniProtKB/TrEMBL:Q1MN52" /translation="MFLISKLVWIFAQPLSLAFF LVFLALLAGLLRWRTLSILGAAGS ALILFVTLYTTAGNLLMQGLEQRFAPKPAADPDSL QCMIVLGGGFENEVNTARHGIEFN GGADRFIEALRLAQKFPQSRILVSGGDGSISGIY EGDAASERFFPLFGVGRDRLIEE RQSRTTFENAVNTKEFLASQGLSNCLLITSGFHM PRSVGIFRKLGDIVPWPTDYRTD GQVRLGLDFTQPSLNAQNLATAIREWYGLVGYYL AGRTSELYPS" /locus-tag="RL0112"
CDS	141322..142110	
misc-feature	order(141349..141414, 141433..141501)	/inference="protein

		motif:TMHMM:2.0"
		/note="2 probable transmembrane helices predicted at aa 10-31 and 38-60"
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gene	142264..142677	/locus-tag="RL0113"
CDS	142264..142677	/locus-tag="RL0113" /inference="similar to sequence:INSDC:AE008990" /note="similarity:fasta; with=UniProt:Q8UIY6 (EMBL:AE008990); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0155.; length=150; id 43.443; 122 aa overlap; query 5-124; subject 25-144" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05601.1" /db-xref="GI:115254527" /db-xref="UniProtKB/TrEMBL:Q1MN51" /translation="MRRRDHEITAFGNLQVEIIG TAVVIALRPLLPVAGQLALVDHRV DQAVIVDVLPPDETIGKFGRLALLLEMFLLDLR VGDQRLLTEGDSRHGKQDDIQNG EHQRFHGFLLDKGSVAQCMSPKVCSGSRTTTCI T" /locus-tag="RL0114"
gene	142765..143400	/locus-tag="RL0114"
CDS	142765..143400	/locus-tag="RL0114" /inference="similar to sequence:INSDC:AE008990" /note="similarity:fasta; with=UniProt:Q8UIY7 (EMBL:AE008990); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0154.; length=229; id 73.460; 211 aa overlap; query 1-211; subject 18-228" /codon-start=1 /transl-table=11 /product="putative transmembrane protein" /protein-id="CAK05602.1" /db-xref="GI:115254528" /db-xref="GOA:Q1MN50" /db-xref="UniProtKB/TrEMBL:Q1MN50" /translation="MSLLVYLDYAGIALFAATGA LAASRKQLDLIGFLFFAMVTGTGG GTVRDIVLGRVPVFWVLNPAYILVCCIVGVMVFF TAHLLESRYRLLIWLDAILGLAAYC VIGAAKGLAATGSPTIAIVTGTLTATFGGILRDL MANEPSVLLRPEIYVTAALIGAGV FTLANGLGMQLYLASACGVVAAFVGRGGALWFGW TFPTYRHKPGRHPDDVM"

sig-peptide	142765..142828	/locus-tag="RL0114" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0114 by SignalP 2.0 HMM (Signal peptide probability 0.910) with cleavage site probability 0.839 between residues 22 and 23"
misc-feature	order(142774..142833, 142852..142920, 142930..142998, 143032..143085, 143095..143163, 143197..143265, 143278..143346)	/locus-tag="RL0114"  /inference="protein motif:TMHMM:2.0" /note="7 probable transmembrane helices predicted at aa 4-23, 30-52, 56-78, 90-107,111-133, 145-167 and 172-194"
misc-feature	142774..143031	/locus-tag="RL0114" /inference="protein motif:Pfam:PF03458.3" /note="Pfam match to entry PF03458.3 UPF0126"
misc-feature	143032..143301	/locus-tag="RL0114" /inference="protein motif:Pfam:PF03458.3" /note="Pfam match to entry PF03458.3 UPF0126"
gene	complement(143477..143899)	/gene="irr"
CDS	complement(143477..143899)	/locus-tag="RL0115" /gene="irr"  /locus-tag="RL0115" /inference="similar to sequence:INSDC:AF073772" /inference="similar to sequence:INSDC:RLE492871" /note="similarity:fasta; with=UniProt:O85719 (EMBL:AF073772); Bradyrhizobium japonicum.; irr; Iron response regulator.; length=163; id 61.111; 126 aa overlap; query 14-139; subject 38-163 similarity:fasta; with=UniProt:Q8KLU1 (EMBL:RLE492871); Rhizobium leguminosarum (biovar viciae).; irr; Iron response regulator protein.; length=139; id 98.561; 139 aa overlap; query 2-140; subject 1-139" /codon-start=1 /transl-table=11 /product="iron response regulator" /protein-id="CAK05603.1" /db-xref="GI:115254529" /db-xref="GOA:Q1MN49" /db-xref="UniProtKB/TrEMBL:Q1MN49"

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misc-feature	complement(143498..143854)	/gene="irr"  /locus-tag="RL0115" /inference="protein motif: Pfam: PF01475.6" /note="Pfam match to entry PF01475.6 FUR"
gene	144197..144712	/gene="fabA" /locus-tag="RL0116"
CDS	144197..144712	/gene="fabA" /locus-tag="RL0116" /EC-number="4.2.1.60" /inference="similar to sequence: INSDC: C97377" /inference="similar to sequence: INSDC: HSDD9B1D" /note="similarity: fasta; with=UniProt: FABA-ECOLI (EMBL: HSDD9B1D); Shigella flexneri.; fabA; 3-hydroxydecanoyl-[acyl-carrier-pr otein] dehydratase (EC 4.2.1.60) (Beta-hydroxydecanoyl thioester dehydrase).; length=171; id 55.952; 168 aa overlap; query 4-171; subject 3-170 similarity: fasta; with=UniProt: Q8UIZ0 (EMBL: C97377); Agrobacterium tumefaciens (strain C58/ATCC 33970).; fabA; D-3-hydroxydecanoyl-(Acyl carrier-protein) dehydratase.; length=acyl carrier-p ( 185; id 88.889; 171 aa overlap; query 1-171; subject 15-185" /codon-start=1 /transl-table=11 /product="putative 3-hydroxydecanoyl-[acyl-carrier-pr otein] dehydratase (Beta-hydroxydecanoyl thioester dehydrase) " /protein-id="CAK05604.1" /db-xref="GI:115254530" /db-xref="GOA:Q1MN48" /db-xref="UniProtKB/TrEMBL:Q1MN48" /translation="MTTRQSSFSYEELIACAHGE LFGPGNAQLPLPPMLMVHRITEIS ETGGTFDKGYLRAEYDVRPDDWYFPCHFEGNPIM PGCLGLDGMWQLTGFFLGWLGEEG RGMALSTGEVKFKGMVRPQTKLIEYGIDFKRVMR GRLVLGTADGWLKADGETIYQAAD LRVGLSKDKTA"
gene	144791..145990	/gene="fabB" /locus-tag="RL0117"
CDS	144791..145990	/gene="fabB"



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with=UniProt:FABB-ECOLI
(EMBL:AE016764); Escherichia coli
06.; fabB;
3-oxoacyl-[acyl-carrier-protein]
synthase I (EC 2.3.1.41) (Beta-
ketoacyl-ACP synthase I) (KAS I).;
length=406; id 59.091; 396 aa
overlap; query 1-396; subject
12-403 similarity:fasta;
with=UniProt:Q8UIZ1
(EMBL:AE008989); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; fabB;
3-oxoacyl-(Acyl-carrier-protein)
synthase I.;
length=acyl-carrier-protein; id
90.226; 399 aa overlap; query
1-399; subject 12-407; putative
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protein] synthase I
(Beta-ketoacyl-ACP synthase I)
(KAS I)."
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/db-xref="UniProtKB/TrEMBL:Q1MN47"
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RTLIEAAEITIKNNSPKRIGPFAVPKAMSSTASA
TLATWFKIHGVNYSISSACSTSAH
CIGNAAEMIQWKGQDVMFAGGHEDLDWTMSNLF
DAMGAMSSKYNDTPDSASRAYDVNR
DGFVIAGGAGVLVLEELERAKARGAKIYAEIVGY
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/note="Pfam match to entry

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		/EC-number="1.3.1.9"
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		/inference="similar to
		sequence:INSDC:SME591783"
		/note="similarity:fasta;
		with=UniProt:FABI-ECOLI
		(EMBL:HS757242); Shigella
		flexneri.; fabI;
		Enoyl-[acyl-carrier-protein]
		reductase [NADH] (EC 1.3.1.9)
		(NADH- dependent enoyl-ACP
		reductase).; length=261; id
		52.510; 259 aa overlap; query
		3-260; subject 1-259
		similarity:fasta;
		with=UniProt:FAI2-RHIME
		(EMBL:SME591783); Rhizobium
		meliloti (Sinorhizobium
		meliloti).; fabI2;
		Enoyl-[acyl-carrier-protein]
		reductase [NADH] 2 (EC 1.3.1.9)
		(NADH- dependent enoyl-ACP
		reductase 2).; length=268; id
		85.448; 268 aa overlap; query
		1-268; subject 1-268"
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		/transl-table=11
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		reductase [NADH] (NADH-dependent
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		/db-xref="UniProtKB/TrEMBL:Q1MN46"
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		GLYADTTRENF SRTMVISCF SFTEIAKRCAPLME
		DGGAMLT LT YNGSTRVIPN YN VMG
		VAKAALEASVRYLAADYGPRGIRVN AISAGPIRT
		LAGAGISDARAILSWNQ RNAPLRK
		TVTIDQVGSSALYLLSDLSSGVTGEVHFVDAGFN
		VTSMPTLET LRKADVE"
misc-feature	146058..146750	/gene="fabI"
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		/inference="protein
		motif: Pfam: PF00106.11"
		/note="Pfam match to entry
		PF00106.11 adh-short"
gene	complement(146893..147909)	/locus-tag="RL0119"
CDS	complement(146893..147909)	/locus-tag="RL0119"
		/EC-number="2.1.1.52"

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(EMBL:U00096); Escherichia coli.;
rsmC; Ribosomal RNA small subunit
methyltransferase C (EC 2.1.1.52)
(rRNA
(guanine-N(2)-)-methyltransferase)
(16S rRNA m2G1207
methyltransferase).; length=342;
id 31.366; 322 aa overlap; query
23-336; subject 18-333
similarity:fasta;
with=UniProt:Q92KT0
(EMBL:SME591783); Rhizobium
meliloti (Sinorhizobium
meliloti).; Hypothetical protein
SMc00325.; length=338; id 70.710;
338 aa overlap; query 1-338;
subject 1-338"
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small subunit methyltransferase"
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SLSAVQGFRLPYRQLLAQRIEAKPEIDGEDYDAA
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GGLIVVAGAKEDGIQPLRKRMEGFNLAVDYMPKY
HGVAFWFGRPADADEIISKAKAP
VRVDGRFNATAGMFSHDRIDAGSELLTSRLPEDF
TGDVADFGAGWGYLSVEMARKSVG
LTRLDLYEADHAALAAARDNLAKNCPNAPARFFW
HDLAGEPVKDKYDLIIMNPPFHEG
HAAEPALGQAMIKTAASALRGGGRLMLVANRGLP
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PF05175.2 MTS"
gene              complement(147985..1501 /gene="pnp"
23)
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CDS               complement(147985..1501 /gene="pnp"
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sequence:INSDC:AE007950"
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sequence:INSDC:HS106228"
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with=UniProt:PNP-ECOLI

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(EMBL:HS106228); Escherichia coli.; pnp; Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8) (Polynucleotide phosphorylase) (PNPase).; length=711; id 56.802; 713 aa overlap; query 1-712; subject 1-708 similarity:fasta; with=UniProt:Q8UJ56 (EMBL:AE007950); Agrobacterium tumefaciens (strain C58/ATCC 33970).; pnpA; Polyribonucleotide nucleotidyltransferase (AGR-C-124p).; length=713; id 92.546; 711 aa overlap; query 1-711; subject 1-711" /codon-start=1 /transl-table=11 /product="putative Polynribonucleotide nucleotidyltransferase (Polynucleotide phosphorylase) (PNPase) " /protein-id="CAK05608.1" /db-xref="GI:115254534" /db-xref="GOA:Q1MN44" /db-xref="UniProtKB/TrEMBL:Q1MN44" /translation="MFDTHTVEIEWAGRPLKLET GKJARQADGAVLATYGETVVLATV VSAKAPKAGQDFFPLTVNYQEKTYAAGKIPGGYF KREGRPSEKETLVSRLIDRPIRPL FPEGYKNDTQVVVTVIQHDLENDPDVLSMVSATSA ALTLSGVPFMGPVGGARVGYINGE YVLNPHLDEMDESSLDLVVAGTYDAVLMVESEAK ELNEDVMLGAVMFGHKGFPVLDA IIKLAEVAAKEPRDFQPADYSALESEMLGLAEGE LRNAYKITQKADRYAAVDAVKAKV KAHFLPEEGEAKYTAEVGAIFKHLQAKIVRWNI LDTKSRIDGRNLETVRPIVSEVGL LPRTHGSALFTRGETQAIVVATLGTGEDEQYVDS LTGMYKERFLLHYNFPPYSVGETG RMGSPGRREIGHGKLAWRAIRPMLPTPEQFPYTL RVVSEITESNGSSSMATVCGTSLA LMDAGVPLAKPVAGIAMGLILEGDRFAVLSDILG DEDHLGDMDFKVAGTADGITSLQM DIKITGITEEIMKVALGQAQGGRVHILGEMSKAI TESRGQLGEFAPRIEVMNIPVDKI REVIGSGGKVIREIVEKTGAKINIEDDGTVKIAS SSGKEIEAARKWIHSIVAEP EIGQ VYEGTVVKTADFGAFVNFFGARDGLVHISQLASE RVAKTQDVVKEGDKVWVKLLGFDE RGKVRLSMKVVDQATGQEIPNEKKKEEAAE"

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misc-feature complement(148285..148458)

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misc-feature	complement(149692..150090)	/locus-tag="RL0120" /inference="protein motif: Pfam: PF01138.10" /note="Pfam match to entry PF01138.10 RNase-PH" /gene="rpsO"
gene	complement(150472..150741)	/locus-tag="RL0121" /gene="rpsO"
CDS	complement(150472..150741)	/locus-tag="RL0121" /inference="similar to sequence: INSDC: BS29668" /inference="similar to sequence: INSDC: SME591783" /note="similarity: fasta; with=UniProt: RS15-BACSU (EMBL: BS29668); Bacillus subtilis.; rpsO; 30S ribosomal protein S15 (BS18).; length=BS18 (88; id 64.773; 88 aa overlap; query 2-89; subject 1-88 similarity: fasta; with=UniProt: Q92SW1 (EMBL: SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; PROBABLE 30S RIBOSOMAL PROTEIN S15.; length=89; id

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PF00312.9 Ribosomal-S15"  
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33)  
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33)  
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with=UniProt:Q89EE1  
(EMBL:AP005961); Bradyrhizobium  
japonicum.; Oxidoreductase.;  
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DVWGHQVADFAKDHLVIVADSRHGHRSTRSQPF  
GYDLMTSDYVALLDYLKIDKVTLV  
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VPVTLAIGDHDEAVKLDHTEMMAK  
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GR"  
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/inference="protein  
motif: Pfam:PF00561.8"  
/note="Pfam match to entry  
PF00561.8 Abhydrolase-1"  
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CDS complement(151863..1527 /gene="truB"

95)

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with=UniProt:TRUB-ECOLI  
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truB; tRNA pseudouridine synthase  
B (EC 4.2.1.70) (tRNA  
pseudouridine 55 synthase) (Psi55  
synthase) (Pseudouridylate  
synthase) (Uracil hydrolyase)  
(Protein p35).; length=314; id  
37.460; 315 aa overlap; query  
1-308; subject 1-308  
similarity:fasta;  
with=UniProt:TRUB-AGRT5  
(EMBL:HS368258); Agrobacterium  
tumefaciens (strain C58/ATCC  
33970).; truB; tRNA pseudouridine  
synthase B (EC 4.2.1.70) (tRNA  
pseudouridine 55 synthase) (Psi55  
synthase) (Pseudouridylate  
synthase) (Uracil hydrolyase).;  
length=315; id 82.803; 314 aa  
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pseudouridine 55 synthase) (Psi55  
synthase) (Pseudouridylate  
synthase) (Uracil hydrolyase) "  
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AYDLAREGETIEIPSREVDIFRLT  
LLACPDADSAHFEVECGKGTIVRALARDFGRELG  
CYGHVSGLRRTFVAPFAEGAMVPL  
ADLVALEAIEDMDERLAALDALLIDTCEALSSLP  
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/inference="protein  
motif:Pfam:PF01509.7"  
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PF01509.7 TruB-N"
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gene              complement(152809..153213)      /gene="rbfA"

CDS	complement(152809..153213)	/locus-tag="RL0124" /gene="rbfA"  /locus-tag="RL0124" /inference="similar to sequence:INSDC:HS134244" /inference="similar to sequence:INSDC:SME591783" /note="similarity:fasta; with=UniProt:RBFA-ECOLI (EMBL:HS134244); Shigella flexneri.; rbfA; Ribosome-binding factor A (P15B protein).; length=132; id 33.929; 112 aa overlap; query 12-120; subject 6-114 similarity:fasta; with=UniProt:RBFA-RHIME (EMBL:SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; rbfA; Ribosome-binding factor A.; length=135; id 84.328; 134 aa overlap; query 1-134; subject 1-134" /codon-start=1 /transl-table=11 /product="putative ribosome-binding factor protein" /protein-id="CAK05612.1" /db-xref="GI:115254538" /db-xref="GOA:Q1MN40" /db-xref="UniProtKB/TrEMBL:Q1MN40" /translation="MTRPTSSAPSQRMLRIGEQV RAAITQVLQRGEVRDDVIEATVIS VSEVRMSPDLKIATAYVTPLGVSDHSIVIEALNR HARFIRGLGPQLRQMKYMPEVRF RDDTSFDNYKKIDELLRSPEVSRDLGDGNDNQ"
misc-feature	complement(152860..153180)	/gene="rbfA"  /locus-tag="RL0124" /inference="protein motif: Pfam:PF02033.5" /note="Pfam match to entry PF02033.5 RBFA"
gene	complement(153364..156117)	/gene="infB"
CDS	complement(153364..156117)	/locus-tag="RL0125" /gene="infB"  /locus-tag="RL0125" /inference="similar to sequence:UniProtKB:Q8UJ51" /inference="similar to sequence:UniProtKB:Q9ZF31" /note="similarity:fasta; SWALL:IF2-SALTY (SWALL:Q9ZF31); Salmonella typhimurium; translation initiation factor if-2; infB; length 892 aa; 909 aa overlap; query 11-917 aa; subject 53-891 aa similarity:fasta; SWALL:IF2-AGRT5 (SWALL:Q8UJ51); Agrobacterium tumefaciens;



translation initiation factor  
if-2; infB; length 913 aa; 935 aa  
overlap; query 1-917 aa; subject  
1-913 aa"  
/codon-start=1  
/transl-table=11  
/product="putative translation  
initiation factor IF-2"  
/protein-id="CAK05613.1"  
/db-xref="GI:115254539"  
/db-xref="GOA:Q1MN39"  
/db-xref="UniProtKB/TrEMBL:Q1MN39"  
/translation="MTDSNDDKTISVAGKKTLL  
KPSGMSQGTVRQDMGRGRTKAVVV  
ETRRRRPMPREDEKPIITPVAPAAPVRAEPAPAP  
VQARPQQPTPAPRVQQGNNNQTNQ  
RPPQQSHQPPRQNDPRPVVLNHLSPPEMDARRR  
ALADSQARDAQDAIRRAEEEEKRRA  
AEEVIRKAAEAEAAARRAAEEAIRQAEAPAVAEP  
AAAEAPAPAEARTDAPRPPQPASSA  
PAARRPDAAGAPAAPAPGAAVPGAVRGRRDEKE  
EDDRGAARGGPVRGRVVRPEPAKP  
VTTRPKTDEERRRGKLTITTANVDGEDNARGRSL  
SAMRRRQEKFRRGQMQETREKISR  
EVVLPETITITIELSQRMSERAVDVIKYLMEGQM  
MKPGDVIDADLAEIAGEFGHTVR  
RVSESDVELGIFNVSDDEGELVSRPPVVTIMGHV  
DHGKTSLLDAIRHANVVSGEAGGI  
TQHIGAYQVEQNGQKITFIDTPGHAAFTAMRARG  
AQATDIAILVVAADDSVMPQTIES  
INHAKAAGVPIIVAINKVDKHEADPQKVRNQLLQ  
HEVFVESMGGEVLDVEVSAKTGKN  
LDKLLEAILLQAEILDLKANANRTAEGTVIEAQL  
DRGRGSVATVLVQKGTLRPGQIIV  
AGDVWGRVRALVTDKGDHVKEAGPATPVEVLGLS  
GTPQAGDKFAVVESESRAREISEY  
RQRLARDKAAARQSGQRGSLEQMMMQRQSVGIKE  
FPLVIKGDVQGSIEAIAGALEKLG  
TDEVRRARIVHSGAGGITESDISLAEASNAIIIGF  
NVRANTQARQFAEREGIEIRYYNI  
IYDLVDDVKAAMSGLLSPERRETFIGNAEILEVF  
NITKVGKVAGCRVVEGKVERGAGV  
RLIRNDVVVHEGKLKTLKRFKDEVSEVPMGQECG  
MAFENYEDMRAGDVIECFRVEHIT RTL"

misc-feature complement(153400..1536  
06)

/gene="infB"  
/locus-tag="RL0125"  
/inference="protein  
motif: Pfam: PF03144.8"  
/note="Pfam match to entry  
PF03144.8 GTP-EFTU-D2"

misc-feature complement(154114..1543  
05)

/gene="infB"  
/locus-tag="RL0125"  
/inference="protein  
motif: Pfam: PF03144.8"  
/note="Pfam match to entry  
PF03144.8 GTP-EFTU-D2"

misc-feature complement(154372..1548  
75)

/gene="infB"  
/locus-tag="RL0125"  
/inference="protein"

		motif: Pfam: PF00009.10"
		/note="Pfam match to entry
		PF00009.10 GTP-EFTU"
misc-feature	complement(154948..155103)	/gene="infB"
		/locus-tag="RL0125"
		/inference="protein"
		motif: Pfam: PF04760.3"
		/note="Pfam match to entry
		PF04760.3 IF2-N"
gene	complement(156219..156911)	/locus-tag="RL0126"
CDS	complement(156219..156911)	/locus-tag="RL0126"
		/inference="similar to
		sequence: INSDC: C97369"
		/note="similarity: fasta;
		with=UniProt: Q8UJ50 (EMBL: C97369);
		Agrobacterium tumefaciens (strain
		C58/ATCC 33970).; Hypothetical
		protein Atu0088 (AGR-C-134p).;
		length=233; id 71.304; 230 aa
		overlap; query 4-230; subject
		5-233"
		/codon-start=1
		/transl-table=11
		/product="conserved hypothetical
		protein"
		/protein-id="CAK05614.1"
		/db-xref="GI:115254540"
		/db-xref="UniProtKB/TrEMBL: Q1MN38"
		/translation="MMTAHEPDAPLEDDDLGYD
		VNGRMCIVTRESGSPEELIRFVAA
		PDGTVVADLKRELPGRCWVKIDRSLVDRAVAKK
		LFARALKTDVKAADDLGESVDRL
		AAQLMQMMNMARKAGQFVSGSSKVDAAVRSGAAL
		AVFHSTGAADDGVRKIDQARKAWH
		LGMETEEEEIPSFRLFSESEMEGLMGQNAFIHAAV
		LAGQAGEGVVKRAKMLEQYRIGGQ
		SRAAGGAGRLKQ"
misc-feature	complement(156606..156851)	/locus-tag="RL0126"
		/inference="protein"
		motif: Pfam: PF04296.2"
		/note="Pfam match to entry
		PF04296.2 DUF448"
gene	complement(156908..158509)	/gene="nusA"
		/locus-tag="RL0127"
CDS	complement(156908..158509)	/gene="nusA"
		/locus-tag="RL0127"
		/inference="similar to
		sequence: INSDC: AE007950"
		/inference="similar to
		sequence: INSDC: B91135"
		/note="similarity: fasta;
		with=UniProt: NUSA-ECOLI
		(EMBL: B91135); Shigella flexneri.;
		nusA; Transcription elongation
		protein nusA (N utilization
		substance protein A) (L factor).;

length=495; id 43.697; 476 aa  
 overlap; query 9-480; subject  
 4-479 similarity:fasta;  
 with=UniProt:Q8UJ49  
 (EMBL:AE007950); Agrobacterium  
 tumefaciens (strain C58/ATCC  
 33970).; nusA; N-utilization  
 substance protein A (AGR-C-136p).;  
 length=538; id 91.011; 534 aa  
 overlap; query 1-533; subject  
 1-532"  
 /codon-start=1  
 /transl-table=11  
 /product="putative transcription  
 elongation protein (N utilization  
 substance protein A) (L factor)"  
 /protein-id="CAK05615.1"  
 /db-xref="GI:115254541"  
 /db-xref="GOA:Q1MN37"  
 /db-xref="UniProtKB/TrEMBL:Q1MN37"  
 /translation="MAVSANRLELLQIADAVARE  
 KVIDREIVLAAMADAIQKAARSRY  
 GTESNIRADINPKTGEIRLQRLLEVVEKAEDYST  
 QIPLELARDRNPDAALGDFIADPL  
 PPMDFGRIAAQSAKQVIVQKVREAERDRQFDEFK  
 DRVGEIVNGTVKRVEYGNVIVDLG  
 RGEIIRDEMIPRENVRYGDRVRAYVYDVRREQ  
 RGPQIFLSRTHPQFMVKLFTMEVP  
 EIYDGIIQVKSVDPPGSRAKIAVISNDSSIDPV  
 GACVGMGRSRVQAVVGELQGEKID  
 IIPWSQDPATFVVNALQPAEVAKVVLDEDAERIE  
 VVVPDEQLSLAIGRRGQNVRLASQ  
 LTGWDIDIMTEAEESERRQKEFNERTNLFMDSL  
 VDEMVGQVLASEGFAAVEELAYVD  
 LDEISSIDGFDEETAQEIIQQRAREFLERLEAEMD  
 EKRKALGVQDELREINGMTAQMMV  
 ALGEDGIKSIEDFAGCAADDLVGWSERKNGETKK  
 FEGLFSKFDVSRVEAEQMIVQARL  
 SAGWITQEDLAKGTEEEVTEAEQEA"

misc-feature complement(157442..1575  
88)

/gene="nusA"  
 /locus-tag="RL0127"  
 /inference="protein  
 motif: Pfam: PF00013.12"  
 /note="Pfam match to entry  
 PF00013.12 KH-1"

misc-feature complement(157904..1581  
04)

/gene="nusA"  
 /locus-tag="RL0127"  
 /inference="protein  
 motif: Pfam: PF00575.9"  
 /note="Pfam match to entry  
 PF00575.9 S1"

gene complement(158569..1591  
74)

/locus-tag="RL0128"

CDS complement(158569..1591  
74)

/locus-tag="RL0128"  
 /inference="similar to  
 sequence: INSDC: SME591783"  
 /note="similarity: fasta;  
 with=UniProt: Y236-RHIME  
 (EMBL: SME591783); Rhizobium

		meliloti (Sinorhizobium meliloti).; Hypothetical UPF0090 protein R00236.; length=205; id 77.612; 201 aa overlap; query 1-200; subject 1-201" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05616.1" /db-xref="GI:115254542" /db-xref="UniProtKB/TrEMBL:Q1MN36" /translation="MSDLTNADNEREPRLITETG LDQRLADIIEPVLVDLGFRLIRVR MMNQNGATMQVMAERN DGTMTVQDCEEVSMAISP VLDVEDPVDKEYHLEVSSPGIDRP MVRKSD FVRWQGH LVKCETSILIDNRKRFRGKIV EAGTDGFTLERDQIAYGEEQKVTI PFTALSDAKLILTDDLIRDALRADKLAKAQAANQ NEADDEE"
misc-feature	complement(158665..159093)	/locus-tag="RL0128"  /inference="protein motif: Pfam: PF02576.5" /note="Pfam match to entry PF02576.5 DUF150"
gene	159373..161052	/locus-tag="RL0129"
CDS	159373..161052	/locus-tag="RL0129" /inference="similar to sequence: INSDC: AE007951" /note="similarity: fasta; with=UniProt: Q8UJ47 (EMBL: AE007951); Agrobacterium tumefaciens (strain C58/ATCC 33970).; MFS permease (AGR-C-139p).; length=542; id 73.371; 537 aa overlap; query 22-558; subject 6-542" /codon-start=1 /transl-table=11 /product="putative transmembrane transport protein" /protein-id="CAK05617.1" /db-xref="GI:115254543" /db-xref="GOA: Q1MN35" /db-xref="UniProtKB/TrEMBL: Q1MN35" /translation="MRIYCRWRAITKAGEIVAYT SSTLAPLRHDTYRTIWFASLSSNF GGLIQAVGAAWMMTTITASEDMVALVQTSTALPI MLFSLISGALADNYDRRRVMLTAQ CMMLTVSALLTASALLGWITPWLLLFFTFLLIGCG TALNNPSWQASVGMVPRADLPAA VTLNSMGFNITRSVGAIGGVIVAAAGAAAFV NTLSYLALIYALLRWRPAAPVSTL PREALGSAIFAGLRYVSMSPNLEKVLVRGLLFGI GASSILALLPVVALDLVAGGPLTY GFMLGAFGIGAIGGAVLNARLRQVLSSEMIVRLS FAGFALSAVIAALSPSAVLTSAGL LVSGACWVSALSLENTIVQLSTPRWVVGRALSLY QTVTFGGIAGGSWLWGIAADRYGV ADALLMSSVVMLLGIAIGLRFSPAFASLNLDPL NRFIEPALSLDITPRSGPIVIQVD

		YEIADEDLAEFMELMGERRRIRIRDGARNWALMR DLENPSLWTETYHTPTWVEYIRHN QRRRTQADAENTDRLRALHRGEGPLHVHRMIERQA IPPDNDVFHKAPIDLHH"
misc-feature	159433..160998	/locus-tag="RL0129" /inference="protein motif: Pfam:PF05977.1" /note="Pfam match to entry PF05977.1 DUF894"
misc-feature	order(159475..159543, 159571..159639, 159700..159768, 159913..159981, 160102..160170, 160183..160251, 160288..160356, 160369..160428, 160465..160533, 160543..160611)	/locus-tag="RL0129"
		/inference="protein motif: TMHMM:2.0" /note="10 probable transmembrane helices predicted at aa 35-57, 67-89, 110-132, 181-203, 244-266, 271-293, 306-328, 333-352, 365-387 and 391-413"
gene	161049..161531	/locus-tag="RL0130"
CDS	161049..161531	/locus-tag="RL0130" /inference="similar to sequence: INSDC:BX640432" /inference="similar to sequence: INSDC:SGPHNOL" /note="similarity: fasta; with=UniProt:Q54244 (EMBL:SGPHNOL); Streptomyces griseus.; phnO-like; Regulatory protein for C-P lyase.; length=150; id 55.102; 147 aa overlap; query 14-160; subject 7-150 similarity: fasta; with=UniProt:Q7W6J0 (EMBL:BX640432); Bordetella parapertussis.; Putative acetyltransferase.; length=154; id 61.486; 148 aa overlap; query 13-160; subject 7-153" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator/acetyltransferase" /protein-id="CAK05618.1" /db-xref="GI:115254544" /db-xref="GOA:Q1MN34" /db-xref="UniProtKB/TrEMBL:Q1MN34" /translation="MRPAMQRSIGYRFLARQSD LAAIVRLLADDNLGGTREIVSDPV DARYLSAFAAIEADANQLLAVANDATDRVVGCLQ LSFVPGLSRTGMWRGQIESVRVAS DLRGSLGSHFIEWAIAQCAERGCGLVQLTPDKT RGDAIRFYERLGFVASHEGLKRNL
misc-feature	161241..161498	/locus-tag="RL0130" /inference="protein"

		motif: Pfam: PF00583.9"
		/note="Pfam match to entry PF00583.9 Acetyltransf-1"
gene	complement(161538..162812)	/locus-tag="RL0131"
CDS	complement(161538..162812)	/locus-tag="RL0131"
		/inference="similar to sequence: INSDC: AF458045" /inference="similar to sequence: INSDC: SME591783" /note="similarity: fasta; with=UniProt: Q8RP11 (EMBL: AF458045); Pseudomonas syringae (pv. maculicola).; Type III effector HopPmaG.; length=413; id 35.782; 422 aa overlap; query 14-424; subject 10-412 similarity: fasta; with=UniProt: Q92SW8 (EMBL: SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE TRANSGLYCOSYLASE TRANSMEMBRANE PROTEIN.; length=412; id 69.343; 411 aa overlap; query 14-424; subject 2-412" /codon-start=1 /transl-table=11 /product="conserved hypothetical exported protein" /protein-id="CAK05619.1" /db-xref="GI:115254545" /db-xref="GOA: Q1MN33" /db-xref="UniProtKB/TrEMBL: Q1MN33" /translation="MRGLHMLKDGPRRLRIFALA LAAALLPLSCYAAPSKADVEVQFE KVVQADLWPEAKANGISEKVFQAAFSGITLNWNL PDLAPPGFPPPKEQKQTQAEFSSP APYFNEDQLKKLAATGRGFAAQYGSTLKRIEKTY GVPGSIVLAIWGRETGFGAAKIPN SAIEVLATKAFMSTRKEMFRTELVAALHILDGGD VTPANFKGSWAGALGQPQFMPTSY LKYAVDFDGDGHRNIWTSVPDTLASIANYLVKKG WQRNRDWGFVSIPEAVSQAQEGP DLAKPLSHWTS LGIDRISGKGFPSGEMKAEGMML VPAGRDGPEFIVTPNFYIIKEYNN SDLYALYIGNLADRIAYNGGAFQGWGDVGKMLR SDVAAMQKALERQGYDVGGSDGLP GYKTRRSIGQWQAKNGMKPTCFPEATMKGKLK"
misc-feature	complement(162708..162776)	/locus-tag="RL0131"
		/inference="protein motif: TMHMM: 2.0" /note="1 probable transmembrane helix predicted at aa 13-35"
sig-peptide	complement(162713..162812)	/locus-tag="RL0131"
		/inference="protein motif: SignalP-HMM: 2.0" /note="Signal peptide predicted for RL0131 by SignalP 2.0 HMM"

		(Signal peptide probability 1.000) with cleavage site probability 0.980 between residues 32 and 33"
gene	complement(162809..1634 14)	/gene="recR"
CDS	complement(162809..1634 14)	/locus-tag="RL0131A" /gene="recR"  /locus-tag="RL0131A" /inference="similar to sequence:INSDC:HST35386" /inference="similar to sequence:INSDC:SME591783" /note="similarity:fasta; with=UniProt:RECR-STRCO (EMBL:HST35386); Streptomyces coelicolor.; recR; Recombination protein recR.; length=199; id 44.271; 192 aa overlap; query 10-201; subject 6-197 similarity:fasta; with=UniProt:RECR-RHIME (EMBL:SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; recR; Recombination protein recR.; length=201; id 89.055; 201 aa overlap; query 1-201; subject 1-201" /codon-start=1 /transl-table=11 /product="putative recombination protein" /protein-id="CAK05620.1" /db-xref="GI:115254546" /db-xref="GOA:Q1MN32" /db-xref="UniProtKB/TrEMBL:Q1MN32" /translation="MAKRVGTGPEIEKLIQLLAKV PGLGPRSARRAALHLIKKKDQLLG PLSHAMGEAYDKVKICSRGCVDTVDPCIVCTDV QRDQSVIIIVVEDVSDLWALERAGA MNAAYHVLGGTLSPLDGVGPDDLNIIRGLIDRVGE GGIRELIIAVNATVEGQTTAHYIT DQLQGLDVKITRLAHGVPVGGELDYLDDEGTLAA LRARTVI"
gene	163433..164101	/locus-tag="RL0132"
CDS	163433..164101	/locus-tag="RL0132" /inference="similar to sequence:INSDC:A97370" /note="similarity:fasta; with=UniProt:Q8UJ44 (EMBL:A97370); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0094 (AGR-C-144p).; length=AGR-C ( 229; id 52.657; 207 aa overlap; query 11-216; subject 23-229" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05621.1" /db-xref="GI:115254547"

		/db-xref="GOA:Q1MN31" /db-xref="UniProtKB/TrEMBL:Q1MN31" /translation="MERKRNRRGRIGHMPKILALC TGNPESLPGKSYKTGIFKHAVTGA VMIDAEGLVGDAICNRKHHGGVDQAVYVEGSLTL DWWSRELGRPYEPGTFGENMVISD LDNRDVAVGDRFLTGDVLVLEVTSCRMPCATFAAR MADPKFVKRYTAAARPGIYCRVIR GGVVEPGMPMEYTSFSGDKITMPELMEAFGRRLP GADRTRYLAAPIHYKLRLAMLESQA DEAR"
misc-feature	163580..163948	/locus-tag="RL0132" /inference="protein" motif: Pfam:PF03473.5" /note="Pfam match to entry PF03473.5 MOSC"
gene	complement(164124..164447)	/locus-tag="RL0133"
CDS	complement(164124..164447)	/locus-tag="RL0133"  /inference="similar to sequence:INSDC:SME591783" /note="similarity:fasta; with=UniProt:Y231-RHIME (EMBL:SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; Hypothetical UPF0133 protein R00231.; length=107; id 83.178; 107 aa overlap; query 1-107; subject 1-107" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05622.1" /db-xref="GI:115254548" /db-xref="GOA:Q1MN30" /db-xref="UniProtKB/TrEMBL:Q1MN30" /translation="MRDIMGMMGKVKEMQAKMEQ MQAEIAELTAEGKAGGGLVTVLIS GKGDLSKSLKIDPSLKFEDDVEILEDLIVAHHKDA KDKAEALAAEKTALTAGLPIPPG FKLPPF"
misc-feature	complement(164148..164426)	/locus-tag="RL0133"  /inference="protein" motif: Pfam:PF02575.4" /note="Pfam match to entry PF02575.4 DUF149"
gene	complement(164470..166347)	/gene="dnaX"
CDS	complement(164470..166347)	/locus-tag="RL0134" /EC-number="2.7.7.7" /inference="similar to sequence:INSDC:C97370" /inference="similar to sequence:INSDC:U00096" /note="similarity:fasta; with=UniProt:DP3X-ECOLI (EMBL:U00096); Escherichia coli.; dnaX; DNA polymerase III subunit



		tau (EC 2.7.7.7) [Contains: DNA polymerase III subunit gamma].; length=643; id 36.170; 564 aa overlap; query 18-560; subject 3-540 similarity:fasta; with=UniProt:Q8UJ42 (EMBL:C97370); Agrobacterium tumefaciens (strain C58/ATCC 33970).; DNA polymerase III, tau subunit (AGR-C-147p).; length=624; id 76.874; 627 aa overlap; query 1-625; subject 1-624" /codon-start=1 /transl-table=11 /product="putative DNA polymerase III" /protein-id="CAK05623.1" /db-xref="GI:115254549" /db-xref="GOA:Q1MN29" /db-xref="UniProtKB/TrEMBL:Q1MN29" /translation="MSDTERQSKDAASTGTGYRV LARKYRPKDFTDLMVGQEPMVRTL TNAFETGRIAQAYMLTGVRGVGKTTTARILARAL NYKTSEIDKPTIDLRAPGEHCQAI MEGRHVDVIEMDAASHTGIDDIREIIEQVRYRPV SARYKVYIIDEVHMLSTQAFNGLL KTLEEPPEHVKFIFATTEIRKVPITVLSRCQRFD LRRISASDLVGLFTTIAAKEGIEA EPDALAMIARAAEGSARDGLSLLDQAIAHGAGVV QAEAVRGMLGLADRARIVDLFQHI VKGDVAAALGEFQNQYEAGANPVVVLTDLADFTH LVTRLKYVPDAANDPSLSEVERTK AAEFAKCVAVTTLSRIWQMLLKGIPETEGSSRTA GAAEMVLIRLAHAAHLPAPEDAAR RLAEFGDNTGPRPSSSPSGNGGSGTRVPYQSS VAARAAETAPSQPPSSAPVAMLRA VPSSQSETMAVGRIEKPAPAEAPKPLVPVNSVNDI VNLATEKRDPKPKAMVRTFLRPVR IEAGRLDVSLAPGAPTLLNELAVKLKEWTGIHW IVLSRDEGQPTLVEAEARTREQH VIDARQDPDVAAILAHFPGAKIIDVRVRAPEPEE EGEATPPAAAESEEGDILPGDDIE F" /gene="dnaX"
misc-feature	complement(165595..166182)	/locus-tag="RL0134" /inference="protein motif: Pfam:PF00004.12" /note="Pfam match to entry PF00004.12 AAA"
gene	166459..166989	/locus-tag="RL0135"
CDS	166459..166989	/locus-tag="RL0135" /inference="similar to sequence: INSDC:AE007951" /note="similarity:fasta; with=UniProt:Q8UJ41 (EMBL:AE007951); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0097 (AGR-C-148p).; length=174; id 62.069; 174 aa overlap; query 1-174; subject 1-174" /codon-start=1

		/transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05624.1" /db-xref="GI:115254550" /db-xref="UniProtKB/TrEMBL:Q1MN28" /translation="MASGSSTTNLPDAHIGNIVI KSKPTCEKTASRRKRQEECPKGF ALDPRLENDSVSIMVTGLCDLRLSKDARWPWLIL VPRRADITEIFELTPLDQVLLAFE TELVAKALKKITGATKINIGALGNIVRQLHVHVI ARFEGDANWPGPVWGFGRAPYED GKRDEFTAKLREALSS" /locus-tag="RL0135" /inference="protein motif: Pfam:PF01230.10" /note="Pfam match to entry PF01230.10 HIT"
misc-feature	166582..166881	
gene	166986..167945	/locus-tag="RL0136" /locus-tag="RL0136" /inference="similar to sequence: INSDC:AE007951" /note="similarity: fasta; with=UniProt:Q8UJ40 (EMBL:AE007951); Agrobacterium tumefaciens (strain C58/ATCC 33970).; MutT/nudix family protein (AGR-C-150p).; length=320; id 69.085; 317 aa overlap; query 1-317; subject 2-318" /codon-start=1 /transl-table=11 /product="putative MutT/nudix family protein" /protein-id="CAK05625.1" /db-xref="GI:115254551" /db-xref="UniProtKB/TrEMBL:Q1MN27" /translation="MSHSLFSDSDVPHPEPSNLTA FAANDLNRDSEHRDEQSVEKALAK EGTTHFAFTRDKLVLKHDGQVLDPLFARYELQEL QPDWDET VLLGYRKSGEPRLAVPV GIDVDDLTSQYKPADGRTLFREMLIDEVLLGEFA QAASLIRWNGDNRF CGRCGSAMEI HIGGYKRVCAACEHVIFPRTPVIMLTVDQQRD LCLLGRSPHFAPGMYSCLAGFLEP GETIENAVRRETLEESGIRTGRIRYHASQPWPMP HSLMIGCYAEAKSTEISRDETELE DCRWFTREETIEMLERPSATGRASPPKGAIAHRL MRDWVEWKR"
CDS	166986..167945	
misc-feature	167523..167906	/locus-tag="RL0136" /inference="protein motif: Pfam:PF00293.12" /note="Pfam match to entry PF00293.12 NUDIX"
gene	167950..168645	/locus-tag="RL0137" /locus-tag="RL0137" /inference="similar to sequence: INSDC:SME591782" /note="similarity: fasta; with=UniProt:Q92SX3 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium
CDS	167950..168645	

		meliloti).; PUTATIVE TRANSCRIPTION REGULATOR PROTEIN.; length=230; id 67.111; 225 aa overlap; query 3-227; subject 1-225" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="CAK05626.1" /db-xref="GI:115254552" /db-xref="UniProtKB/TrEMBL:Q1MN26" /translation="MPVARSERLLTLLQTLRRYR RPVTGTVLAQETGVSLRTLRYDIA SLQAQGAMIEGEAGIGYVLKPGFMLPPMMFSEEE LEALVLGSRWVARAAEPRLAGAGA DALAKIAAVLPADMREMIDSAALFVGPKRRDEDK ADVSAIRRAIRLERILELHYGDEQ GRISRRRVWPFGLGYEHVRVLMAWCEL RQDFRH FRTDRIIDMALHEVRYPRRRTVLL KEWRETQDVP MEN"
gene	169172..169540	/locus-tag="RL0138"
CDS	169172..169540	/locus-tag="RL0138" /inference="similar to sequence:INSDC:AF451953" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:Q8GPH6 (EMBL:AF451953); Pantoea agglomerans.; EhpR.; length=129; id 33.333; 123 aa overlap; query 3-121; subject 10-129 similarity:fasta; with=UniProt:Q92KT5 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; Hypothetical protein SMc02901.; length=122; id 63.115; 122 aa overlap; query 1-122; subject 1-122" /codon-start=1 /transl-table=11 /product="putative glyoxalase/dioxygenase" /protein-id="CAK05627.1" /db-xref="GI:115254553" /db-xref="GOA:Q1MN25" /db-xref="UniProtKB/TrEMBL:Q1MN25" /translation="MTSPNLIIILYVKDPGESASF YRNLLNREPAVEAPNFVAFPLEGG FTLGLWRRSKVEPQPSAIGNRGEVAFMVEGENAV ARHYEDWRQRGLPIAQELTELDGF PTFVVLDPDGHRRLRVCEPDK"
misc-feature	169178..169522	/locus-tag="RL0138" /inference="protein motif: Pfam:PF00903.11" /note="Pfam match to entry PF00903.11 Glyoxalase"
gene	complement(169654..1705 08)	/locus-tag="RL0139"
CDS	complement(169654..1705 08)	/locus-tag="RL0139"

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/EC-number="4.2.1.51"
/inference="similar to
sequence:INSDC:A30261"
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sequence:INSDC:AE007951"
/note="similarity:fasta;
with=UniProt:PHEA-ECOLI
(EMBL:A30261); Shigella flexneri.;
pheA; P-protein [Includes:
Chorismate mutase (EC 5.4.99.5)
(CM); Prephenate dehydratase (EC
4.2.1.51) (PDT)].; length=386; id
32.143; 280 aa overlap; query
1-275; subject 99-375
similarity:fasta;
with=UniProt:Q7D273
(EMBL:AE007951); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; AGR-C-151p.; length=287;
id 87.324; 284 aa overlap; query
1-284; subject 1-284"
/codon-start=1
/transl-table=11
/product="putative P-protein
[includes: chorismate mutase and
prephenate dehydrogenase]"
/protein-id="CAK05628.1"
/db-xref="GI:115254554"
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/db-xref="UniProtKB/TrEMBL:Q1MN24"
/translation="MNIKTNRIAFQGEFGANSDM
ASRDMFPTMEPLPCQTFEDAFTAV
DNGDADIGMPIIENTIAGRVADIIHLLPESRLHI
IGEYFMPPIRFQLMVLPGVTKDEIR
TVHSHIHALGQCRKIVRANGWKPVIAAGDTAGAAK
LVQETGDRSMAALAPRLAADLYGL
EIIAENVEDTENNVTFRVVLRSDEEWAQRNSAEE
KVVTTTFVFNVRNIPAALYKALGGF
ATNNINMTKLESYQLGGKFVATQFYADIEGHPND
PNVRRALEELRFFSEKVRILGVYK GHAMRGLL"
misc-feature    complement(169693..1699 /locus-tag="RL0139"
17)
/inference="protein
motif: Pfam: PF01842.8"
/note="Pfam match to entry
PF01842.8 ACT"
misc-feature    complement(169954..1704 /locus-tag="RL0139"
87)
/inference="protein
motif: Pfam: PF00800.8"
/note="Pfam match to entry
PF00800.8 PDT"
gene            complement(170519..1712 /gene="kdsB"
74)
/locus-tag="RL0140"
CDS             complement(170519..1712 /gene="kdsB"
74)
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sequence:INSDC:A26322"
/inference="similar to

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sequence:INSDC:SME591782"
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with=UniProt:KDSB-ECOLI
(EMBL:A26322); Escherichia coli.;
kdsB; 3-deoxy-manno-octulosonate
cytidyltransferase (EC 2.7.7.38)
(CMP-KDO synthetase)
(CMP-2-keto-3-deoxyoctulosonic
acid synthetase) (CKS).;
length=247; id 45.122; 246 aa
overlap; query 10-243; subject
3-243 similarity:fasta;
with=UniProt:Q92SX6
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PROBABLE
3-DEOXY-MANNO-OCTULOSONATE
CYTIDYLYLTRANSFERASE (CMP-KDO
SYNTHETASE) PROTEIN (EC
2.7.7.38).; length=250; id 77.500;
240 aa overlap; query 10-249;
subject 10-249; putative
3-deoxy-manno-octulosonate
cytidyltransferase (CMP-KDO
synthetase)
(CMP-2-keto-3-deoxyoctulosonic
acid synthetase) "
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/transl-table=11
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te cytidyltransferase (CMP-KDO
synthetase)
(CMP-2-keto-3-deoxyoctulosonic
acid synthetase) (CKS)."
/protein-id="CAK05629.1"
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/translation="MSDSNLDGVLVLIPARMAST
RLPGKPLADICGLPMIVQVAMRAR
EAAIGRVVAVDETRVFDVAAAGFEVVMTRVDH
QSGSDRIFEALTKVDPEGKAKIIV
NIQGDLPITIDPETVRAALRPLENEAVDIGTLTTE
IDNEEDKTAPHIVKIIGSPISGMR
LHALYFTRATAPYQGPLYHHIGLYAYRRAALER
FVSLGPSTLEKRESLEQLRALEAG
MRIDAEEVVDTPVPLGVDTTPADLEKARRILSAKSN"

misc-feature      complement(170612..1712
47)               /gene="kdsB"

                  /locus-tag="RL0140"
                  /inference="protein
motif:PFam:PF02348.6"
                  /note="Pfam match to entry
PF02348.6 CTP-transf-3"

gene              171429..171992  /gene="cycM"
                  /locus-tag="RL0141"

CDS               171429..171992  /gene="cycM"
                  /locus-tag="RL0141"
                  /inference="similar to
sequence:INSDC:AP005940"
                  /inference="similar to
sequence:INSDC:HS370249"

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		/note="similarity:fasta; with=UniProt:CYCM-BRAJA (EMBL:AP005940); Bradyrhizobium japonicum.; cycM; Cytochrome c homolog.; length=184; id 48.913; 184 aa overlap; query 1-180; subject 1-180 similarity:fasta; with=UniProt:CYCM-AGRT5 (EMBL:HS370249); Agrobacterium tumefaciens (strain C58/ATCC 33970).; cycM; Cytochrome c homolog.; length=192; id 70.213; 188 aa overlap; query 1-185; subject 1-187" /codon-start=1 /transl-table=11 /product="putative cytochrome c" /protein-id="CAK05630.1" /db-xref="GI:115254556" /db-xref="GOA:Q1MN22" /db-xref="UniProtKB/TrEMBL:Q1MN22" /translation="MNSYVNTAVGALLGTIFVLM SVSIASEGIFHSEAPEKEGFAIVA EEAPAAGGEAAPAVAVPIAQLLASADAKAGETVF KKCQACHDGTKGGPNKVGPNLFGV VDRPIASHAGFAYSAPMKDFSCKGSEKWTFEYLN KFLAPKKDIPGTAMGFAGLAKDQ ERANVILYLHTLADSPGPLPDPNAATQ" /gene="cycM" /locus-tag="RL0141" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0141 by SignalP 2.0 HMM (Signal peptide probability 0.996) with cleavage site probability 0.974 between residues 25 and 26"
sig-peptide	171429..171501	
misc-feature	171447..171515	/gene="cycM" /locus-tag="RL0141" /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted at aa 7-29"
misc-feature	171642..171947	/gene="cycM" /locus-tag="RL0141" /inference="protein motif:Pfam:PF00034.8" /note="Pfam match to entry PF00034.8 Cytochrom-C"
gene	complement(172062..173015)	/locus-tag="RL0142"
CDS	complement(172062..173009)	/locus-tag="RL0142" /inference="similar to sequence:INSDC:AE007950" /note="similarity:fasta; with=UniProt:Q8UJ58 (EMBL:AE007950); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Permease (AGR-C-121p).; length=AGR-C-121p; id 65.815; 313 aa overlap; query 1-313; subject

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1-313"
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permease protein"
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/db-xref="GI:115254557"
/db-xref="GOA:Q1MN21"
/db-xref="UniProtKB/TrEMBL:Q1MN21"
/translation="MSAIIFDVLPVFILILIGWV
IVRSGLMASNVGEALSEFVFKIAV
PLLLFRTIAEADFHGASPFRLWIVYFSGVAITWT
AGHIAATRLFGRDERIGVLAGVSS
AFANNIFIGLPLVERTVGDEGLVALSILLAVHLP
VMMVAGTVLMEHAERKIAGKSDRS
MVLVLRQIAVNLVRNPLVIGLAAGMAMHLSGLTM
PTTLATVVGQIAGIAGPAALISLG
MALERYGVSGNLGIASVTSSLKLLLLPGCVWAAS
RLLGLSPEWTA AIVLTSSVPTGVN
AWLIANRFGVGHSLAASTITVTALGAITVSLWA
YFLGA"

misc-feature      complement(join(172077. /locus-tag="RL0142"
.172145,172164..172232,
172260..172328,
172347..172415,
172443..172511,
172572..172640,
172668..172727,
172746..172814,
172947..173015))

/inference="protein
motif:TMHMM:2.0"
/note="9 probable transmembrane
helices predicted at aa 21-43,
88-110, 117-136, 146-168,189-211,
221-243, 250-272, 282-304 and
311-333"

misc-feature      complement(172080..1730 /locus-tag="RL0142"
03)

/inference="protein
motif:Pfam:PF03547.6"
/note="Pfam match to entry
PF03547.6 Auxin-eff"

gene              173497..174489 /locus-tag="RL0143"
CDS               173497..174489 /locus-tag="RL0143"

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sequence:INSDC:B97368"
/inference="similar to
sequence:INSDC:BCAJ3322"
/note="similarity:fasta;
with=UniProt:O44015
(EMBL:BCAJ3322); Babesia canis.;
adk; Adenosine kinase.;
length=368; id 29.338; 317 aa
overlap; query 6-313; subject
36-346 similarity:fasta;
with=UniProt:Q8U5P4 (EMBL:B97368);
Agrobacterium tumefaciens (strain
C58/ATCC 33970).; AGR-C-118p.;
length=330; id 82.121; 330 aa
overlap; query 1-330; subject
1-330"

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misc-feature	173581..174456	/locus-tag="RL0143" /inference="protein motif: Pfam:PF00294.10" /note="Pfam match to entry PF00294.10 PfkB"
gene	complement(174482..175021)	/locus-tag="RL0144"
CDS	complement(174482..175021)	/locus-tag="RL0144"
		/inference="similar to sequence:INSDC:A97368" /note="similarity:fasta; with=UniProt:Q8UJ60 (EMBL:A97368); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0078.; length=200; id 73.889; 180 aa overlap; query 1-179; subject 24-200 Similar, but truncated at the N-terminus, to Agrobacterium tumefaciens (strain C58/ATCC 33970) Hypothetical protein Atu0078 (200 aa)" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05633.1" /db-xref="GI:115254559" /db-xref="UniProtKB/TrEMBL:Q1MN19" /translation="MRSKVLKSLALAIALAASM GSVEFAHAQAAGKPSGLPLPRFVT LKSKRVNLRIGPGTDYAVSWMYLKSGLPVEIIQE YDNWRRIRDADGTEGWVNQSLLSG QRAAIAAPWMKTKGKIYVNLRRQAQPSASIVAK LEPGVMLTIGECNGDWCRAESDGA SGWVAQSEIWGAYPGEAFK"
misc-feature	complement(174485..174910)	/locus-tag="RL0144" /inference="protein motif: Pfam:PF06347.1" /note="Pfam match to entry PF06347.1 DUF1058"



sig-peptide	complement(174934..175021)	/locus-tag="RL0144"
		/inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0144 by SignalP 2.0 HMM (Signal peptide probabiltiy 1.000) with cleavage site probability 0.446 between residues 28 and 29"
gene	175207..176208	/gene="gyaR" /locus-tag="RL0145"
CDS	175207..176208	/gene="gyaR" /locus-tag="RL0145" /EC-number="1.1.1.26" /inference="similar to sequence:INSDC:AB033995" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:GYAR-THELI (EMBL:AB033995); Thermococcus litoralis.; gyaR; Glyoxylate reductase (EC 1.1.1.26) (Glycolate reductase).; length=331; id 46.364; 330 aa overlap; query 6-329; subject 2-321 similarity:fasta; with=UniProt:Q92T15 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE HYDROXYACID DEHYDROGENASE PROTEIN (EC 1.1.1.-).; length=334; id 86.787; 333 aa overlap; query 1-333; subject 1-333" /codon-start=1 /transl-table=11 /product="putative glyoxylate reductase" /protein-id="CAK05634.1" /db-xref="GI:115254560" /db-xref="GOA:Q1MN18" /db-xref="UniProtKB/TrEMBL:Q1MN18" /translation="MTAKKKPKVYITRKLPDAVE TRMRELFDAELNIDDAPRSVPELI AAVKTADVLVPTVTDRIDAAALIEQAGPQMKLIA FSNGTDHIDVEAAARKGITVTNTP NVLTEDTADMTMALILAVPRRLGEGARVLTDPKG EWAGWSPTWMLGRRIHGKRIGIVG MGRIGTAVARRAKAFGLSIHYHNRKRVNPAVEDE LEATYWESLDQMLARVDIVSVNCP STPATFHLISARRLALLQPTAYLVNTARGDVVDE AALIKCLREGRIAGAGLDVFENEP AVNPRLIKLANEGKVVLPHMSSATIEGRIDMGD KVIINIRTFIDGHRPPNRVLPGR"
misc-feature	175225..175515	/gene="gyaR" /locus-tag="RL0145" /inference="protein motif:Pfam:PF00389.14" /note="Pfam match to entry PF00389.14 2-Hacid-dh"
misc-feature	175531..176094	/gene="gyaR"

		/locus-tag="RL0145" /inference="protein motif: Pfam: PF02826.5" /note="Pfam match to entry PF02826.5 2-Hacid-dh-C"
gene	complement(176222..176710)	/locus-tag="RL0146"
CDS	complement(176222..176710)	/locus-tag="RL0146"  /inference="similar to sequence: INSDC: SME591782" /note="similarity: fasta; with=UniProt: Q92T05 (EMBL: SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE ACETYLTRANSFERASE PROTEIN (EC 2.3.1.-).; length=156; id 62.821; 156 aa overlap; query 1-156; subject 1-156" /codon-start=1 /transl-table=11 /product="putative acetyltransferase" /protein-id="CAK05635.1" /db-xref="GI:115254561" /db-xref="GOA: Q1MN17" /db-xref="UniProtKB/TrEMBL: Q1MN17" /translation="MRIVPLDQTFTRWDELLALI LSAFASMNGRIDPPSSALKLTTAS LAEKAGTEIGHVAIDGEKLIGCLFLRPEADCLYV GKLA VLPEVQGKGLGKRL LALAE TAAALDLPALRLETRIELTDNHAVFAAWGFCRTA EKAHPGFARTTFVEMRKVLAPPIC VA"
misc-feature	complement(176312..176548)	/locus-tag="RL0146"
		/inference="protein motif: Pfam: PF00583.9" /note="Pfam match to entry PF00583.9 Acetyltransf-1"
gene	complement(176707..177531)	/locus-tag="RL0147"
CDS	complement(176707..177531)	/locus-tag="RL0147"  /inference="similar to sequence: INSDC: AE007949" /inference="similar to sequence: INSDC: HS53223" /note="similarity: fasta; with=UniProt: O54307 (EMBL: HS53223); Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).; moeB; MPT-synthase sulfurylase.; length=391; id 48.770; 244 aa overlap; query 21-264; subject 11-247 similarity: fasta; with=UniProt: Q7D290 (EMBL: AE007949); Agrobacterium tumefaciens (strain C58/ATCC 33970).; AGR-C-111p.; length=285; id 75.836; 269 aa overlap; query

		2-266; subject 13-281"
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		/db-xref="UniProtKB/TrEMBL:Q1MN16"
		/translation="MTEAAFPGVGRHDNIGAMEP LSPEEIARYHRHILLPEIGGAGQQ KLKAARVLVIGAGGLGAPVLQYLAAAGVGTGLGIV DDDRVSLSNLQRQVIHDSGTIGEL KTESAFAIARLNPHVRLIRFEERFSPEAARRQL SGFDLLIDGSDNFDTRYAAADAAD EARIPLVTGAVGRFDGSLTVLKPYETAEDGTPNP RYRDLFPEAPPAGLIPACAEAGII GALTGVIGTMMAMEAIKLVTGIGEPLVGRLLLYD ALSARFDTIRYKRRRTTQRQAG"
misc-feature	complement(176713..176961)	/locus-tag="RL0147"
		/inference="protein motif: Pfam:PF05237.1" /note="Pfam match to entry PF05237.1 MoeZ-MoeB"
misc-feature	complement(176989..177393)	/locus-tag="RL0147"
		/inference="protein motif: Pfam:PF00899.8" /note="Pfam match to entry PF00899.8 ThiF"
gene	complement(177528..178652)	/gene="recF"
		/locus-tag="RL0148"
CDS	complement(177528..178652)	/gene="recF"
		/locus-tag="RL0148" /inference="similar to sequence: INSDC:AF008187" /note="similarity: fasta; with=UniProt:RECF-RHIME (EMBL:AF008187); Rhizobium meliloti (Sinorhizobium meliloti).; recF; DNA replication and repair protein recF.; length=374; id 75.000; 372 aa overlap; query 1-372; subject 1-372" /codon-start=1 /transl-table=11 /product="putative DNA replication and repair protein" /protein-id="CAK05637.1" /db-xref="GI:115254563" /db-xref="GOA:Q1MN15" /db-xref="UniProtKB/TrEMBL:Q1MN15" /translation="MPHKVLSRLKLTDFRNYAA AALALDGRHAVLTGDNGAGKTNLM EAVSLLSPGRGLRRAAYGDITRVGAAGGFSIFAA LDGMEGDVEIGTGIETGEETTARK LRINGTTAKTADELTDHLRLLWLTTPAMDGLFTGA SSDRRRFLDRLVLSLDPAHGRRAS"

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DFERAMRSRNKLLDEGRFDPSWLAGIEEQMASLG
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SPFPSASLQLSGFMDGQFSRPSVDLEDDYAAMLA
ESRYRDAGAGRTLLEGPHRADLIVH
HREKAMEAERCSTGEQKALLVGLVLAHARLVGNL
TGHAPILLLLDEIAAHLDEGRRAAL
FDLIDGLGGQAFMTGTDRAMFSALGDKAQFFTVA
DGRVFE"
misc-feature    complement(178509..1786 /gene="recF"
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                /inference="protein
motif: Pfam: PF02463.6"
                /note="Pfam match to entry
PF02463.6 SMC-N"
gene            179034..179399 /locus-tag="RL0149"
CDS             179034..179399 /locus-tag="RL0149"
                /inference="similar to
sequence: INSDC: AP005937"
                /inference="similar to
sequence: INSDC: SME591783"
                /note="similarity: fasta;
with=UniProt: Y410-RHIME
(EMBL: SME591783); Rhizobium
meliloti (Sinorhizobium
meliloti).; Putative HTH-type
transcriptional regulator R00410.;
length=139; id 42.609; 115 aa
overlap; query 2-111; subject
8-116 similarity: fasta;
with=UniProt: Q89WA2
(EMBL: AP005937); Bradyrhizobium
japonicum.; B110790 protein.;
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transcriptional regulator"
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                /db-xref="UniProtKB/TrEMBL:Q1MN14"
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RVSQLELGEALGLTFQQIQKYEKG
ANRVSASKLHQIAVFLDVDISALFEGAGMSPFGS
RVELSPDAYALALS YDKLNSPAGK
EAVKTIIVTLMTGESAETTA"
misc-feature    179070..179234 /locus-tag="RL0149"
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motif: Pfam: PF01381.9"
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PF01381.9 HTH-3"
gene            complement(179558..1797 /locus-tag="RL0150"
58)
CDS             complement(179558..1797 /locus-tag="RL0150"
58)
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sequence: INSDC: SME591784"
                /note="similarity: fasta;
with=UniProt: Q92S48
(EMBL: SME591784); Rhizobium

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		meliloti (Sinorhizobium meliloti).; Hypothetical protein SMc02277.; length=70; id 33.333; 60 aa overlap; query 1-60; subject 1-58; hypothetical protein smc02277" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05639.1" /db-xref="GI:115254565" /db-xref="UniProtKB/TrEMBL:Q1MN13" /translation="MAPAFSSQSEDVDVLAGAIY TWCAERNIKLRSQQGLSIASIAID LYHAGHQTQDDLLMALHECELH"
gene	complement(180070..181197)	/gene="dnaJ"
CDS	complement(180070..181197)	/locus-tag="RL0151" /gene="dnaJ" /locus-tag="RL0151" /inference="similar to sequence:INSDC:I39586" /note="similarity:fasta; with=UniProt:DNAJ-AGRT5 (EMBL:I39586); Agrobacterium tumefaciens (strain C58/ATCC 33970).; dnaJ; Chaperone protein dnaJ.; length=377; id 91.534; 378 aa overlap; query 1-375; subject 1-377" /codon-start=1 /transl-table=11 /product="putative chaperone protein" /protein-id="CAK05640.1" /db-xref="GI:115254566" /db-xref="GOA:Q1MN12" /db-xref="UniProtKB/TrEMBL:Q1MN12" /translation="MAKADFYETLGVAKSADKE LKSAFRKLAMKYHPDKNPDDKDAE RKFKEINEAYEMLKDPQKRAAYDRYGHAAFEHGG MGGGGGGFAGGGFSDIFEDIFGEM MGGGRARQRSSGGRERGADLRNMEITLEESFSG KTAQIRVPTSITCDVCSGSGAKPG TQPKNCGTCQGTGRVRAAQGFFSIERTCPTCHGR GQIIPDPCPKCHGQGRVTEERSLS VNIPAGIEDGTRIRLQGEAGEAGRGPGAGDLYIF LSVKPHEFYQRDGADLYCAVPISM TTAALGGTFDVATLDGTSRVTVPGETQVGKQFR LKGKGMPLVRSVQTGDLYIQIQIE TPQKLTKRQRELLQEFELSSKENNPSTGFFAR MKEFFEG"
misc-feature	complement(180145..180513)	/gene="dnaJ" /locus-tag="RL0151" /inference="protein motif: Pfam:PF01556.7" /note="Pfam match to entry PF01556.7 DnaJ-C"
misc-feature	complement(180550..1807	/gene="dnaJ"

92)

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		/note="Pfam match to entry
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		/note="Pfam match to entry
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		dnaK (Heat shock protein 70) (Heat
		shock 70 kDa protein) (HSP70).;
		length=Heat sh ( 633; id 93.103;
		638 aa overlap; query 1-638;
		subject 1-633 similarity: fasta;
		with=UniProt: DNAK-RHILE
		(EMBL: RLDNAKJ); Rhizobium
		leguminosarum.; dnaK; Chaperone
		protein dnaK (Heat shock protein
		70) (Heat shock 70 kDa protein)
		(HSP70).; length=Heat sh ( 638; id
		96.708; 638 aa overlap; query
		1-638; subject 1-638"
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		/transl-table=11
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		GGGTFDISILEIGDGVFEVKSTNG
		DTFLGGEDFDMRLVEYLVGEFKRDNGIDLKNDKL
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		TIAPCKAALKDAGVTAAEIDEVVL
		VGGMSRMPKVQEVVKQLFGKEPHKGVNPDEVVAL

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gene	complement(183536..185872)	/locus-tag="RL0153"
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CDS               complement(186083..1863 /locus-tag="RL0154"
04)
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sig-peptide       complement(186247..1863 /locus-tag="RL0154"
04)
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                  /note="Signal peptide predicted
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                  with cleavage site probability
                  0.712 between residues 18 and 19"
gene              complement(186908..1875 /locus-tag="RL0155"
58)
CDS               complement(186908..1875 /locus-tag="RL0155"

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58)

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meliloti).; Hypothetical protein.;
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overlap; query 1-200; subject
14-204"
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0.995 between residues 23 and 24"
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21)
CDS complement(187564..1878 /locus-tag="RL0156"
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misc-feature complement(187990..189312)

/locus-tag="RL0157" /inference="protein motif: Pfam:PF01546.12" /note="Pfam match to entry PF01546.12 Peptidase-M20"

gene 189588..191972  
CDS 189588..191972

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with=UniProt:Q7WYW5  
 (EMBL:AY323811); Pseudomonas  
 putida.; MorA.; length=1282; id  
 38.889; 522 aa overlap; query  
 261-760; subject 742-1263  
 similarity:fasta;  
 with=UniProt:Q8U728  
 (EMBL:HS161255); Agrobacterium  
 tumefaciens (strain C58/ATCC  
 33970).; GGDEF family protein.;  
 length=779; id 49.935; 773 aa  
 overlap; query 1-765; subject  
 1-766"  
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 VARLGGDEFATIQLAGQQPAAQK  
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                     189825..189893,  
                     189930..189989,  
                     190017..190085,  
                     190119..190187,  
                     190230..190298)

/inference="protein  
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gene	complement(192083..192499)	/locus-tag="RL0159"
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misc-feature	complement(192107..192418)	/locus-tag="RL0159"  /inference="protein motif: Pfam: PF01047.8" /note="Pfam match to entry PF01047.8 MarR"
gene	192994..196044	/gene="polA" /locus-tag="RL0160"
CDS	192994..196044	/gene="polA" /locus-tag="RL0160" /EC-number="2.7.7.7" /inference="similar to sequence: INSDC: U86403" /note="similarity: fasta;

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 KRRET  
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 LDLDALVLEPQNGPKLIGFLKTMEFTTLTR  
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 TA  
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gene	196319..198664	/locus-tag="RL0161"
CDS	196319..198664	/locus-tag="RL0161" /inference="similar to sequence: INSDC: A64828" /inference="similar to sequence: INSDC: C96030" /note="Codons 60 to the C-terminus are similar to codons 650 to the C-terminus of Escherichia coli. ftsK FTSK-ECOLI (EMBL: A64828) ( DNA translocase ftsK.), and codons 180 to the C-terminus are similar to Rhizobium meliloti (Sinorhizobium meliloti). Putative cell division protein FtsK like protein. Q92TK5 (EMBL: C96030) (611) similarity: fasta; with=UniProt: FTSK-ECOLI (EMBL: A64828); Escherichia coli.; ftsK; DNA translocase ftsK.; length=1329; id 43.490; 722 aa overlap; query 63-775; subject 649-1324 similarity: fasta; with=UniProt: Q92TK5 (EMBL: C96030); Rhizobium meliloti (Sinorhizobium meliloti).; Putative cell division protein FtsK like protein.; length=611; id 79.500; 600 aa overlap; query 187-779; subject 6-600" /codon-start=1 /transl-table=11 /product="putative cell division DNA translocase protein" /protein-id="CAK05650.1" /db-xref="GI: 115254576" /db-xref="GOA: Q1MN02" /db-xref="UniProtKB/TrEMBL: Q1MN02" /translation="MRFPRTNLT DAGDFSSEIET DLPEENPGEKPA APIWQSNFSLAP NVRFT RTPETLISR RAPNEPVRDDSQIGQQAIR IEPVAVDVPFDIYLPEPDEISAAP QRIELQQSPLLDEAAAPAFRASAE LSSISDFAFV EVMAFEEAEPVRAPPLISFPKTET SPESITSLFRIMEWRPGRPAPAQVVS RPAPQPAA VSAKVAVRPAA AISLEKPRRIAVE APVMLAPQAAPTPQLAPAPHIASAPQAAPAPQRT PPVA AVLPSRLAARPEKIDASGY EFP PRALLQEPPERLGEIMSQETLEQNAGLLESV

		LEDFGIKGEIIHVRPGPVVTLYEF EPAPGVKSSRVIGLADDIARSMSALSARVAVVPG RNVIGIELPNVTRETIVYFREMIES QDFEKSgyKLALGLGKTIGGEPVIAELAKMPHLL VAGTTGSGKSVAINTMILSLLYRM TPEQCRLIMVDPKMLELSVYDGIPHLLTPVVTDP KKAVMALKWAVREMEERYRKMSRL GVRNIDGYNDRVAQAREKGETIHVMVQVGFDKGT GTPIEESQALDLTPMPYIVVIVDE MADLMMVAGKDIEGAIQRLAQMARAAAGIHLIMAT QRPSVDVITGTIKANFPTRISFQV TSKIDSRTILGEQGAEQLLGQGDMLHMQGGGRIS RVHGPFVSDVEVEKVVAHLKTQGR PEYLDTVTADEEEETEETEEAGAVFDKSAMASEDG NELYEQAVKVVMRDKKCSTSYIQR RLGIGYNRAASLVERMEKEGLVGPNHVGKREIV SGRGDGE"
misc-feature	197471..198133	/locus-tag="RL0161" /inference="protein" motif: Pfam: PF01580.8" /note="Pfam match to entry PF01580.8 FtsK-SpoIIIE"
gene	complement(198700..199203)	/locus-tag="RL0162"
CDS	complement(198700..199203)	/locus-tag="RL0162"  /inference="similar to sequence: INSDC: AE011062" /inference="similar to sequence: INSDC: BF39410" /note="similarity: fasta; with=UniProt: GRPB-BACPF (EMBL: BF39410); Bacillus pseudofirmus.; grpB; Glutamate-rich protein grpB.; length=174; id 28.395; 162 aa overlap; query 4-158; subject 9-169 similarity: fasta; with=UniProt: Q8TK81 (EMBL: AE011062); Methanosarcina acetivorans.; Hypothetical protein MA3535.; length=186; id 38.509; 161 aa overlap; query 4-161; subject 21-181" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05651.1" /db-xref="GI: 115254577" /db-xref="UniProtKB/TrEMBL: Q1MN01" /translation="MRAIKVVDYDPSWPRLFAEI SAEVSALLGDRLLSIDHIGSTSV GLAAKPKIDLAAVMISDAFLPAAIEIVRAADFVF HGDTGEQRWAFTRDHDGYGFRLYL CGPDNRAHRGRILFRDYLRNHPERAKAYADLKRR LAEEADDDWDFYTGGKTDVSETV RLAALKT"
misc-feature	complement(198715..199203)	/locus-tag="RL0162"  /inference="protein" motif: Pfam: PF04229.3" /note="Pfam match to entry

		PF04229.3 UPF0157"
gene	complement(199223..199819)	/gene="phnN"
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CDS	complement(199223..199819)	/gene="phnN"
		/locus-tag="RL0163"
		/inference="similar to sequence:INSDC:B97379"
		/inference="similar to sequence:INSDC:HSPD32662"
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		/codon-start=1
		/transl-table=11
		/product="putative ATP-binding phosphonate metabolism protein"
		/protein-id="CAK05652.1"
		/db-xref="GI:115254578"
		/db-xref="GOA:Q1MN00"
		/db-xref="UniProtKB/TrEMBL:Q1MN00"
		/translation="MMSHEPHAGAGAERGTMVVV VGPSGAGKDTLMNLAARRFKGRED VHFVRRVITRHRDAGGEDHLSVSLQGFAAMEQSG SFAVWWEAHGLKYGIPAEISVALS KGHIVVANGSRSAHHRFQAAPRLKVINVTARPE VLAGRLETRGRETHEDIMARLARG PLTVRGEYDVVELDNSGSLEAEQKMIEILNGLL TKTP"
gene	complement(199816..200988)	/gene="phnM"
		/locus-tag="RL0164"
CDS	complement(199816..200988)	/gene="phnM"
		/locus-tag="RL0164"
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		/inference="similar to sequence:INSDC:RME591985"
		/note="similarity:fasta; with=UniProt:PHNM-ECOLI (EMBL:ECPHN); Escherichia coli.; phnM; PhnM protein.; length=378; id 47.340; 376 aa overlap; query 17-389; subject 2-377 similarity:fasta; with=UniProt:Q92V74 (EMBL:RME591985); Rhizobium meliloti (Sinorhizobium meliloti).; Putative enzyme protein.; length=379; id 76.781;



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379 aa overlap; query 12-390;
subject 1-379"
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metabolism protein"
/protein-id="CAK05653.1"
/db-xref="GI:115254579"
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TTVFDCLRMGADE DGGFEHGEMREMADAIQSAET
EGRLRAEHLIHLRCEVSADNVLEH
FADFESDRHVR LVSLMDHAPGQRQFQTMDQYIFY
YQKKRGLSDEAFARFVAKRQAESA
RNSTPHRNAIAKVCAERGITVASHDDATLSHVDE
AIDNGVRLAEFPTSFDAARASHEH
GMSVLMGAPNIVRGKSHSGNIAARDLAEMGVLDV
LSSDYVPLSLLHAPFILADEVESI
SLPKAIAMVTSTPARTVSLDDRGRIATGLRADLV
RVHRSHGVPVTRSVWRQGRRVA"
misc-feature    complement(199876..2008 /gene="phnM"
14)
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                /inference="protein
motif: Pfam: PF01979.7"
                /note="Pfam match to entry
PF01979.7 Amidohydro-1"
gene            complement(200969..2016 /locus-tag="RL0165"
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CDS             complement(200969..2016 /locus-tag="RL0165"
64)
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sequence: INSDC: AE008991"
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with=UniProt: Q8UIX1
(EMBL: AE008991); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; Hypothetical protein
Atu0170.; length=232; id 59.292;
226 aa overlap; query 1-226;
subject 4-222"
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                /transl-table=11
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protein"
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M
TVAEDFARRTQAFEIPELVLGQLG
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TDMARRNPEKLSDSQRAHLKRWGY
PYVMEDFGFHMTLSGQVPETRAEVMKAILTERFA
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KVHSWLPLAGAKS"
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64)

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gene	complement(201786..203138)	
CDS	complement(201786..203138)	/locus-tag="RL0166" /gene="phoT"  /locus-tag="RL0166" /inference="similar to sequence: INSDC: AE007958" /inference="similar to sequence: INSDC: HSH95946" /note="similarity: fasta; with=UniProt: Q52909 (EMBL: HSH95946); Rhizobium meliloti (Sinorhizobium meliloti).; phoT; PhoT (Phosphate uptake ABC transporter permease protein).; length=Phosphate uptake ABC transpor ( 505; id 49.105; 503 aa overlap; query 1-447; subject 1-503 similarity: fasta; with=UniProt: Q8UIX0 (EMBL: AE007958); Agrobacterium tumefaciens (strain C58/ATCC 33970).; phnE; ABC transporter, membrane spanning protein (AGR-C-284p).; length=449; id 70.667; 450 aa overlap; query 1-450; subject 1-449" /codon-start=1 /transl-table=11 /product="putative permease component of phosphate uptake ABC transporter protein" /protein-id="CAK05655.1" /db-xref="GI:115254581" /db-xref="GOA:Q1MMZ7" /db-xref="UniProtKB/TrEMBL:Q1MMZ7" /translation="MSSVPTINAAERERLLSAYP DVFHRSFMQRWGLLLISAAVFVYL AFCFAFFNVIPTFVNGNWDRAAIYVQDWYSWRAQ PRLRFQNDQVVPQWTSRRQYPEGA DINWLKPNADGSRYTIVTFGSDGDRMEVTPSRVDV YIDGKLYPVTITHDRASLPSDAPA RMQQDDNKVNVYYGFAGQAEIRTNQVYIQRRFLG WANFFFDTHSPFWGRSLPEVVGLM FSGERLDPNQSNASLALDNFLNNASWQHGDILSK LMQTLVMAFVGTLFGTLVAFPLAF IAARNIMRSRAANWGKRLFDLRSIDMLIWALF FTRAFGPGPLPGIAAIFFTDTGAL GKVYAEALENIDDKQREGVRSVGAAPVAVQRYGV IPQVLPVFISQSLYFWESNTRSAT AIGAVGAGGIGLKLLESMKTNSDWDK VAYMVLII LLVVFAFDNLSNALRSRVMGKKGH
misc-feature	complement(201801..202382)	/gene="phoT"  /locus-tag="RL0166" /inference="protein motif: Pfam: PF00528.10"

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                                .201884,202155..202223,
                                202302..202370,
                                202977..203045))

                                /locus-tag="RL0166"
                                /inference="protein
                                motif:TMHMM:2.0"
                                /note="4 probable transmembrane
                                helices predicted at aa 32-54,
                                257-279, 306-328 and 419-441"
gene            complement(203138..2041 /gene="phoE"
                                18)

                                /locus-tag="RL0167"
CDS             complement(203138..2041 /gene="phoE"
                                18)

                                /locus-tag="RL0167"
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                                sequence:INSDC:AE008991"
                                /note="similarity:fasta;
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                                Rhizobium meliloti (Sinorhizobium
                                meliloti).; phoE; PhoE (Phosphate
                                uptake ABC transporter permease
                                protein).; length=Phosphate uptake
                                ABC transpor ( 320; id 59.683; 315
                                aa overlap; query 9-323; subject
                                6-320 similarity:fasta;
                                with=UniProt:Q8UIW9
                                (EMBL:AE008991); Agrobacterium
                                tumefaciens (strain C58/ATCC
                                33970).; phnE; ABC transporter,
                                membrane spanning protein.;
                                length=328; id 81.620; 321 aa
                                overlap; query 6-326; subject
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                                transporter"
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                                /db-xref="GOA:Q1MMZ6"
                                /db-xref="UniProtKB/TrEMBL:Q1MMZ6"
                                /translation="MAHSAGADSLSGLQEGSRTI
                                LDHYQSQVRTRRIYTVVSIVVFLI
                                ILGASLDFANSANSKGKFFERLPYFFDFMKSFVDP
                                SPLEIFRAMFDLPSPFSDGSIKYD
                                YTSDRVWITDSFYIPNFFYQLAITLNIAIVSTIL
                                GASGAFLLCFFASTNLVGAGVTRW
                                VVRRIMEIMRAFPEIVVAGLLAAILSIGPISAI
                                AVVWHTVGALGKLFFEVENADMK
                                PDEGLRAAGAGWLERVRFALPQVLPNFVSYTLL
                                RTEINVRASTIIIGAVGGGGIGEVF
                                SLSIGRDHAAKTYAIIILLITVICVDQFSAWLR
                                RRLIGKQSFEEFGQGA"
misc-feature    complement(203174..2037 /gene="phoE"
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misc-feature	complement(join(203192.. 203251,203285..203353, 203528..203596, 203633..203701, 203711..203779, 203954..204022))	
		/locus-tag="RL0167" /inference="protein motif: TMHMM: 2.0" /note="6 probable transmembrane helices predicted at aa 33-55, 114-136, 140-162, 175-197,256-278 and 290-309"
gene	complement(204187..2051 10)	/gene="phoD"
CDS	complement(204187..2051 10)	/locus-tag="RL0168" /gene="phoD"
		/locus-tag="RL0168" /inference="similar to sequence: INSDC: B95947" /inference="similar to sequence: INSDC: HS379248" /note="similarity: fasta; with=UniProt: Q52907 (EMBL: B95947); Rhizobium meliloti (Sinorhizobium meliloti).; phoD; PhoD precursor (Phosphate uptake ABC transporter periplasmic solute- binding protein).; length=Phosphate uptake AB ( 301; id 60.000; 300 aa overlap; query 8-307; subject 2-301 similarity: fasta; with=UniProt: Q8UIW8 (EMBL: HS379248); Agrobacterium tumefaciens (strain C58/ATCC 33970).; phnD; ABC transporter, substrate binding protein (AGR-C-288p).; length=301; id 74.000; 300 aa overlap; query 8-307; subject 2-301" /codon-start=1 /transl-table=11 /product="putative solute-binding component of phosphate uptake ABC transporter" /protein-id="CAK05657.1" /db-xref="GI:115254583" /db-xref="GOA: Q1MMZ5" /db-xref="UniProtKB/TrEMBL: Q1MMZ5" /translation="METSMSAFRKILMATIAVAA LAGNAAAQDVKVLRIGLDGGGENA DQVRRTECVKPLIAATGVSEVQLFPPNYNGVI QGLLGGTIDLAVMGAASYAAIYIK DPNAVTPVLTTKQADGSTGYYSIMVARKDSGIKT LADAKGKKLGFADPDSTSGYLVPN VALPKDTGAPVKQYFSETGFGGGHENLVLGVLDK

KFDVGTTFGSGQGDWAQGYSSGNL  
 HQMVTKGLLDMD DIVEVWKSPLIPNGPLMVSQKL  
 PADLQKKVTTYFAELPKTDKSCFE  
 SFTGGGYVDWVPVDQSFYQTIIDARKAVIGG"

gene complement(205369..2064 /locus-tag="RL0169"  
 36)

CDS complement(205369..2064 /locus-tag="RL0169"  
 36)

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 (EMBL:AE016960); Coxiella  
 burnetii.; Transposase for  
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 IS1111A.; length=339; id 26.706;  
 337 aa overlap; query 9-337;  
 subject 7-335 similarity:fasta;  
 with=UniProt:Q6LB66  
 (EMBL:OCA82447); Oligotropha  
 carboxidovorans (Pseudomonas  
 carboxydovorans).; Transposase  
 ISC1190.; length=300; id 87.667;  
 300 aa overlap; query 57-355;  
 subject 1-300; transposase for  
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 is1111a"  
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 LAHLLRADLVPEAWAPSESRDLRVALRERMFYV  
 RLRTMTKNRIVTVFDRYPEQTAQL  
 KKLGD LFGKAGRVQLAQVNVSEIDRIQIDRGLAF  
 IGDIDMRIKQSEATIRAMTKANAN  
 VKLLKTIPGIGEFFARLIDAEIDDISRFRH  
 SKKL  
 AAYAGLVPSTHSSGGKTFHGKIIK  
 QGNKWLRFVFAVAPAIASDPQLRAQYEH  
 LKIK  
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 RAYEPRGESTMEGASTISRLS"

misc-feature complement(205525..2058 /locus-tag="RL0169"  
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gene complement(206639..2074 /gene="phoC"  
 84)

CDS complement(206639..2074 /gene="phoC"  
 84)

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(EMBL:RM59229); Rhizobium meliloti
(Sinorhizobium meliloti).; phoC;
PhoC.; length=270; id 80.695; 259
aa overlap; query 2-260; subject
1-256 similarity:fasta;
with=UniProt:Q8UIW7 (EMBL:A97380);
Agrobacterium tumefaciens (strain
C58/ATCC 33970).; phnC; ABC
transporter, nucleotide
binding/ATPase protein.;
length=290; id 83.846; 260 aa
overlap; query 1-260; subject
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transporter"
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MAGGRVVFDDGKPSeltaEAVKEIYGTDKDGAGID
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misc-feature complement(206819..2074
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/locus-tag="RL0170"
/inference="protein
motif:PFam:PF00005.11"
/note="Pfam match to entry
PF00005.11 ABC-tran"
gene complement(207600..2082
17) /locus-tag="RL0171"
CDS complement(207600..2082
17) /locus-tag="RL0171"
/inference="similar to
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/inference="similar to
sequence:INSDC:B97380"
/note="similarity:fasta;
with=UniProt:CAT4-ECOLI
(EMBL:AF047479); Escherichia
coli.; catB2; Chloramphenicol
acetyltransferase (EC 2.3.1.28).;
length=210; id 39.053; 169 aa
overlap; query 23-188; subject
26-190 similarity:fasta;
with=UniProt:Q8UIW6 (EMBL:B97380);

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Agrobacterium tumefaciens (strain
C58/ATCC 33970).;
Acetyltransferase (AGR-C-291p).;
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WRRANRVTIGNDVWIGHGATILPGVSVGNNAVIG
AGAVVSKDVAPYTI VGGVPAKLIR
ERFPREVGGERMDRLSWWDWEHDLRQALEDFRNL
DAEDFLSRYGG"
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42)
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96)
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motif: Pfam:PF00132.9"
/note="Pfam match to entry
PF00132.9 Hexapep"
misc-feature      complement(208008..2080 /locus-tag="RL0171"
61)
/inference="protein
motif: Pfam:PF00132.9"
/note="Pfam match to entry
PF00132.9 Hexapep"
misc-feature      complement(208110..2081 /locus-tag="RL0171"
63)
/inference="protein
motif: Pfam:PF00132.9"
/note="Pfam match to entry
PF00132.9 Hexapep"
gene              complement(208214..2089 /locus-tag="RL0172"
21)
CDS               complement(208214..2089 /locus-tag="RL0172"
21)
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sequence: INSDC:HSH96023"
/note="similarity: fasta;
with=UniProt: AAR91740; length=234;
id 56.828; 227 aa overlap; query
1-227; subject 1-227
similarity: fasta;
with=UniProt: Q92TQ1
(EMBL:HSH96023); Rhizobium
meliloti (Sinorhizobium
meliloti).; Putative phosphonate
uptake ABC transporter ATP-binding

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subject 1-235"
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component of phosphate uptake ABC
transporter"
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/translation="MATPLVVSEVSKSFTMHLRD
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LASIDPRTVLNVRRNTLGYVSQFL
RTVPRVAAIDVVAEPLVARGEDAVTAREKAGALL
ARLNLPETLWQLPPATFSGGEQQR
VNIARGFITEHTILLLLDEPTASLDARNRAVVVGM
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13)

/inference="protein
motif:Pfam:PF00005.11"
/note="Pfam match to entry
PF00005.11 ABC-tran"
gene            complement(208948..2097 /gene="phnK"
24)

/locus-tag="RL0173"
CDS             complement(208948..2097 /gene="phnK"
24)

/locus-tag="RL0173"
/inference="similar to
sequence:INSDC:ECPHN"
/inference="similar to
sequence:INSDC:RME591985"
/note="similarity:fasta;
with=UniProt:PHNK-ECOLI
(EMBL:ECPHN); Escherichia coli.;
phnK; Phosphonates transport
ATP-binding protein phnK.;
length=252; id 68.235; 255 aa
overlap; query 3-257; subject
2-251 similarity:fasta;
with=UniProt:Q52988
(EMBL:RME591985); Rhizobium
meliloti (Sinorhizobium
meliloti).; phnK; PhnK protein
(Putative phosphonate uptake ABC
transporter ATP-binding protein).;
length=Putative phosphonate ( 258;
id 89.535; 258 aa overlap; query
1-258; subject 1-258"
/codon-start=1
/transl-table=11
/product="putative ATP-binding
component of phosphate uptake ABC
transporter"
/protein-id="CAK05662.1"
/db-xref="GI:115254588"
/db-xref="GOA:Q1MMZ0"

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		/db-xref="UniProtKB/TrEMBL:Q1MMZ0" /translation="MSDTPLLKVHDSKFGNRI GCRDVSFELWPGEVLAIVGESGSG KTTLLNCLSTRLLPSTGSVEYHMRDGSYRDLYRM NEAERRFLMRTDWGFVHQNPADGL RMTVSAGANVGERLMATGDRHYGKIRASAIWLE RVEIDADRIDDQPRAFSGGMRQRL QIARNLVTGPRLVFMDEPTGGLDVSVQARLLDLV RGLVNDLGLSAIIVTHDLAVARLL SHRMMVMKDGIVIEHGLTDRVLDDPREPYTQLLV SSILQV"
misc-feature	complement(209041..209631)	/gene="phnK"  /locus-tag="RL0173" /inference="protein" motif: Pfam: PF00005.11" /note="Pfam match to entry PF00005.11 ABC-tran"
gene	complement(209721..210596)	/gene="phnJ"  /locus-tag="RL0174"
CDS	complement(209721..210596)	/gene="phnJ"  /locus-tag="RL0174" /inference="similar to sequence: INSDC: RME591985" /note="similarity: fasta; with=UniProt: PHNJ-RHIME (EMBL: RME591985); Rhizobium meliloti (Sinorhizobium meliloti).; phnJ; PhnJ protein.; length=297; id 90.722; 291 aa overlap; query 1-291; subject 1-291" /codon-start=1 /transl-table=11 /product="putative phosphonate metabolism protein" /protein-id="CAK05663.1" /db-xref="GI:115254589" /db-xref="GOA:Q1MMY9" /db-xref="UniProtKB/TrEMBL:Q1MMY9" /translation="MTDLASYNFAYLDEQTKRMI RRAILKAIAIPGYQVPFASREMPM PYGWTGGVQVTASIIIGPDDVLKVIDQGADDTTN AVSIRAFFQKVANVAVTHTTKDAT IIQTRHRIPEEKLGVGQVLVYQVPIPEPLRFLEP RETETRKMHALEEYGLMHVKLYED IAHNGRISRITYAYPVKVHGRYVMDPSPTPKFDNP KMHMSDALQLFGAGREKRIYAVPP YTDVVS LDFEDYPFDIQRFDKPCALCGAEDVYLD EVVLDDKGGRMFVCSDTDHCEDRR AHGHAGEMLAREAAE"
misc-feature	complement(209754..210590)	/gene="phnJ"  /locus-tag="RL0174" /inference="protein" motif: Pfam: PF06007.1" /note="Pfam match to entry PF06007.1 PhnJ"
gene	complement(210593..211699)	/gene="phnI"

CDS	complement(210593..211699)	/locus-tag="RL0175" /gene="phnI"  /locus-tag="RL0175" /inference="similar to sequence:INSDC:AE007959" /inference="similar to sequence:INSDC:RME591985" /note="similarity:fasta; with=UniProt:PHNI-RHIME (EMBL:RME591985); Rhizobium meliloti (Sinorhizobium meliloti).; phnI; PhnI protein.; length=368; id 81.351; 370 aa overlap; query 1-368; subject 1-368 similarity:fasta; with=UniProt:Q8UIW2 (EMBL:AE007959); Agrobacterium tumefaciens (strain C58/ATCC 33970).; phnI; Hypothetical protein phnI (AGR-C-299p).; length=369; id 82.656; 369 aa overlap; query 1-368; subject 1-369" /codon-start=1 /transl-table=11 /product="putative phosphonate metabolism protein" /protein-id="CAK05664.1" /db-xref="GI:115254590" /db-xref="GOA:Q1MMY8" /db-xref="UniProtKB/TrEMBL:Q1MMY8" /translation="MYVAVKGGETAIAHRLLA DRRRGDRSLPAIGIDQIVAQLALA VDRVMAEASLFDRTLAALAIRQSRGDMIEAIFLL RAYRTTLPRFGYSRPLDTADMTIE RRISATYKDLPGGQLLGPTFDYTHRLLDPSLLSD EAVETPAQRAAETGRVMRVSEILG EEGLIEADGDMPEDHEIGDLTREPMEFPMTRDLR LQALARGDEGFLLALGYSTQRGYG RNHPFTGEIRIGDVEVEFDVPELGFVSLGTIQI TECQMVNQFKGSAKAPPQFTRGYG LVFGQSERKAMAMSLVDRALRAEELGEDITAPAQ DEEFVISHSDNVQATGFVEHLKLP HYVDFQAELDLVRRMRREFEAAANGGEDMKEAAE "
misc-feature	complement(210632..211699)	/gene="phnI"  /locus-tag="RL0175" /inference="protein motif:Pfam:PF05861.1" /note="Pfam match to entry PF05861.1 PhnI"
gene	complement(211704..212312)	/gene="phnH"
CDS	complement(211704..212312)	/locus-tag="RL0176" /gene="phnH"  /locus-tag="RL0176" /inference="similar to sequence:INSDC:AE007959" /inference="similar to

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sequence:INSDC:RME591985"
/note="similarity:fasta;
with=UniProt:PHNH-RHIME
(EMBL:RME591985); Rhizobium
meliloti (Sinorhizobium
meliloti).; phnH; PhnH protein.;
length=200; id 58.883; 197 aa
overlap; query 1-197; subject
1-197 similarity:fasta;
with=UniProt:Q8UIW1
(EMBL:AE007959); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; phnH; Hypothetical
protein phnH (AGR-C-302p).;
length=203; id 64.677; 201 aa
overlap; query 1-201; subject
2-202"
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/product="putative phosphonate
utilisation protein"
/protein-id="CAK05665.1"
/db-xref="GI:115254591"
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/db-xref="UniProtKB/TrEMBL:Q1MMY7"
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EAGTALSSFGLFASGTQEYPDRSTTLIELAELE
GGRRRLALMGPGIQSVAEIAPIGLP
ETFLRLWTENRALFPRGVDIVLTAGKRFLCLPRT
TKITATEI"
misc-feature    complement(211716..2122 /gene="phnH"
97)

/locus-tag="RL0176"
/inference="protein
motif: Pfam:PF05845.1"
/note="Pfam match to entry
PF05845.1 PhnH"
gene            complement(212312..2127 /gene="phnG"
88)

/locus-tag="RL0177"
CDS             complement(212312..2127 /gene="phnG"
88)

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/inference="similar to
sequence:INSDC:C96023"
/inference="similar to
sequence:INSDC:HS380249"
/note="similarity:fasta;
with=UniProt:PHNG-RHIME
(EMBL:C96023); Rhizobium meliloti
(Sinorhizobium meliloti).; phnG;
PhnG protein.; length=156; id
60.127; 158 aa overlap; query
1-158; subject 1-156
similarity:fasta;
with=UniProt:Q8UIW0
(EMBL:HS380249); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; phnG; Hypothetical

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		protein phnG (AGR-C-303p).; length=153; id 61.589; 151 aa overlap; query 8-158; subject 3-153"
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		/transl-table=11
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		/protein-id="CAK05666.1"
		/db-xref="GI:115254592"
		/db-xref="GOA:Q1MMY6"
		/db-xref="UniProtKB/TrEMBL:Q1MMY6"
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misc-feature	complement (212315..212755)	/gene="phnG"
		/locus-tag="RL0177"
		/inference="protein
		motif: Pfam: PF06754.1"
		/note="Pfam match to entry PF06754.1 PhnG"
gene	212906..213643	/locus-tag="RL0178"
CDS	212906..213643	/locus-tag="RL0178"
		/inference="similar to
		sequence: INSDC: AE007959"
		/note="similarity: fasta;
		with=UniProt: Q8UIV9
		(EMBL: AE007959); Agrobacterium
		tumefaciens (strain C58/ATCC
		33970).; Transcriptional
		regulator, GntR family
		(AGR-C-306p).; length=245; id
		64.490; 245 aa overlap; query
		1-245; subject 1-245"
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		/transl-table=11
		/product="putative GntR family
		transcriptional regulator"
		/protein-id="CAK05667.1"
		/db-xref="GI:115254593"
		/db-xref="GOA:Q1MMY5"
		/db-xref="UniProtKB/TrEMBL:Q1MMY5"
		/translation="MSG LKQVQRQTGVALWRQIA
		DRIREAISNGAYDETGMVPPETML
		ALQFGVNRHTVRSALAALAQEGIVRAVQGRGTLI
		ERKERLNFPI TRRTRFTAGIGDQA
		REMRGLLLEEAKKEEASAEIARWLGLKPGEVIRL
		ETLRQADKRPVSRATSWFPAKRFA
		GIGEAYRTEESITKAF AELGLPDYVRATTEVTAA
		HASAADMADLELTPGAILLI AKAM
		NTDLEGVPVQYSISRFAADRVQFTIEN"
misc-feature	212948..213139	/locus-tag="RL0178"
		/inference="protein
		motif: Pfam: PF00392.9"
		/note="Pfam match to entry
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gene	complement (213683..214318)	/gene="gpmA"

CDS	complement(213683..214318)	/locus-tag="RL0179" /gene="gpmA"  /locus-tag="RL0179" /EC-number="5.4.2.1" /inference="similar to sequence:INSDC:AY074773" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:GPMA-BARHE (EMBL:AY074773); Bartonella henselae (Rochalimaea henselae).; gpmA; 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (EC 5.4.2.1) (Phosphoglyceromutase) (PGAM) (BPG-dependent PGAM) (dPGM).; length=206; id 62.745; 204 aa overlap; query 1-204; subject 1-204 similarity:fasta; with=UniProt:GPMA-RHIME (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; gpmA; 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (EC 5.4.2.1) (Phosphoglyceromutase) (PGAM) (BPG-dependent PGAM) (dPGM).; length=211; id 88.152; 211 aa overlap; query 1-211; subject 1-211; putative 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (Phosphoglyceromutase) (PGAM) (BPG-dependent PGAM) (dPGM)" /codon-start=1 /transl-table=11 /product="2,3-bisphosphoglycerate- dependent phosphoglycerate mutase (phosphoglyceromutase) (pgam) (bpg-dependent pgam) (dpgm)" /protein-id="CAK05668.1" /db-xref="GI:115254594" /db-xref="GOA:Q1MMY4" /db-xref="UniProtKB/TrEMBL:Q1MMY4" /translation="MSGTLVLVRHGQSDWNLKLN FTGWKDPDLTELGIQEANTGGAAL AEYGIKFDVAYTSVLVRAQHTLKLILDKVGQPD LTIRDQALNERDYGDLGSLNKDDA RAKWGEEQVHIWRRSYDVPPPGGESLRDTGARVW PYYLTEILPRVLRGEKVLVAAHGN SLRSLVMVLDKLSREGVLALNLATGVPMVYKLKA DSTVASKEVLGDMSGAH"
misc-feature	complement(213713..214312)	/gene="gpmA"  /locus-tag="RL0179" /inference="protein motif:PFam:PF00300.9" /note="Pfam match to entry PF00300.9 PGAM"
gene	complement(214340..2151)	/gene="dapB"

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			/inference="similar to
			sequence:INSDC:SME591782"
			/note="similarity:fasta;
			with=UniProt:DAPB-ECOLI
			(EMBL:ECAPAH02); Escherichia
			coli.; dapB; Dihydrodipicolinate
			reductase (EC 1.3.1.26) (DHP)
			length=273; id 46.350; 274 aa
			overlap; query 1-273; subject
			1-272 similarity:fasta;
			with=UniProt:DAB1-RHIME
			(EMBL:SME591782); Rhizobium
			meliloti (Sinorhizobium
			meliloti).; dapB;
			Dihydrodipicolinate reductase (EC
			1.3.1.26) (DHP).; length=272; id
			80.074; 271 aa overlap; query
			1-271; subject 1-271"
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			dihydrodipicolinate reductase"
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			/db-xref="GOA:Q1MMY3"
			/db-xref="UniProtKB/TrEMBL:Q1MMY3"
			/translation="MSDAAMKLVVGAAGRMGQT
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			VGKDAGEIAGLGPTGVIIIGDDPLNAFLDAEGVLD
			FTSPAATVEFSGLAQAQARIVHVVG
			TTGCSADDNTKIAAAARHARIVKSGNMSLGVNLL
			SVLAEQAARALDPDDWDIEILEMH
			HKHKVDAPSGTALLIGEAAKGRGIDLASQSVRV
			RDGHTGAREAGTIGFATLRGGSVI
			GEHSVLFAGEGEIVTLSHSAADRSIFARGAIKAA
			LWARDKKPGLYSMLDVLGLSSS"
misc-feature	complement(214355..2147	/gene="dapB"	
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			/locus-tag="RL0180"
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			/note="Pfam match to entry
			PF05173.2 DapB-C"
misc-feature	complement(214778..2151	/gene="dapB"	
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			/locus-tag="RL0180"
			/inference="protein
			motif:PFam:PF01113.9"
			/note="Pfam match to entry
			PF01113.9 DapB-N"
gene	complement(215180..2169	/locus-tag="RL0181"	
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CDS	complement(215180..2169	/locus-tag="RL0181"	
	67)		

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(EMBL:C85617); Escherichia coli.;
msbA; Lipid A export
ATP-binding/permease protein
msbA.; length=582; id 36.380; 558
aa overlap; query 34-587; subject
26-579 similarity:fasta;
with=UniProt:Q92T26
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE ATP-BINDING
ABC TRANSPORTER PROTEIN.;
length=601; id 75.966; 595 aa
overlap; query 1-594; subject
1-594"
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component of ABC transporter"
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KRIIAENGRDHLWGYVFAIACLIV
VALSTAFTAWIMRAIIDEAFANRRADVWIICLS
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DIVARYQRRLYAHLMTLSVGFFSEARSAHIAAQV
SQNVSGIRDVLNLTITSTVRDLLT
FVSL LAVMIIQDPLLSLAVFIMAPPLLYALRYVS
KRLRSATREAVHLNSHVLGAMQET
IQGIAIVKAFTMEEELERKVNKLIKGAESRANRI
ARLSERTSPLTESFAGFAVASVLA
YAAYRSIYFNVPPGAFFSFVTALLLAYDPARRLA
RLQVQMERAVVNARMIYELLDMEP
RQRDLDPARPLTVTQARIEFRNVSFAYGKESVLS
GVSFIAEGGGTTALVGPSGAGKST
VISLIPRFYDPREGEILIDGQDIAHITKKSRLRQQ
LAYVSQQPYLFEGTIRDNIRYGRP
EATDAEVEEAARLAYAHDFISAQPQGYETPVGEN
GVTLSGGQRQLSIARALVRNAPI
LLLDEATSALDTESEAAVQKALDEAMSGRTVVVI
AHLRSTVVRADKIVVMQQGRVVEE
GNHETLAKVSDGLYARLNNLQRPSASDSN"
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39)

/inference="protein
motif: Pfam:PF00005.11"
/note="Pfam match to entry
PF00005.11 ABC-tran"
misc-feature      complement(216050..2168 /locus-tag="RL0181"
65)

/inference="protein
motif: Pfam:PF00664.9"
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misc-feature      complement(join(216062. /locus-tag="RL0181"

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216566..216634,
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helices predicted at aa 32-54,
69-91, 112-134, 168-190 and
283-302"
gene      complement(217115..2181 /gene="glk"
40)

/locus-tag="RL0182"
CDS      complement(217115..2181 /gene="glk"
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/note="similarity:fasta;
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(EMBL:AE005470); Escherichia coli
O157:H7.; glk; Glucokinase (EC
2.7.1.2) (Glucose kinase).;
length=EC 2.7.1.2; id 37.097; 310
aa overlap; query 16-325; subject
6-314 similarity:fasta;
with=UniProt:GLK-AGRT5
(EMBL:C97381); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; glk; Glucokinase (EC
2.7.1.2) (Glucose kinase).;
length=EC 2.7.1.2; id 72.189; 338
aa overlap; query 4-340; subject
6-343"
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/db-xref="UniProtKB/TrEMBL:Q1MMY1"
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TADFATIDEAIIQQGVLDKTAVQPRSAI LAVAGPI
NDDEIPLTNCDWVVRPKTMIEGLG
MEDVLVVNDFEAQALAI AALSDENRERIGDATRD
MIASRVVLGPGTGLGVGGLVHAQH
SWIPVPGEGGHVDLGPRSKRDYDIFPHIETIEGR
VSAEQILCGRGLVNLYHAICVVDG
IEPTMKDPADITSHALAGSDKAAVETVSLFATYL
GRVAGDLAMVFMARGGVYLSGGIS
QKIIPALKKPEFRIAFEDKAPHTALLRTIPTYV
VTHPLAALAGLSSYARMPANFGVST EGRRWRR"
misc-feature complement(217160..2181 /gene="glk"
10)

/locus-tag="RL0182"
/inference="protein
motif:Pfam:PF02685.4"
/note="Pfam match to entry

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gene complement(218158..2185 /locus-tag="RL0183"  
 38)

CDS complement(218158..2185 /locus-tag="RL0183"  
 38)

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 /inference="similar to  
 sequence:INSDC:SME591782"  
 /note="similarity:fasta;  
 with=UniProt:MGSA-ECOLI  
 (EMBL:AE005286); Shigella  
 flexneri.; mgsA; Methylglyoxal  
 synthase (EC 4.2.3.3) (MGS).;  
 length=152; id 50.442; 113 aa  
 overlap; query 5-117; subject  
 12-123 similarity:fasta;  
 with=UniProt:MGSA-RHIME  
 (EMBL:SME591782); Rhizobium  
 meliloti (Sinorhizobium  
 meliloti).; mgsA; Methylglyoxal  
 synthase (EC 4.2.3.3) (MGS).;  
 length=126; id 83.471; 121 aa  
 overlap; query 1-121; subject  
 1-121; putative methylglyoxal  
 synthase"  
 /codon-start=1  
 /transl-table=11  
 /product="methylglyoxal synthase  
 (mgs) "  
 /protein-id="CAK05672.1"  
 /db-xref="GI:115254598"  
 /db-xref="GOA:Q1MMY0"  
 /db-xref="UniProtKB/TrEMBL:Q1MMY0"  
 /translation="MAGGKCLALIAHDQKKDDMA  
 AFARANRDILSRWKIVATGTTGGR  
 VLDAAPDLDVRLKSGPLGGDQQIGALISTGEVD  
 ALIFFVDPLTPMPHDVDVKALMRL  
 AIVYDIPMALNHATAIKLLPTLEA"

misc-feature complement(218203..2184 /locus-tag="RL0183"  
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/inference="protein  
 motif:Pfam:PF02142.8"  
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 PF02142.8 MGS"

gene complement(218624..2197 /locus-tag="RL0184"  
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CDS complement(218624..2197 /locus-tag="RL0184"  
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 sequence:INSDC:SME591782"  
 /note="Similar, but extended at  
 the N and C-termini, to Shigella  
 flexneri. mepA MEPA-ECOLI  
 (EMBL:AE015256)  
 (Penicillin-insensitive murein  
 endopeptidase precursor (EC  
 3.4.99.-)  
 (D-alanyl-D-alanine-endopeptidase)

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(DD-endopeptidase).), and to
entire protein of Rhizobium
meliloti (Sinorhizobium meliloti).
PUTATIVE MUREIN ENDOPEPTIDASE
TRANSMEMBRANE PROTEIN (EC 3.4.99.-
). Q92T29 (EMBL:SME591782) (355)
similarity:fasta;
with=UniProt:MEPA-ECOLI
(EMBL:AE015256); Shigella
flexneri.; mepA;
Penicillin-insensitive murein
endopeptidase precursor (EC
3.4.99.-)
(D-alanyl-D-alanine-endopeptidase)
(DD-endopeptidase).; length=274;
id 38.372; 258 aa overlap; query
52-307; subject 29-270
similarity:fasta;
with=UniProt:Q92T29
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE MUREIN
ENDOPEPTIDASE TRANSMEMBRANE
PROTEIN (EC 3.4.99.-).;
length=355; id 61.708; 363 aa
overlap; query 1-358; subject
1-355"
/codon-start=1
/transl-table=11
/product="putative murein
endopeptidase
(d-alanyl-d-alanine-endopeptidase)
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/db-xref="UniProtKB/TrEMBL:Q1MMX9"
/translation="MAFGFAQAFRTLGLTLAGA
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RFSQDAVRYAGWPGILVGDIAQPRGGPMLNGHSS
HQIGLDADIWFSMPARRMTAQER
EDLPFTSMLQKDKFLTVNPKVWTESRARLLMLAA
SYPEVERIFVNPAIKKKMCDTWGG
DRTNLGLRPIYGHDSHFHIRIKPPGAAGCTPQ
APVPAGDGCDKSLAYWFTPAPWAP
PKPPKPGAKPPKPPREMMVTDLPNACA AVLDAAS
VASMQAATYGGPSAASALAATPAA
ASADDTDGALPDVGPVPNDKPAIQ"
misc-feature      complement(218768..2195 /locus-tag="RL0184"
29)
/inference="protein
motif:Pfam:PF03411.3"
/note="Pfam match to entry
PF03411.3 Peptidase-U6"
sig-peptide      complement(219613..2197 /locus-tag="RL0184"
00)
/inference="protein
motif:SignalP-HMM:2.0"
/note="Signal peptide predicted
for RL0184 by SignalP 2.0 HMM

```

gene	219976..221808	(Signal peptide probability 0.937) with cleavage site probability 0.632 between residues 28 and 29"
CDS	219976..221808	/locus-tag="RL0185" /locus-tag="RL0185" /inference="similar to sequence:INSDC:RSAE104" /note="Similar, but truncated at the C-terminus, to Rhizobium sp. (strain NGR234). Hypothetical protein Y4WM precursor. Y4WM-RHISN (EMBL:RSAE104) (663) similarity:fasta; with=UniProt:Y4WM-RHISN (EMBL:RSAE104); Rhizobium sp. (strain NGR234).; Hypothetical protein Y4WM precursor.; length=663; id 67.833; 600 aa overlap; query 11-609; subject 16-614" /codon-start=1 /transl-table=11 /product="putative solute-binding component of ABC transporter" /protein-id="CAK05674.1" /db-xref="GI:115254600" /db-xref="GOA:Q1MMX8" /db-xref="UniProtKB/TrEMBL:Q1MMX8" /translation="MAALWSKIGLFLSLAGALAP MTATAQDQPFLIGSSVISEMKYKP GFAHFDYVNPDPKGGDLRLSASGAFTDNPLLA KGQAAVGLTLVYDTLMKPADDELL VSYGLLAEGLSFPTDVSSATFRLRKEAKWSDGQP VTPEDVIFSLDKTKELNPLTANY RHVAKAEKTGDRDVTFTFDEKNNRELNPILGQLV VVPKHWEGQGPDPKPRDISKTTL EPVMGSGPYKIASFSPGATIRYELRDDYWGKDLN VNVGQNNFRNVIYTYFGDRDVEFE AFRAGNSDYWQETTAARWATGYDFPAVKEGRVKK EEVANPLRATGIMQALVPNMRRDL FKDIRVREALNYGLDFEELNRTVAFNSYKRIDS FWNTEASSGLPQGRELEILQGMK DKVPAEIFTTPYTNPVAGDPQKSRDNLRKAIAL KEAGWEIKGNRMVNSKTGQPMSE ILLSSPMLERWAVPYASNLRKIGIDARVRTVDAS QAVNRERSFDYDMIWNVWAETMNP GNEQADYWGSGSVNQGSRNYAGIANPAVDELIR MVIFAPNRDEQIAAIKAMDRVLLA NHYVIPLFYRDTYNIAYWNTVTHPAEFPAYSLGF PDAWWSTSAK" /locus-tag="RL0185" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0185 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.999 between residues 25 and 26"
sig-peptide	219976..220048	/locus-tag="RL0185" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0185 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.999 between residues 25 and 26"
misc-feature	220003..221790	/locus-tag="RL0185" /inference="protein motif:Pfam:PF00496.8" /note="Pfam match to entry

gene	221959..223047	PF00496.8 SBP-bac-5"
CDS	221959..223047	/locus-tag="RL0186"
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		/inference="similar to
		sequence:INSDC:AE007959"
		/note="similarity:fasta;
		with=UniProt:Q8UIV3
		(EMBL:AE007959); Agrobacterium
		tumefaciens (strain C58/ATCC
		33970).; ABC transporter, membrane
		spanning protein (AGR-C-318p).;
		length=364; id 87.637; 364 aa
		overlap; query 1-362; subject
		1-364"
		/codon-start=1
		/transl-table=11
		/product="putative transmembrane
		component of ABC transporter"
		/protein-id="CAK05675.1"
		/db-xref="GI:115254601"
		/db-xref="GOA:Q1MMX7"
		/db-xref="UniProtKB/TrEMBL:Q1MMX7"
		/translation="MGAYILRRLLLMIPTIVGIM
		AISFVVIQFAPGGPVEQVIAQLTG
		QADSADQRLSGGGDLLGGGGSDEGSKYRGAQGLD
		PELIAKLEKQFGFDKPPLTRFGEM
		MWNYIRFDFGESFFRNTSVLELIKEKLPVSISLG
		IWILIFSIAISIPLGIRKAVKDGS
		TFDVWTSGVIVVGAVPSFLFGILLIVLFAGGSF
		YDWFPLRGLVSDNFDQLAWWQKPL
		DYFWHLTLPLISLSLSAFATTTLLTKNSFIEEIK
		KQYVVTARAKGLNERQVLYGHIFR
		NAMLIIIAGFPGAFISAFFTGSLLIENIFSLDGL
		GRLGYLSVINRDYPIVFATLYIFS
		LLGLVSVSLVSDLIYTWIDPRIDFERRDV"
misc-feature	order(221983..222051,	/locus-tag="RL0186"
	222343..222411,	
	222460..222528,	
	222619..222687,	
	222793..222861,	
	222931..222999)	
		/inference="protein
		motif:TMHMM:2.0"
		/note="6 probable transmembrane
		helices predicted at aa 9-31,
		129-151, 168-190, 221-243,279-301
		and 325-347"
misc-feature	222343..223029	/locus-tag="RL0186"
		/inference="protein
		motif:Pfam:PF00528.10"
		/note="Pfam match to entry
		PF00528.10 BPD-transp-1"
gene	223047..224195	/locus-tag="RL0187"
CDS	223047..224195	/locus-tag="RL0187"
		/inference="similar to
		sequence:INSDC:HS381248"
		/note="similarity:fasta;
		with=UniProt:Q8UIV2
		(EMBL:HS381248); Agrobacterium
		tumefaciens (strain C58/ATCC
		33970).; ABC transporter, membrane
		spanning protein.; length=395; id

		84.656; 378 aa overlap; query 5-382; subject 18-395" /codon-start=1 /transl-table=11 /product="putative transmembrane component of ABC transporter" /protein-id="CAK05676.1" /db-xref="GI:115254602" /db-xref="GOA:Q1MMX6" /db-xref="UniProtKB/TrEMBL:Q1MMX6" /translation="MDAAANPVITTPVKPPRKGL LSPTNIRRWHNFKANGRGYWSLWL FLVLFVLSLFAEFLANDRPPIIASYKGEVLFVPLI DYPEEKFGGFLAETDYRSSVIAD INANGWMIWPPIRYSYRSVNSNIPHSAPTAPFWL MTNEERCAGYPQGVNDPCTLGNL NWLGTDDQARDVLARVIYGFRI SVLFGLVLTICS AVIGVTAGAVQGYFGGWTDLLLQR FIEIWSSMPVLYILLIIAALLPPGFFVLLGIMLL FSWVGFGVIVRAEFLRARNFEYVR AARALGVNNRTIMWRHLLPNAMVATLTFLPFILS GSITTLTSLDFLGFGMPPGSPSLG EMIAQGKTNLQAPWLGLTAFFAMSIMLSLLIFIG EAVRDAFDPRKTFQ" /locus-tag="RL0187"
misc-feature	order(223158..223226, 223590..223658, 223728..223832, 223923..223991, 224082..224150)	
		/inference="protein motif:TMHMM:2.0" /note="5 probable transmembrane helices predicted at aa 38-60, 182-204, 228-262, 293-315 and 346-368"
misc-feature	223584..224189	/locus-tag="RL0187" /inference="protein motif:Pfam:PF00528.10" /note="Pfam match to entry PF00528.10 BPD-transp-1"
gene	224192..225829	/locus-tag="RL0188"
CDS	224192..225829	/locus-tag="RL0188" /inference="similar to sequence:INSDC:A97382" /note="similarity:fasta; with=UniProt:Q8UIV1 (EMBL:A97382); Agrobacterium tumefaciens (strain C58/ATCC 33970).; ABC transporter, nucleotide binding/ATPase protein (AGR-C-320p).; length=549; id 83.364; 541 aa overlap; query 5-545; subject 9-549" /codon-start=1 /transl-table=11 /product="putative ATP-binding component of ABC transporter" /protein-id="CAK05677.1" /db-xref="GI:115254603" /db-xref="GOA:Q1MMX5" /db-xref="UniProtKB/TrEMBL:Q1MMX5" /translation="MSDMTEPLLSVRDLSVAFHQ GGETSLAVDHISFDIAKGEVVALV

		GESGSGKSVSANSILRLLPYPSASHPSGEILFKG KDLLKASERALREVRGNDITMIFQ EPMTSLNPLHTIEKQIAEILALHQGLTGQSARQR VLELLNQVGIREPEKRLKAYPHEL SGGQRQVRMIAMALANRPELLIADEPTTALDVTV QAQILELLRQLKAVHGMSMLFITH DLGIVRKFADRVCMVTKGKIVETGTVEEVFANPK HDYTRHLLASEPRGEPPLADPSKP LVMEGSDIRVWFPIKSGLMRRVVDHVKAVDGIDL SLRAGQTLGVVGESGSGKTTLGLA LTRLISSEGRIAFVGKDIAGYSFNEMRPLRNQLQ VVFQDPYGSLSPRMSVGDIVAEG KVHERSLTSEERDQRCWALEEVGLDPLTRWRYP HEFSGGQRQRIAIARAMVLKPRFV MLDEPTSALDMSVQAQVVDLLRDLQKKHDLAYLF ISHDLKVVKALANDVIVMRFGKV EQGPSADIFRAPKDDYTRALMAAAFNIEAVPTPA VQQ"
misc-feature	224303..224899	/locus-tag="RL0188" /inference="protein" motif: Pfam: PF00005.11" /note="Pfam match to entry PF00005.11 ABC-tran"
misc-feature	225134..225706	/locus-tag="RL0188" /inference="protein" motif: Pfam: PF00005.11" /note="Pfam match to entry PF00005.11 ABC-tran"
gene	225838..226797	/locus-tag="RL0189"
CDS	225838..226797	/locus-tag="RL0189" /inference="similar to sequence: INSDC: SME591782" /note="similarity: fasta; with=UniProt: Q92T34 (EMBL: SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE HYDROXYACID DEHYDROGENASE PROTEIN (EC 1.1.1.-).; length=319; id 61.755; 319 aa overlap; query 1-319; subject 1-319" /codon-start=1 /transl-table=11 /product="putative 2-hydroxyacid dehydrogenase" /protein-id="CAK05678.1" /db-xref="GI:115254604" /db-xref="GOA:Q1MMX4" /db-xref="UniProtKB/TrEMBL:Q1MMX4" /translation="MPATPPVLVDIKFNAEGVAR VLKTAFAADRGSLNADPRNRARDL RAVEYALLWKPDADLFARAPNLKVIFSGGAGVDH IIGMDGLPEIPIVRFVDRSLTTRM SEWVVMQCLMHLRGQYTHDSHQREWAKLIAPE AAEVTVGVMGLGILGQDAVAKLRV MGFNVIGWSRSRKQIDGVETFDASELDSFLARTD ILVGLLPLTPETSGFYDAGLFAKL RRNGALGQPVFINAGRGKSQVEADIVSAIRDGTL GGASLDVFEEPLASDHPLWELRN VFITPHDAAVSEENALFCHVETQIARFERGEPLQ FVVDRAAGY"
misc-feature	226141..226683	/locus-tag="RL0189"

gene	226886..227233	/inference="protein motif: Pfam: PF02826.5" /note="Pfam match to entry PF02826.5 2-Hacid-dh-C" /locus-tag="RL0190" /locus-tag="RL0190" /inference="similar to sequence: INSDC: SME591787" /note="similarity: fasta; with=UniProt: Q92KE7 (EMBL: SME591787); Rhizobium meliloti (Sinorhizobium meliloti).; HYPOTHETICAL TRANSMEMBRANE PROTEIN.; length=117; id 33.333; 105 aa overlap; query 2-105; subject 1-99" /codon-start=1 /transl-table=11 /product="putative transmembrane protein" /protein-id="CAK05679.1" /db-xref="GI: 115254605" /db-xref="GOA: Q1MMX3" /db-xref="UniProtKB/TrEMBL: Q1MMX3" /translation="MMAHQTDTRWEKSNGKLHKE EQIPPVKARQGRMGYRILTVLIVA LVLAFFVVWIPVEIWGNREANEVAPQQPGQQLQSQ QPAPAPAPALQNGTAVPTETPNTT PAAPNVAPATPAQ"
CDS	226886..227233	
misc-feature	226994..227062	/locus-tag="RL0190" /inference="protein motif: TMHMM: 2.0" /note="1 probable transmembrane helix predicted at aa 37-59"
gene	227421..228725	/locus-tag="RL0191"
CDS	227421..228725	/locus-tag="RL0191" /EC-number="2.4.2.11" /inference="similar to sequence: INSDC: AE007962" /inference="similar to sequence: INSDC: ECD731" /note="similarity: fasta; with=UniProt: PNCB-ECOLI (EMBL: ECD731); Escherichia coli.; pncB; Nicotinate phosphoribosyltransferase (EC 2.4.2.11) (NAPRTase).; length=399; id 35.135; 407 aa overlap; query 19-420; subject 6-387 similarity: fasta; with=UniProt: PNCB-AGRT5 (EMBL: AE007962); Agrobacterium tumefaciens (strain C58/ATCC 33970).; pncB; Nicotinate phosphoribosyltransferase (EC 2.4.2.11) (NAPRTase).; length=434; id 85.253; 434 aa overlap; query 1-434; subject 1-434; putative nicotinate phosphoribosyltransferase" /codon-start=1

		/transl-table=11 /product="nicotinate phosphoribosyltransferase (naprtase)" /protein-id="CAK05680.1" /db-xref="GI:115254606" /db-xref="GOA:Q1MMX2" /db-xref="UniProtKB/TrEMBL:Q1MMX2" /translation="MARTDIARRVYNHAWKLDPI IRSLIDTDFYKLLMLQMIWKLYPD VNASFTLINRTKRVRLAEELDEGELREQLDHART LRLSKKEMIWLAGNSFYGRAQIFE PEFLAWLSNFQLPEYELSKKDGQYVLDHGSWKE TTMWEIPALAIVNELRSRSAMKAL GPFTLDVLYARAKAKMWSKVERLKELPGLRISDF GTRRRHSFLWQRWCVEALKEGIGP AFAGTSNVLLAMDSLEAVGTNAHELPMVAAALA ETDEQLRNAPYKILRDWNKLYGGN LLIVLPDAFGTAAFLRDAPEWVADWTGFRPDSAP PIEGGEKIIDWWKKMGRDPRQKLL IFSDGLDVD AI IDTYRHFEGVRMSFGWGTNLTN DFSGCAPIEISGLNPISVVCKVSD ANGRPAVKLSDN PQKATGEP AEV ERYLKFFGAED RIDQTVLV"
misc-feature	227484..228698	/locus-tag="RL0191" /inference="protein motif: Pfam: PF04095.4" /note="Pfam match to entry PF04095.4 NAPRTase"
gene	complement(229362..229760)	/locus-tag="RL0192"
CDS	complement(229362..229760)	/locus-tag="RL0192"  /inference="similar to sequence: INSDC: AE012107" /note="C-terminus from codon 60 is similar to Xanthomonas campestris (pv. campestris). Hypothetical protein XCC0125. Q8PE56 (EMBL: AE012107) (85) similarity: fasta; with=UniProt: Q8PE56 (EMBL: AE012107); Xanthomonas campestris (pv. campestris).; Hypothetical protein XCC0125.; length=85; id 32.836; 67 aa overlap; query 62-128; subject 18-84" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05681.1" /db-xref="GI:115254607" /db-xref="UniProtKB/TrEMBL:Q1MMX1" /translation="MCWIRARPNNEMARLPAYPR GRRSDGAARFRRSKIPDFLPCSFT ASLHVWVYRLPKSKTEVKQVEELSVKSKIIKTVY FSQEDGRLRICFKNGEERLFEGVP SSEAHAMTVAPSPGHYYLDRI RTRFRRLAA"
gene	complement(229806..230375)	/locus-tag="RL0193"



CDS	complement(229806..230375)	/locus-tag="RL0193" /inference="similar to sequence:INSDC:AP002998" /note="similarity:fasta; with=UniProt:Q98JQ9 (EMBL:AP002998); Rhizobium loti (Mesorhizobium loti).; Mll1824 protein.; length=177; id 59.412; 170 aa overlap; query 7-176; subject 1-170" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05682.1" /db-xref="GI:115254608" /db-xref="UniProtKB/TrEMBL:Q1MMX0" /translation="MIRGKDMKDIIILPGIGGSG EAHWQTRWERSNPYMRRFQPTNWE KPDLADWISALERAVGASTTPPLLVAHSLACLLV AHWQQVSSLAVAGAFLLVAVPDPQS ASFPKEAAGFADPPSQMRFP TLIIASGDDPFGT LDHAHARADLWGSGLV AIGPFGHI NGQSGLEDWGQGKALLTAFSAGLARSRA"
misc-feature	complement(229839..230348)	/locus-tag="RL0193" /inference="protein motif: Pfam:PF06821.1" /note="Pfam match to entry PF06821.1 DUF1234"
gene	230468..230944	/locus-tag="RL0194"
CDS	230468..230944	/locus-tag="RL0194" /inference="similar to sequence:INSDC:AP002998" /note="similarity:fasta; with=UniProt:Q98JQ8 (EMBL:AP002998); Rhizobium loti (Mesorhizobium loti).; Probable transcriptional regulator.; length=160; id 77.483; 151 aa overlap; query 6-156; subject 5-155" /codon-start=1 /transl-table=11 /product="putative AsnC transcriptional regulator" /protein-id="CAK05683.1" /db-xref="GI:115254609" /db-xref="GOA:Q1MMW9" /db-xref="UniProtKB/TrEMBL:Q1MMW9" /translation="MAFQENNRVQLDPTDIAIE AMQENGRIAVSELGRRVGLSQPAA SERVKRLED RGIIIVGYAARIDPTALGIGMTAVLR LRTTHEHIKCLKQFAEMPQVMEV LRLTGEDCFLKVLVPAPGELETIVDTIARFGAV TTSLVLRSENP KPIGRALLQRP"
misc-feature	230570..230869	/locus-tag="RL0194" /inference="protein motif: Pfam:PF01037.8" /note="Pfam match to entry PF01037.8 AsnC-trans-reg"

gene	complement(231045..231134)	/gene="tRNA-Ser"
tRNA	complement(231045..231134)	/gene="tRNA-Ser"
		/product="tRNA-Ser"
		/note="anticodon GGA"
gene	231363..231680	/locus-tag="RL0195"
CDS	231363..231680	/locus-tag="RL0195"
		/inference="similar to sequence:INSDC:SME591782"
		/note="similarity:fasta; with=UniProt:Q92SY6 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; CONSERVED HYPOTHETICAL SIGNAL PEPTIDE PROTEIN.;
		length=105; id 52.381; 105 aa overlap; query 1-105; subject 1-105"
		/codon-start=1
		/transl-table=11
		/product="putative transmembrane protein"
		/protein-id="CAK05684.1"
		/db-xref="GI:115254610"
		/db-xref="GOA:Q1MMW8"
		/db-xref="UniProtKB/TrEMBL:Q1MMW8"
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misc-feature	order(231381..231449, 231576..231644)	/locus-tag="RL0195"
		/inference="protein motif:TMHMM:2.0"
		/note="2 probable transmembrane helices predicted at aa 7-29 and 72-94"
gene	231998..232990	/locus-tag="RL0196"
CDS	231998..232990	/locus-tag="RL0196"
		/inference="similar to sequence:INSDC:B97374"
		/note="similarity:fasta; with=UniProt:Q8UJ15 (EMBL:B97374); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Membrane lipoprotein (AGR-C-200p).;
		length=337; id 86.970; 330 aa overlap; query 1-330; subject 8-337"
		/codon-start=1
		/transl-table=11
		/product="putative outer membrane basic protein"
		/protein-id="CAK05685.1"
		/db-xref="GI:115254611"
		/db-xref="GOA:Q1MMW7"
		/db-xref="UniProtKB/TrEMBL:Q1MMW7"
		/translation="MKKSLTLFAVAAMSTTALA ADVKPALVYGTGGKFDKSFNEAAY NGAEKFKAETGIAYRDFEPTGDTQGEQAIRNFAS RGFNPVVAVSFAWTSIAIEKVAAEF"

		PDTKFIIVDSVVDKPNVRSVVYKEEEGSYLVGVL AGMASKTGKVGFGVGGMDIPLIRKF ECGYEQGARSVKADIEVFQNMGTGTTGAAWNPDVPR GGELTKNQIDQGADVYAAAGATG LGVLQTAADNKKLSIGVDSNQNLHPGSVLTSMV KRVDLAVYNAYNDTKNDKFTAGVQ ALGVKEDGVGAAIDNNKSLITPEMQAAVDKAKA DIIAGTIKVHDYTSNACPK"
sig-peptide	231998..232055	/locus-tag="RL0196" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0196 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.999 between residues 20 and 21"
misc-feature	232001..232966	/locus-tag="RL0196" /inference="protein motif:PFam:PF02608.4" /note="Pfam match to entry PF02608.4 Bmp"
gene	233067..234590	/locus-tag="RL0197"
CDS	233067..234590	/locus-tag="RL0197" /inference="similar to sequence:INSDC:C97374" /note="Similar to Agrobacterium tumefaciens (strain C58/ATCC 33970). ABC transporter, nucleotide binding/ATPase protein. Q8UJ14 (EMBL:C97374) (501) similarity:fasta; with=UniProt:Q8UJ14 (EMBL:C97374); Agrobacterium tumefaciens (strain C58/ATCC 33970).; ABC transporter, nucleotide binding/ATPase protein.; length=501; id 87.976; 499 aa overlap; query 9-507; subject 3-501" /codon-start=1 /transl-table=11 /product="putative ATP-binding component of ABC transporter" /protein-id="CAK05686.1" /db-xref="GI:115254612" /db-xref="GOA:Q1MMW6" /db-xref="UniProtKB/TrEMBL:Q1MMW6" /translation="MEPAVTDKPAIELVGIDKKF GAVHANKDINLTVAKGTIHGIIGE NGAGKSTLMSIIYGFYHADSGEIRVNGNPVTIRD SQAAIATGIGMVHQHFMLVDNFTV LENIMLGAEGGMLLARGVASARAELKRLETEYGL EVDPDALIEELPVGLQQRVEILKA MYRGAEILILDEPTGVLTPAEADHLFRILKVLRLD QGKTIILITHKLREIMAITDTVSV MRRGEMVATRKTAETTVEELAEMLVGRRVLLRVQ KGEANPGSAVLSVRNLTVKDNRGV TMVDNVSFVDRAGEIVGIAGVAGNGQSELLEAIA GIRKPTSGEILLDGQTIDKADPAR LRDLGLAHIPEDRHHMGLVLKFEEYENSVLGYHR RPAYSKGPLLDLEAIRKDAMEKIE KYDIRPPNPRLKTANFSGGNQKIVVAREIERDL KMLIIGQPTRGVDIGAIEFIHRI

		IEMRDAGKAILLVSVLDELIRSLSDRILVMFAGH VVGEKTPDAGEQTLGLMMAGIAA" /locus-tag="RL0197" /inference="protein motif: Pfam: PF00005.11" /note="Pfam match to entry PF00005.11 ABC-tran"
misc-feature	233172..233732	
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gene	234598..235701	/locus-tag="RL0198"
CDS	234598..235701	/locus-tag="RL0198" /inference="similar to sequence: INSDC: AE007954" /note="similarity: fasta; with=UniProt: Q8UJ13 (EMBL: AE007954); Agrobacterium tumefaciens (strain C58/ATCC 33970).; ABC transporter, membrane spanning protein (AGR-C-205p).; length=367; id 81.199; 367 aa overlap; query 1-367; subject 1-367" /codon-start=1 /transl-table=11 /product="putative transmembrane permease component of ABC transporter" /protein-id="CAK05687.1" /db-xref="GI:115254613" /db-xref="GOA: Q1MMW5" /db-xref="UniProtKB/TrEMBL: Q1MMW5" /translation="MSTASVPLPNWINYGLIPIL NLIVAF LISGFV VWLIGESPLDAL SLLIEGALGN GEFIGFTLFYATSFIFTGLSVAVA IHAGLFNIGSEGQAYMGGLGCALV ALS LDNYVPWYVTMPVAVVGAALFGAVAAFI PAW LQAKRGSHIVITTIMFNIIASLM NYLLVHV LIVPGKMAPETRTFLEGGQLPKLTWLM EIFGTKLGAAPLNVSFIIALVMCY VWLLIWR TKLGFEMRTLGV SPTAASYAGIPYVR IVMIAMMLSGALAGMMALNPVMGA SARLQVGFVGGAGFVGIAVSLMGRNHPLGIILAA FLFGILYQGGDWISFEMP NITREM ILVIQGLVILFAGALEYMF RPAMVRLYQQFKRG" /locus-tag="RL0198"
misc-feature	order(234640..234708, 234766..234834, 234940..235008, 235045..235113, 235204..235272, 235339..235407, 235435..235494, 235513..235572, 235600..235656)	/inference="protein motif: TMHMM: 2.0" /note="9 probable transmembrane helices predicted at aa 15-37, 57-79, 115-137, 150-172, 203-225, 248-270, 280-299, 306-325 and

misc-feature	234766..235638	335-353" /locus-tag="RL0198" /inference="protein motif: Pfam: PF02653.5" /note="Pfam match to entry PF02653.5 BPD-transp-2"
gene	235712..236683	/locus-tag="RL0199"
CDS	235712..236683	/locus-tag="RL0199" /inference="similar to sequence: INSDC: AE007954" /note="similarity: fasta; with=UniProt: Q8UJ12 (EMBL: AE007954); Agrobacterium tumefaciens (strain C58/ATCC 33970).; ABC transporter, membrane spanning protein (AGR-C-207p).; length=323; id 80.805; 323 aa overlap; query 1-323; subject 1-323" /codon-start=1 /transl-table=11 /product="putative transmembrane permease component of ABC transporter" /protein-id="CAK05688.1" /db-xref="GI: 115254614" /db-xref="GOA: Q1MMW4" /db-xref="UniProtKB/TrEMBL: Q1MMW4" /translation="MDYYDIFISVLASTIRLSIP LIFTALAGLFSERAGIFDIGLEGK MLGSAFAAACVAYLTDSA WLGLGAGILCSVALSL VHGFASITNRGNQIVSGVAINFFI AGITIVLGQAWFGQGGRTPLAPDSRFAPILPG ADVARDIPIIGPLYANVISGNNIL TYLAFLAVPFSWWVLYRTRFGLRLRAVGENPGAV DTAGISVAWLRYRAVMCAGILCGF AGTYLAIAQSAAFIKDMSAGKGYIALAALVFAKW KQVPVVMFACLLFGFLDALANFMQG KQVPLIGEVPVQVFQALPYVLTVCVLLAGFIGVAT PPKAGGVPYTKER" /locus-tag="RL0199"
misc-feature	order(235730..235798, 235898..235966, 235985..236053, 236186..236239, 236333..236401, 236444..236512, 236570..236638)	/inference="protein motif: TMHMM: 2.0" /note="7 probable transmembrane helices predicted at aa 7-29, 63-85, 92-114, 159-176, 208-230, 245-267 and 287-309"
misc-feature	235739..236617	/locus-tag="RL0199" /inference="protein motif: Pfam: PF02653.5" /note="Pfam match to entry PF02653.5 BPD-transp-2"
gene	236685..237074	/gene="cdd" /locus-tag="RL0200"
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misc-feature	236685..236996	/gene="cdd" /locus-tag="RL0200" /inference="protein motif: Pfam:PF00383.9" /note="Pfam match to entry PF00383.9 dCMP-cyt-deam"
gene	237071..237871	/gene="punA" /locus-tag="RL0201"
CDS	237071..237871	/gene="punA" /locus-tag="RL0201" /EC-number="2.4.2.1" /inference="similar to sequence:INSDC:AE007954" /inference="similar to sequence:INSDC:BSJH6421" /note="similarity:fasta; with=UniProt:PUNA-BACSU (EMBL:BSJH6421); Bacillus subtilis.; punA; Purine nucleoside phosphorylase I (EC 2.4.2.1) (PNP I) (PU-NPASE I) (Inosine phosphorylase).; length=271; id 46.586; 249 aa overlap; query 17-262; subject 20-268 similarity:fasta; with=UniProt:Q8UJ10 (EMBL:AE007954); Agrobacterium

		tumefaciens (strain C58/ATCC 33970).; deoD; Purine nucleoside phosphorylase (AGR-C-210p).; length=266; id 75.769; 260 aa overlap; query 5-264; subject 6-265; putative purine nucleoside phosphorylase" /codon-start=1 /transl-table=11 /product="purine nucleoside phosphorylase i (pnp i) (pu-npase i) (inosine phosphorylase)" /protein-id="CAK05690.1" /db-xref="GI:115254616" /db-xref="GOA:Q1MMW2" /db-xref="UniProtKB/TrEMBL:Q1MMW2" /translation="MKATVSLLAALLGGIKPRHG IVLGSGLGSLVGELDGAVRVPYRD LPGFVPVSAVSGHAGEVVAGRLGGVPVVMLSGRVH YYEKGDANAMRLPIEVLKALGVEA LILTNSAGSLRDDMPPGSVMQITDHINYSGMNPL IGEESDHRFVGMTNAYDAGLAAAM QRAAAKLEIELAQGVYMWFSGPSFETPAEIRMAR ILGADAVGMSTVPEVVISRMLGLR VAAASVITNYGAGMTGNELSHEETKDMAPIGGAR LAAILKDMIAAGRG" /gene="punA" /locus-tag="RL0201" /inference="protein motif:Pfam:PF00896.9" /note="Pfam match to entry PF00896.9 Mtap-PNP"
misc-feature	237116..237865	
gene	237987..238763	/gene="deoC" /locus-tag="RL0202" /EC-number="4.1.2.4" /inference="similar to sequence:INSDC:AE016772" /inference="similar to sequence:INSDC:HS374251" /note="similarity:fasta; with=UniProt:DEOC-ECOLI (EMBL:AE016772); Escherichia coli 06.; deoC; Deoxyribose-phosphate aldolase (EC 4.1.2.4) (Phosphodeoxyriboaldolase) (Deoxyriboaldolase) (DERA).; length=259; id 56.000; 250 aa overlap; query 13-255; subject 11-258 similarity:fasta; with=UniProt:DEOC-AGRT5 (EMBL:HS374251); Agrobacterium tumefaciens (strain C58/ATCC 33970).; deoC; Deoxyribose-phosphate aldolase (EC 4.1.2.4) (Phosphodeoxyriboaldolase) (Deoxyriboaldolase) (DERA).; length=259; id 71.705; 258 aa overlap; query 1-258; subject 3-259"
CDS	237987..238763	

		/codon-start=1 /transl-table=11 /product="putative deoxyribose-phosphate aldolase" /protein-id="CAK05691.1" /db-xref="GI:115254617" /db-xref="GOA:Q1MMW1" /db-xref="UniProtKB/TrEMBL:Q1MMW1" /translation="MNSHSNRETA AVALSLLDLT NLRDDCTEAQIDALCARAQT PYGT SAAICIWPRFVAQARNILGTGHAVRIATVVNLP S GDMEVADVAAEAREAIADGADEID LVIPYRKLLAGNEKAVTDMVKAVRAECAGPVLLK VIIETGELKDAALIRHASELAIEA GADFIKTSTGKVAVNATLEAADIMIRAIRESGRK VGFKPAGGIGSVADAALYLSLAET IMTPDWAMPSTFRFGASDLLDDILSVLSGTQSAS AAASGY"
misc-feature	238017..238676	/gene="deoC" /locus-tag="RL0202" /inference="protein motif: Pfam:PF01791.6" /note="Pfam match to entry PF01791.6 DeoC"
gene	238765..240072	/gene="deoA" /locus-tag="RL0203"
CDS	238765..240072	/gene="deoA" /locus-tag="RL0203" /EC-number="2.4.2.4" /inference="similar to sequence: INSDC:AE007954" /inference="similar to sequence: INSDC:U00096" /note="similarity:fasta; with=UniProt:TYPH-ECOLI (EMBL:U00096); Escherichia coli.; deoA; Thymidine phosphorylase (EC 2.4.2.4) (TdrPase).; length=EC 2.4 ( 440; id 52.778; 432 aa overlap; query 2-431; subject 3-434 similarity:fasta; with=UniProt:Q8UJ08 (EMBL:AE007954); Agrobacterium tumefaciens (strain C58/ATCC 33970).; deoA; Thymidine phosphorylase (AGR-C-214p).; length=438; id 69.142; 431 aa overlap; query 1-431; subject 3-433" /codon-start=1 /transl-table=11 /product="putative thymidine phosphorylase" /protein-id="CAK05692.1" /db-xref="GI:115254618" /db-xref="GOA:Q1MMW0" /db-xref="UniProtKB/TrEMBL:Q1MMW0" /translation="MIPQEIIIRKRDGDELDAE ISSFIAALAAGQLSEGQIGAFAMA VWFKGMSRTETVALTLAMADSGDRLQWADVDRPI ADKHSTGGVGDNVSLMLAPIAAAC GLAVPMISGRGLGHTGGTLDKLESIPGYMITPDA



		DLFHKVKEAGCAIIGQTGTLAPA DGRLYAVRDVTATVDSIPLITASILSKKLAAGLE TLVLDVKVGNGAFMVDRGQAETLA QSLVEVANGAGVKTSALITDMNQPLADSAGNAVE MRNCLDFLAGRKADTRLETVVLA AAEMLVKSGIAASSDEAEGMARRALSSGKAAEVF ARMVSM LGGPADLIENPDRYLARA PVAKPVPAARSGWLAACDARGIGVSVIDLGGGRR HPADRIDHRVGFSELLPLGTRVNA GEPIALVHAADDDAAERAVAALAAHYRITEEKPE LTPVIAGLI"
misc-feature	238771..238965	/gene="deoA" /locus-tag="RL0203" /inference="protein motif: Pfam: PF02885.5" /note="Pfam match to entry PF02885.5 Glycos-trans-3N"
misc-feature	238987..239754	/gene="deoA" /locus-tag="RL0203" /inference="protein motif: Pfam: PF00591.9" /note="Pfam match to entry PF00591.9 Glycos-transf-3"
gene	complement(240079..240612)	/locus-tag="RL0204"
CDS	complement(240079..240612)	/locus-tag="RL0204"  /inference="similar to sequence: INSDC: B97375" /note="similarity: fasta; with=UniProt: Q8UJ07 (EMBL: B97375); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0134.; length=180; id 50.000; 176 aa overlap; query 1-175; subject 8-178" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05693.1" /db-xref="GI: 115254619" /db-xref="UniProtKB/TrEMBL: Q1MMV9" /translation="MLVRTVL FASIAAVLATQVP SFFGGTSQQPAETLSANYVSAQTE QPVAPEPVYGSNAIRLQADAQGHYTGSFKINGKP VQGLIDTGATYVALNETLARRLGF TANQLDFRYGVNTANGQTKAAHVTLDRVEIGGIR VREVEAFVLKDDALTTTLVGMSFL QKLASYSVADGSLSLKQ"
sig-peptide	complement(240537..240612)	/locus-tag="RL0204"  /inference="protein motif: SignalP-HMM: 2.0" /note="Signal peptide predicted for RL0204 by SignalP 2.0 HMM (Signal peptide probabiltiy 0.991) with cleavage site probability 0.362 between residues 24 and 25"
gene	complement(240774..241403)	/gene="upp"  /locus-tag="RL0205"

CDS	complement(240774..241403)	/gene="upp" /locus-tag="RL0205" /EC-number="2.4.2.9" /inference="similar to sequence:INSDC:AE005479" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:UPP-ECOLI (EMBL:AE005479); Shigella flexneri.; upp; Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase).; length=208; id 52.427; 206 aa overlap; query 4-209; subject 3-208 similarity:fasta; with=UniProt:UPP-RHIME (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; upp; Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase).; length=209; id 86.124; 209 aa overlap; query 1-209; subject 1-209" /codon-start=1 /transl-table=11 /product="putative uracil phosphoribosyltransferase (UMP pyrophosphorylase)" /protein-id="CAK05694.1" /db-xref="GI:115254620" /db-xref="GOA:Q1MMV8" /db-xref="UniProtKB/TrEMBL:Q1MMV8" /translation="MDGVTVIDHPLVQHKLTIMR RKETSTGSFRLLREISTLLCYEV TRDLELTMETIETPLQTMESPILEGKKLVFASIL RAGNGLLEGMLDLVPSARVSHIGV YRDHETLQPVEYYFKAPEDVAERLIIVDPMLAT GNSSIAAIDKLKERGAHNIRFLCL LAAPEGIRNFRAAHPDVPVFTASIDSHLNEKGYI MPGLGDAGDRMYGTK"
misc-feature	complement(240894..241265)	/gene="upp" /locus-tag="RL0205" /inference="protein motif:Pfam:PF00156.11" /note="Pfam match to entry PF00156.11 Pribosyltran"
gene	complement(241550..242518)	/locus-tag="RL0206"
CDS	complement(241550..242518)	/EC-number="3.5.4.4" /inference="similar to sequence:INSDC:A64919" /inference="similar to sequence:INSDC:AE007955" /note="similarity:fasta; with=UniProt:ADD-ECOLI (EMBL:A64919); Escherichia coli.;

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add; Adenosine deaminase (EC
3.5.4.4) (Adenosine
aminohydrolase).; length=EC
3.5.4.4; id 28.916; 332 aa
overlap; query 1-322; subject
2-330 similarity:fasta;
with=UniProt:ADD-AGRT5
(EMBL:AE007955); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; add; Adenosine deaminase
(EC 3.5.4.4) (Adenosine
aminohydrolase).; length=EC
3.5.4.4; id 75.466; 322 aa
overlap; query 1-322; subject
1-322"
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LAGIDTIYSELIVSPDHGKRIGLG
ADAYISGICEGIRRAREKSGIEARLIVTGERHFG
PESVIGAAEYAARAANPLITGFNL
AGEERMGRVADYARAFDIARDAGLGLTIHAGEVC
GAFSVADALDAVRPSRIGHGVRAI
EDLDLVTRLADLGTVLEICPGSNIALGVFPDFAS
HPLRRLKDAGVRVTISSDDPPFFH
TSLKREYELAAGTFGFGDAEIDAMTRTAIEAAFV
DDETRKALLARI"
misc-feature    complement(241556..2425 /locus-tag="RL0206"
09)

/inference="protein
motif: Pfam:PF00962.10"
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PF00962.10 A-deaminase"
gene            complement(242515..2437 /gene="deoB"
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CDS             complement(242515..2437 /gene="deoB"
35)

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/note="similarity:fasta;
with=UniProt:DEOB-ECOLI
(EMBL:HS137240); Shigella
flexneri.; deoB;
Phosphopentomutase (EC 5.4.2.7)
(Phosphodeoxyribomutase).;
length=EC 5.4.2.7; id 55.746; 409
aa overlap; query 1-406; subject
1-407 similarity:fasta;
with=UniProt:DEOB-AGRT5

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(EMBL:AE007955); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; deoB; Phosphopentomutase
(EC 5.4.2.7)
(Phosphodeoxyribomutase).;
length=EC 5.4.2.7; id 78.818; 406
aa overlap; query 1-406; subject
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phosphopentomutase
(phosphodeoxyribomutase)"
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EADVPGILGNCHASGTEIIARLGE
EHIRTGKPICTSSDSVFQVAAHEVHFGLDRLLA
FCGLARGLLDSYNIGRVIARPFIF
QSASTFQRTGNRRDFSVLPPPEPTLLDRLIEQGRH
VHAVGKIGDIFAHQGISRVIKANG
NEALMDASLSAIDAAEDGDLVFTNFVDFDMIYGH
RRDVPGYAAALEAFDARLPDVHKK
LKPGDLVVLTAADHGCDPTWRGTDHTRERVPVIAY
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                /inference="protein
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                /note="Pfam match to entry
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gene            complement(243895..2444 /locus-tag="RL0208"
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76)
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                /note="similarity: fasta;
                with=UniProt:Q8UIZ4
                (EMBL:AE008989); Agrobacterium
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                33970).; Hypothetical protein
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GITIDAGANAKVLWSWAKDGTVPYAKNTAVTNVP
ADMKTANSFLVRTELSIPYTMFLF
APNFMPDGMRTITISRSYFYRQRQGDSIPCGDC"
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07)

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/note="1 probable transmembrane
helix predicted at aa 24-46"
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11)
CDS             complement(244476..2451 /locus-tag="RL0209"
11)

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/note="similarity:fasta;
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(EMBL:AE007956); Agrobacterium
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33970).; AGR-C-240p.; length=211;
id 53.299; 197 aa overlap; query
18-210; subject 15-205"
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IPKVSTDKYADINTAAFKFAPGGA
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/inference="protein
motif:TMHMM:2.0"
/note="1 probable transmembrane
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gene            complement(245227..2456 /gene="pilQ"
37)

/locus-tag="RL0210"
CDS             complement(245227..2456 /gene="pilQ"
37)

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sequence:INSDC:AE007963"
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/note="putative alternative start
site at codon 13 similarity:fasta;
with=UniProt:Q8UIR6 (EMBL:B97386);
Agrobacterium tumefaciens (strain
C58/ATCC 33970).; PilQ.;

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length=124; id 73.387; 124 aa
overlap; query 14-136; subject
1-124 similarity:fasta;
with=UniProt:Q7D1X0
(EMBL:AE007963); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; AGR-C-384p.; length=136;
id 69.630; 135 aa overlap; query
3-136; subject 2-136"
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transmembrane protein"
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NTVRVYRQTQRSVLSCTPNCEQHAQQAATATSSP
"
misc-feature    complement(245560..2456 /gene="pilQ"
19)
                /locus-tag="RL0210"
                /inference="protein
motif:TMHMM:2.0"
                /note="1 probable transmembrane
helix predicted at aa 33-52"
gene            246017..246202    /gene="pilA"
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CDS             246017..246202    /gene="pilA"
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sequence:INSDC:AP003007"
                /inference="similar to
sequence:INSDC:B87614"
                /note="similarity:fasta;
with=UniProt:Q9L720 (EMBL:B87614);
Caulobacter crescentus.; pilA;
Pilus subunit protein PilA.;
length=Pilus subunit protein PilA;
id 60.000; 55 aa overlap; query
1-55; subject 1-55
similarity:fasta;
with=UniProt:Q98BG0
(EMBL:AP003007); Rhizobium loti
(Mesorhizobium loti).; Fimbriae
associated protein.; length=58; id
65.455; 55 aa overlap; query 1-55;
subject 1-55"
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protein"
                /protein-id="CAK05700.1"
                /db-xref="GI:115254626"
                /db-xref="UniProtKB/TrEMBL:Q1MMV2"
                /translation="MTKLFSRFLKDESGATAIEY
GLIAALISVALITGATTLGDRIGT
TFNNLGTKMNTGVTASN"

```

misc-feature	246038..246178	/gene="pilA" /locus-tag="RL0211" /inference="protein motif: Pfam:PF04964.3" /note="Pfam match to entry PF04964.3 Flp-Fap"
misc-feature	246074..246133	/gene="pilA" /locus-tag="RL0211" /inference="protein motif: TMHMM:2.0" /note="1 probable transmembrane helix predicted at aa 20-39"
gene	246327..246839	/gene="cpaA"
CDS	246327..246839	/locus-tag="RL0212" /gene="cpaA" /locus-tag="RL0212" /inference="similar to sequence: INSDC:A87614" /inference="similar to sequence: INSDC:SME591782" /note="similarity: fasta; with=UniProt:Q9L719 (EMBL:A87614); Caulobacter crescentus.; cpaA; Pilus assembly protein CpaA.; length= Pilus assembly protein CpaA; id 35.583; 163 aa overlap; query 6-166; subject 8-169 similarity: fasta; with=UniProt:Q92T43 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE PILUS ASSEMBLY TRANSMEMBRANE PROTEIN.; length=174; id 56.805; 169 aa overlap; query 1-169; subject 5-173" /codon-start=1 /transl-table=11 /product="putative pilus assembly protein" /protein-id="CAK05701.1" /db-xref="GI:115254627" /db-xref="GOA:Q1MMV1" /db-xref="UniProtKB/TrEMBL:Q1MMV1" /translation="MIAAAVFVILPLCLAMAAFS DLFTMTIPNRISVILTASFFVLAP LSGLGLAEIGMHLAGAAIVFSACFALFAFNMVGG GDAKLMSAAALWFGLNESLLFLMT DVAMIGGLITLLILLVRGQSDTILAIGLPVPNSV LLAKKIPYGIAIAIGGFMAFPSSP LFLAALES�K"
sig-peptide	246327..246384	/gene="cpaA" /locus-tag="RL0212" /inference="protein motif: SignalP-HMM:2.0" /note="Signal peptide predicted for RL0212 by SignalP 2.0 HMM (Signal peptide probability 0.996) with cleavage site probability 0.861 between residues 20 and 21"
misc-feature	order(246339..246407, 246417..246476,	/gene="cpaA"

	246495..246554, 246612..246680, 246756..246824)	/locus-tag="RL0212" /inference="protein motif:TMHMM:2.0" /note="5 probable transmembrane helices predicted at aa 5-27, 31-50, 57-76, 96-118 and 144-166"
misc-feature	246348..246677	/gene="cpaA" /locus-tag="RL0212" /inference="protein motif:Pfam:PF01478.6" /note="Pfam match to entry PF01478.6 Peptidase-A24"
gene	246950..247765	/gene="cpaB"
CDS	246950..247765	/locus-tag="RL0213" /gene="cpaB" /locus-tag="RL0213" /inference="similar to sequence:INSDC:AE007962" /inference="similar to sequence:INSDC:HS613241" /note="similarity:fasta; with=UniProt:Q9L718 (EMBL:HS613241); Caulobacter crescentus.; cpaB; Pilus assembly protein CpaB.; length=297; id 34.333; 300 aa overlap; query 1-264; subject 1-294 similarity:fasta; with=UniProt:Q8UIS0 (EMBL:AE007962); Agrobacterium tumefaciens (strain C58/ATCC 33970).; ctpC; Components of type IV pilus (AGR-C-380p).; length=AGR-C- ( 268; id 66.914; 269 aa overlap; query 1-269; subject 1-268" /codon-start=1 /transl-table=11 /product="putative pilus assembly protein" /protein-id="CAK05702.1" /db-xref="GI:115254628" /db-xref="UniProtKB/TrEMBL:Q1MMV0" /translation="MKPARLIILAVAVVAAGLAG LLAMQMAGSGGVVTQVRSVVEKEP TVNILVSSANLSVGARLDDQSVHWMMAWPQGGVVP GLITEADKPDPAVKDLQGAVVRLPI FEGEPIRPEKIADSSSRILSSLLPAGKRAVATEI SVATGAGGFILPNDRVDVIMVRKG AEADKLITETVLSNVRVLAIDQQIQEKDDGSKSV VGTTATLELTPDQTKVLAVAQQMA DRLSLALRSVADAQEQDTSAADYLLSGDNGSAII QVIKSGAIVTDASAAPKAE"
sig-peptide	246950..247049	/gene="cpaB" /locus-tag="RL0213" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0213 by SignalP 2.0 HMM"



		(Signal peptide probability 1.000) with cleavage site probability 0.335 between residues 34 and 35"
misc-feature	246968..247036	/gene="cpaB" /locus-tag="RL0213" /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted at aa 7-29"
misc-feature	247232..247627	/gene="cpaB" /locus-tag="RL0213" /inference="protein motif:Pfam:PF06981.1" /note="Pfam match to entry PF06981.1 CpaB"
gene	247771..249276	/gene="rcpA" /locus-tag="RL0214"
CDS	247771..249276	/gene="rcpA" /locus-tag="RL0214" /inference="similar to sequence:INSDC:AE017154" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:Q8KQJ0 (EMBL:AE017154); Haemophilus ducreyi.; rcpA; RcpA (Rough colony protein A).; length=Rough colony protein A; id 26.269; 453 aa overlap; query 62-499; subject 31-455 similarity:fasta; with=UniProt:Q92T41 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE PILUS ASSEMBLY TRANSMEMBRANE PROTEIN.; length=511; id 60.433; 508 aa overlap; query 19-501; subject 11-511" /codon-start=1 /transl-table=11 /product="putative pilus assembly protein" /protein-id="CAK05703.1" /db-xref="GI:115254629" /db-xref="GOA:Q1MMU9" /db-xref="UniProtKB/TrEMBL:Q1MMU9" /translation="MQMGNSMRRAGPLVTGCLSL AIGVSGMVPASFATLFAAGEARAD SDSLVRISQTGSNAHRLKLGLNKAVVVDLPEDA HDILVSDPTMADAVTRTSRRIYLF GKKVGQTNIFVFGAGGQEIYNLDIEIERDVSGLE VNLRRFIRDSNINVEIVSDNIVLT GTVRTPQDATQAADLAQVFLKGGEATTRTETASG TGGDSSVALFAEGRQSSQVVNLLQ IEGEDQVTLKVTIAEVRREVLKQLGFDNLVSNSS GMTVAQLGSPSADSATATVGGGLA ALFKSSIGKYDISTYLNALQAKVVKTLEPTLT AISGQAATFNSGGQQLYSTTDSG NVTVPFNYGINLAFKPVVLSSGRISLQIKTNVS EPVAGSGNATYQRRSAETSVELPS GGSIAGLIRDNVSQTMGGTPGVSKIPLLGTLF

		RQKGFERQETELVIIATPYLVLPV ARNQLNRPDDNFSPENDGATFFLNRVNKVYGRRE APVADAQFHGSIGFIYK"
sig-peptide	247771..247879	/gene="rcpA" /locus-tag="RL0214" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0214 by SignalP 2.0 HMM (Signal peptide probability 0.995) with cleavage site probability 0.396 between residues 37 and 38"
misc-feature	247807..247875	/gene="rcpA" /locus-tag="RL0214" /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted at aa 13-35"
misc-feature	248164..248301	/gene="rcpA" /locus-tag="RL0214" /inference="protein motif:Pfam:PF04972.3" /note="Pfam match to entry PF04972.3 BON"
misc-feature	248446..249114	/gene="rcpA" /locus-tag="RL0214" /inference="protein motif:Pfam:PF00263.9" /note="Pfam match to entry PF00263.9 Secretin-C"
gene	249273..250025	/gene="cpaD"
CDS	249273..250025	/locus-tag="RL0215" /gene="cpaD" /locus-tag="RL0215" /inference="similar to sequence:INSDC:AE005958" /inference="similar to sequence:INSDC:AE007962" /note="similarity:fasta; with=UniProt:Q9L716 (EMBL:AE005958); Caulobacter crescentus.; cpaD; Pilus assembly protein CpaD.; length=225; id 36.842; 133 aa overlap; query 120-249; subject 91-218 similarity:fasta; with=UniProt:Q8UIS2 (EMBL:AE007962); Agrobacterium tumefaciens (strain C58/ATCC 33970).; ctpE; Components of type IV pilus (AGR-C-378p).; length=AGR-C- ( 250; id 55.349; 215 aa overlap; query 28-241; subject 34-246" /codon-start=1 /transl-table=11 /product="putative pilus assembly protein" /protein-id="CAK05704.1" /db-xref="GI:115254630" /db-xref="UniProtKB/TrEMBL:Q1MMU8" /translation="MSGARAAAMAENRDQAMAHM

		NATTPRLGISKALFATVAMSVAIL SGCAGPHDQLTTGGIPDDYRARHPPIIVTEAEQTV DIPVASTDRRLTIAQRDLIRGFAA NYISRASGPVYVLSPOGSPNSAAAYQLRNQVRAE LTSRGIASSKIVNTSYAAVGPDA APIRLSFTGTTAVTTQCGQWPKDISNDLTNQNY NFGCASQNNLAAQIANPEDLVAPR GMTPIDAQRRNNAIQEYRTTTTTIEDAGDSGF"
gene	250040..251317	/gene="cpaE" /locus-tag="RL0216"
CDS	250040..251317	/gene="cpaE" /locus-tag="RL0216" /inference="similar to sequence:INSDC:AF229646" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:Q9L715 (EMBL:AF229646); Caulobacter crescentus.; CpaE.; length=517; id 46.193; 394 aa overlap; query 32-425; subject 124-517 similarity:fasta; with=UniProt:Q92T40 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE RESPONSE REGULATOR PROTEIN.; length=428; id 72.406; 424 aa overlap; query 1-424; subject 1-424" /codon-start=1 /transl-table=11 /product="putative pilus assembly protein" /protein-id="CAK05705.1" /db-xref="GI:115254631" /db-xref="GOA:Q1MMU7" /db-xref="UniProtKB/TrEMBL:Q1MMU7" /translation="MSAIEYEIRNPSELRNAEEA VRMADLENMRPLPRISVHAFCESE ALQHVMECANDRRVAKVSMRITSGGVAAAANMF SGAPTPNLIILETKANAANLLGEL APLAAVCDPTTKVVIIGYYNDIGLYRELIRNGIS EYMQVPVAMPDILTAMASIFVDPD AEPLGRSIAFIGSKGGTGASTIAHNCAFGISNLF STETILADLDLPYGTANIDFDQDP AQGIAEAVFAPDRLDEVFLDRLLTKCSEHLSLLA APSLLDRAVDGQAFQPVLDVLQ RSAPVTVLDPHAWSEWTRSVLSSVDEVVIAAVP DLANLRNAKNMLDALRKMRPNDRP PHLILNQVGMPKRPEISPSDFCEPLEIDPIAIIIP FDINLFGNAANSGRMISEVDPKSP TAETFSQISHIVTGRVAIKKAKKGGLLGLLKRK"
gene	251351..252826	/gene="cpaF" /locus-tag="RL0217"
CDS	251351..252826	/gene="cpaF" /locus-tag="RL0217" /inference="similar to sequence:INSDC:AF229646" /inference="similar to sequence:INSDC:C97385" /note="similarity:fasta;

		with=UniProt:Q9L714 (EMBL:AF229646); Caulobacter crescentus.; CpaF.; length=501; id 67.928; 502 aa overlap; query 1-486; subject 1-501 similarity:fasta; with=UniProt:Q8UIS4 (EMBL:C97385); Agrobacterium tumefaciens (strain C58/ATCC 33970).; ctpG; Component of type IV pilus.; length=491; id 84.615; 494 aa overlap; query 1-489; subject 1-491" /codon-start=1 /transl-table=11 /product="putative component of pilus" /protein-id="CAK05706.1" /db-xref="GI:115254632" /db-xref="GOA:Q1MMU6" /db-xref="UniProtKB/TrEMBL:Q1MMU6" /translation="MFGKRGNEGSGKVGGAIAAPP PPAPAAAPAASSPSILVEPSRESA RQQVTPPQMOTPQKRKPARTDEYYDTKAQVFSAL IDTIDLSQLSKLDGESAREEIRDI VNDIITIKNFAMSISEQEELLEDDICNDVLGYGPL EPLLARDDIADIMVNGAGQTFIEV GGKTIESEIRFRDNAQLLSICQRIVSQVGRRVDE SSPICDARLPDGSRVNVIAPPLSI DGPALTIRKFKKDKLTLDQLVRFGAITPEGATVL QIIGRVRCNVVISGGTGSGKTTL NCLTNYIDRDERVITCEDTAEQLQPPHVVRLET RPPNIEGEGEITMRDLVKNCLMR PERIIVGEVRGPEVFDLLQAMNTGHDGSMGTIHA NTPRECLSRIESMIAMGGFTLPK TVREIISSSVDVVIQAARLRDGSRRITQITEVIG MEGDVIIITQDLMRYEIEGEDANGR LVGRHMSTGVGKPHFWDRARYFNEEKRLAAALDA MEAKTKE" /gene="cpaF" /locus-tag="RL0217" /inference="protein motif: Pfam:PF00437.9" /note="Pfam match to entry PF00437.9 GSPII-E"
misc-feature	251714..252586	
gene	252832..253839	/locus-tag="RL0218" /inference="similar to sequence:INSDC:AJ584609" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:Q6MRH4 (EMBL:AJ584609); Bdellovibrio bacteriovorus.; TadB; TadB protein (Flp pilus assembling protein).; length=Flp pilus assembling ( 291; id 24.806; 258 aa overlap; query 87-335; subject 35-291 similarity:fasta; with=UniProt:Q92T38 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium
CDS	252832..253839	

		meliloti).; HYPOTHETICAL TRANSMEMBRANE PROTEIN.; length=336; id 68.452; 336 aa overlap; query 1-335; subject 1-336" /codon-start=1 /transl-table=11 /product="putative pilus assembly protein" /protein-id="CAK05707.1" /db-xref="GI:115254633" /db-xref="GOA:Q1MMU5" /db-xref="UniProtKB/TrEMBL:Q1MMU5" /translation="MFGFDPIVLAIVVLA AVSAA AVAYALLFSKIEADKKSASRINRV KSAESDRVKVKAARDRVQELSKRRKSVQDNLKDL EKRRQHEKTKKTVMKSRVLVQAGLT ITAAKFYLLISAVFASVLLLIALLVVGASLMVMIGI AVVAGLGLPRWVVGFLIKRRQTKF LNEFPNALDVITRSIKSGLPLNDAIRLIATEGTE PVKSEFLRVIEAQVGLSIPDACA RMTIHMPQLQEVNFFAIVIAIQSQAGGNLSEAIGN LSKVLRERRKMKAKVSALSMEAKA SAVIIGALPFIIVATLVYMTSPNYMMILFTDPRGH FIMGVSAIWMSIGIFVMRNMVNFD I" /locus-tag="RL0218" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0218 by SignalP 2.0 HMM (Signal peptide probability 0.999) with cleavage site probability 0.707 between residues 23 and 24" /locus-tag="RL0218"
sig-peptide	252832..252898	
misc-feature	order(252847..252915, 253153..253212, 253222..253290, 253657..253716, 253759..253827)	/inference="protein motif:TMHMM:2.0" /note="5 probable transmembrane helices predicted at aa 6-28, 108-127, 131-153, 276-295 and 310-332" /locus-tag="RL0218"
misc-feature	253324..253713	/locus-tag="RL0218" /inference="protein motif:Pfam:PF00482.9" /note="Pfam match to entry PF00482.9 GSPII-F"
gene	253855..254841	/gene="tadC"
CDS	253855..254841	/locus-tag="RL0219" /gene="tadC" /locus-tag="RL0219" /inference="similar to sequence:INSDC:AE007962" /inference="similar to sequence:INSDC:AY083157" /note="similarity:fasta; with=UniProt:Q8KQI5 (EMBL:AY083157); Haemophilus ducreyi.; TadC.; length=281; id 24.038; 312 aa overlap; query

		16-324; subject 4-276 similarity:fasta; with=UniProt:Q8UIS6 (EMBL:AE007962); Agrobacterium tumefaciens (strain C58/ATCC 33970).; ctpI; Components of type IV pilus (AGR-C-371p).; length=AGR-C- ( 328; id 74.390; 328 aa overlap; query 1-328; subject 1-328" /codon-start=1 /transl-table=11 /product="putative component of pilus protein" /protein-id="CAK05708.1" /db-xref="GI:115254634" /db-xref="GOA:Q1MMU4" /db-xref="UniProtKB/TrEMBL:Q1MMU4" /translation="MSQDLAATLTNPMSMLIALLV AIAVFATFYTIAVPFFFERGDLNKR MKAVSTEREQIRARERARMNTETGAGKASLRSON NRSVRQIVERFNLRLKALVDENTIN KLRAAGFRSENALNTFLVARFLLPFLFLALAAFV VFGLGNLAEKGTPIRLFAVIGVGY LGFYAPNIYISNRMGKRQHSIKRAWPDALDLMLI CVESGISIEAAMRRVSEELGEQSP ALAEEMVLTTAELSFLPDRRVALENLATRTQIEL VRSVTQALIQAADRYGTPVAQALRV LAQEGRDERMNEAEKKAALPPKLTVPMLFFLP VLIIVILGPAGIQVADKF" /gene="tadC" /locus-tag="RL0219" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0219 by SignalP 2.0 HMM (Signal peptide probability 0.883) with cleavage site probability 0.738 between residues 32 and 33" /gene="tadC"  /locus-tag="RL0219" /inference="protein motif:TMHMM:2.0" /note="4 probable transmembrane helices predicted at aa 15-37, 118-140, 150-172 and 300-322" /gene="tadC" /locus-tag="RL0219" /inference="protein motif:Pfam:PF00482.9" /note="Pfam match to entry PF00482.9 GSPII-F" /locus-tag="RL0220" /locus-tag="RL0220" /inference="similar to sequence:INSDC:AE005613" /inference="similar to sequence:INSDC:AP005079" /note="similarity:fasta;
sig-peptide	253855..253948	
misc-feature	order(253897..253965, 254206..254274, 254302..254370, 254752..254820)	
misc-feature	254410..254808	
gene	255044..255676	
CDS	255044..255676	

		with=UniProt:RHTC-ECOLI (EMBL:AE005613); Escherichia coli O157:H7.; rhtC; Threonine efflux protein.; length=206; id 35.749; 207 aa overlap; query 6-205; subject 4-205 similarity:fasta; with=UniProt:Q87NK6 (EMBL:AP005079); Vibrio parahaemolyticus.; Putative threonine efflux protein.; length=211; id 37.879; 198 aa overlap; query 7-203; subject 8-205" /codon-start=1 /transl-table=11 /product="putative transmembrane efflux protein" /protein-id="CAK05709.1" /db-xref="GI:115254635" /db-xref="GOA:Q1MMU3" /db-xref="UniProtKB/TrEMBL:Q1MMU3" /translation="MSSAGIFISIMAALAVGAMS PGPFSFVVVSRIAISRRLDGLAAA LGMGAGGVVFAVLALAGLTALLSQFEWLYVLLKV AGGAYLVYIAVNIWRSAGQPLEVS DAVNGNRALRLSFMTALLTQLSNPKTIIVYASLF AALLPRTVPLDLIVALPLGVFAVE AGWYSIVAFALSARHPRLYLAAGWIDRAAGAV MGGLGLRLILSGLSAR" /locus-tag="RL0220" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0220 by SignalP 2.0 HMM (Signal peptide probability 0.993) with cleavage site probability 0.697 between residues 26 and 27" /locus-tag="RL0220"
sig-peptide	255044..255119	
misc-feature	order(255056..255124, 255161..255229, 255257..255316, 255374..255442, 255485..255553)	/inference="protein motif:TMHMM:2.0" /note="5 probable transmembrane helices predicted at aa 5-27, 40-62, 72-91, 111-133 and 148-170" /locus-tag="RL0220" /inference="protein motif:PFam:PF01810.7" /note="Pfam match to entry PF01810.7 LysE" /locus-tag="RL0221"
misc-feature	255086..255661	
gene	complement(255786..256619)	/locus-tag="RL0221"
CDS	complement(255786..256619)	/locus-tag="RL0221"
		/inference="similar to sequence:INSDC:HS384249" /note="similarity:fasta; with=UniProt:Q8UIS7 (EMBL:HS384249); Agrobacterium tumefaciens (strain C58/ATCC

gene  
CDS

256764..258155  
256764..258155

33970).; Hypothetical protein  
Atu0215 (AGR-C-369p).; length=289;  
id 65.683; 271 aa overlap; query  
4-272; subject 20-289;  
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ANPGDRNVLAAYGKAQAAAGQFQQALDTIGRAQT  
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ARQRYRDALDIQPNEPSILSNLGMSYVLTGDLRT  
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sequence:INSDC:SME591782"  
/note="Codons 120 to the  
C-terminus are similar to codons  
80 to the C-terminus of Salmonella  
typhimurium. PepB PEPB-SALTY  
(EMBL:AE008815) ( Peptidase B (EC  
3.4.11.23) (Aminopeptidase B).),  
and to Rhizobium meliloti  
(Sinorhizobium meliloti). PUTATIVE  
AMINOPEPTIDASE PROTEIN (EC  
3.4.-.-). Q92T36 (EMBL:SME591782)  
(EC ( 463) similarity:fasta;  
with=UniProt:PEPB-SALTY  
(EMBL:AE008815); Salmonella  
typhimurium.; pepB; Peptidase B  
(EC 3.4.11.23) (Aminopeptidase  
B).; length=EC 3.4.11.23; id  
40.625; 320 aa overlap; query  
122-430; subject 78-396  
similarity:fasta;  
with=UniProt:Q92T36  
(EMBL:SME591782); Rhizobium  
meliloti (Sinorhizobium  
meliloti).; PUTATIVE  
AMINOPEPTIDASE PROTEIN (EC  
3.4.-.-).; length=EC ( 463; id  
83.624; 458 aa overlap; query  
1-458; subject 1-458"  
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/transl-table=11  
/product="putative peptidase"  
/protein-id="CAK05711.1"  
/db-xref="GI:115254637"



		/db-xref="GOA:Q1MMU1" /db-xref="UniProtKB/TrEMBL:Q1MMU1" /translation="MAPYQFIERPTPFNTKGGST LPIFAVTPAHJETGTIDPIALDWA RRAGYKAESGSLLLIPTAEGHLGGALYGLGTNPS EQPYITGRLARALPAGDWHIETAP LTANRLALGFGLGSYRFDYKSEKSPAATLMIPR DADAADIKRQLAGVFLARDLINTP TNDMGPNQLEAVFRGLAAHYKAEMSVISGDDLLT QNFPLVHTVGRASADAPRLLELRW GKKGHRKVTLVGKGVCFTGGLDIKPAASMLLMK KDMGGAANVMGLALMIMDAKLKVD LRVIVPVVENAISSNAFRPGDIYRSRKGLTVQID NTDAEGRILADALAYADEEEPEL LIDMATLTGAARVALGPDLPFFTTDDANLAHDLT EASLETDDPIWRLPLYSGYEKDIR TKFADLTNAPAGGMAGAITAALFLKRFVSKAKSW AHFDIYGWAQSERPHSPGGGEAQA IRALFHHIRESLR"
misc-feature	257211..258131	/locus-tag="RL0222" /inference="protein motif: Pfam:PF00883.9" /note="Pfam match to entry PF00883.9 Peptidase-M17"
gene	258334..258684	/locus-tag="RL0223"
CDS	258334..258684	/locus-tag="RL0223" /inference="similar to sequence: INSDC:SME591782" /note="similarity: fasta; with=UniProt:Q92T35 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE TRANSCRIPTION REGULATOR PROTEIN. PUTATIVE TRANSCRIPTION REGULATOR PROTEIN.; length=114; id 79.825; 114 aa overlap; query 1-114; subject 1-114" /codon-start=1 /transl-table=11 /product="putative MarR family transcriptional regulator" /protein-id="CAK05712.1" /db-xref="GI:115254638" /db-xref="GOA:Q1MMU0" /db-xref="UniProtKB/TrEMBL:Q1MMU0" /translation="MPIELTASQALGLWHGVALD QVRHDDRDLTLRQMAILLHIYLV PPHTVRGLAATLEVTKPVITRALDTMGEMGLVDR VRDDADRRNVIIKRTVGGALYLEN LGDLIRDQARRLPI"
misc-feature	258418..258606	/locus-tag="RL0223" /inference="protein motif: Pfam:PF01047.8" /note="Pfam match to entry PF01047.8 MarR"
gene	258696..259553	/locus-tag="RL0224"
CDS	258696..259553	/locus-tag="RL0224" /inference="similar to sequence: INSDC:BSEPEPII" /inference="similar to sequence: INSDC:SME591782"

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/feature "misc-feature" 259224..259499
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    /note="Similar, but extended at
the N-terminus to Bacillus
sphaericus. Dipeptidyl-peptidase
VI (EC 3.4.22.-) (DPP VI)
(Gamma-D-glutamyl-L- diamino acid
endopeptidase II)
(Gamma-D-glutamyl-MESO-diaminopime
late peptidase II) (Endopeptidase
II). DPP6-BACSH (EMBL:BSEPEPII)
(EC 3.4 ( 271), and similar to
entire protein of Rhizobium
meliloti (Sinorhizobium meliloti).
Hypothetical protein SMc02827.
Q92KU2 (EMBL:SME591782) (284)
similarity:fasta;
with=UniProt:DPP6-BACSH
(EMBL:BSEPEPII); Bacillus
sphaericus.; Dipeptidyl-peptidase
VI (EC 3.4.22.-) (DPP VI)
(Gamma-D-glutamyl-L- diamino acid
endopeptidase II)
(Gamma-D-glutamyl-MESO-diaminopime
late peptidase II) (Endopeptidase
II).; length=EC 3.4 ( 271; id
26.667; 270 aa overlap; query
37-274; subject 4-271
similarity:fasta;
with=UniProt:Q92KU2
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; Hypothetical protein
SMc02827.; length=284; id 64.539;
282 aa overlap; query 3-283;
subject 4-284"
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/transl-table=11
/product="putative
dipeptidyl-peptidase"
/protein-id="CAK05713.1"
/db-xref="GI:115254639"
/db-xref="UniProtKB/TrEMBL:Q1MMT9"
/translation="MTMLDCRLHAYRSDLAEAGL
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ASDGYVGIVKADALLEGRPAATHI
VTVQRTFLYPEPELKRPHQAILSMGSRIHVAGET
EARGNRYVVLEDGTAIFAKHVQPI
GALDGADYVEIVARFLETPYLWGGRSGLGIDCSG
LVQLAMLMTGRAAPRDTDMQAAGL
GQPIDRSELRRGDLVFWKGHVAVFEDPETILHAN
GHSMTVARENFAAAVERIGWLYEQ
PTGYRRPIS"
/locus-tag="RL0224"
/inference="protein
motif: Pfam:PF00877.8"
/note="Pfam match to entry
PF00877.8 NLPC-P60"
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/feature "gene" complement(259554..2609
45)
{
    /locus-tag="RL0225"
}

/feature "CDS" complement(259554..2609
45)
{
    /locus-tag="RL0225"
    /inference="similar to

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sequence:INSDC:AE008241"
/inference="similar to
sequence:INSDC:RSAMDANTH"
/note="similarity:fasta;
with=UniProt:Q53116
(EMBL:RSAMDANTH); Rhodococcus sp.;
amdA; Enantiomerase-selective
amidase.; length=462; id 28.755;
466 aa overlap; query 5-459;
subject 5-458 similarity:fasta;
with=UniProt:Q8U7K8
(EMBL:AE008241); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; gatA; Glutamyl-tRNA
amidotransferase subunit A
(AGR-L-854p).; length=465; id
73.160; 462 aa overlap; query
1-461; subject 1-462"
/codon-start=1
/transl-table=11
/product="putative amidase"
/protein-id="CAK05714.1"
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/db-xref="UniProtKB/TrEMBL:Q1MMT8"
/translation="MTETDLTIHELQRFAKSL
SPLEYWLALEDHIAAWEPSISALY
LYDPESARAQAKASTERWAKAETLGPLDGIPVTL
KELIATKGQPVPSGTRAVELKPAD
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FHPLSRNPWDITQNPGGSSAGASA
AAAAGYGPLHIGTDIGGSVRLPAGWTGIFGFKPS
HGRIPADPYVVGRCVGP MARTVED
AAF5MATLSRPDWRDGTSLPPNDFNWMDL DIDLS
GMKIGLMLDAGCGLAVDDEIRTAV
ETA AKQFEAAGATILSVQPVLTRAMLDGLDNFWR
SRLWGD IADLDEERRDSILPYIRD
WAMGGADISGVDVRGFNQTIEMRKSCGRLFTEV
DALLSPTNP IISYP AEWASPTNDP
ALPFEHIGFTVPWNMSEQPAASINCGFSRSGMPI
GLQIVGPRFDDMRVLR LSKAFEDW
MGGVRSWPQPPIG"
misc-feature      complement(259623..2608 /locus-tag="RL0225"
76)
                  /inference="protein
                  motif: Pfam:PF01425.8"
                  /note="Pfam match to entry
                  PF01425.8 Amidase"
gene              complement(260982..2618 /locus-tag="RL0226"
45)
CDS               complement(260982..2618 /locus-tag="RL0226"
45)
                  /inference="similar to
                  sequence:INSDC:AE008241"
                  /note="similarity:fasta;
                  with=UniProt:Q8U7K9
                  (EMBL:AE008241); Agrobacterium
                  tumefaciens (strain C58/ATCC
                  33970).; ABC transporter, membrane
                  spanning protein (AGR-L-856p).;
                  length=273; id 68.773; 269 aa
                  overlap; query 18-286; subject

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/transl-table=11
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permease component of ABC
transporter"
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/db-xref="GI:115254641"
/db-xref="GOA:Q1MMT7"
/db-xref="UniProtKB/TrEMBL:Q1MMT7"
/translation="MVPIASTAIAGRRRVFRLSR
RMNLIAGAVIIGLLVAVALLSLVW
TPLPPAKMQIIHKLQPPLAFGLLGTQFGHDVLS
MLMAGCWNSLSIAITAVTIGGTLG
SIAGISAAAIRGPFEALLMRICDVIFALPPILSA
MVLGAFLGPGRFTAITAIVFMIP
VFARVTLATSLQAWSRDYVTAARAIGNTRLTISL
RHLVLPNIISQIIIVHGAIQLGLAIL
TEAGLSFLGLGMAPPAPTWGRMLADAQTYLALAP
WLAILPGLAIALTVFGFNMLGDGL
RDLLDPREASR"
misc-feature    complement(260988..261608) /locus-tag="RL0226"
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                motif:Pfam:PF00528.10"
                /note="Pfam match to entry
                PF00528.10 BPD-transp-1"
misc-feature    complement(join(261039..261107,261165..261233,
                261342..261410,
                261423..261491,
                261510..261578,
                261714..261782))
                /inference="protein
                motif:TMHMM:2.0"
                /note="6 probable transmembrane
                helices predicted at aa 22-44,
                90-112, 119-141, 146-168,205-227
                and 247-269"
gene            complement(261849..262796) /locus-tag="RL0227"
CDS             complement(261849..262796) /locus-tag="RL0227"
                /inference="similar to
                sequence:INSDC:AE008241"
                /note="similarity:fasta;
                with=UniProt:Q8U7L0
                (EMBL:AE008241); Agrobacterium
                tumefaciens (strain C58/ATCC
                33970).; ABC transporter, membrane
                spanning protein (AGR-L-857p).;
                length=316; id 71.111; 315 aa
                overlap; query 1-315; subject
                1-315"
                /codon-start=1
                /transl-table=11
                /product="putative transmembrane
                component of ABC transporter"
                /protein-id="CAK05716.1"
                /db-xref="GI:115254642"
                /db-xref="GOA:Q1MMT6"
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/translation="MIPLLARRFVGLIVTLVVVS
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PETLAALRHSLGLDQPLLLRYGQWLAGVLSGDLG
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LMAIVLSVAIALPLGVLAASRRGGIFDVIATLFS
QISIAVPAFWVALLLIILFSTMLG
LMPAGGFPGWSAGLTPALQALVMPAVALAMPQAG
VLTRVARSAVLDTMHEDFARTAVA
KGLSRSAVLWRHIVPNALIPILTMIGLQFTFLVA
GAVLVENVFNLPLGLGRLALQALSQ
RDIIVMQDVVLEFFAGLVIVMNFIVDLSYMAIDPR
MRKAA"
misc-feature      complement(261858..2625 /locus-tag="RL0227"
14)
/inference="protein
motif:PFam:PF00528.10"
/note="Pfam match to entry
PF00528.10 BPD-transp-1"
misc-feature      complement(join(261876. /locus-tag="RL0227"
.261944,262026..262094,
262200..262268,
262311..262379,
262440..262508,
262704..262772))
/inference="protein
motif:TMHMM:2.0"
/note="6 probable transmembrane
helices predicted at aa 9-31,
97-119, 140-162, 177-199,235-257
and 285-307"
gene              complement(262908..2644 /locus-tag="RL0228"
37)
CDS               complement(262908..2644 /locus-tag="RL0228"
37)
/inference="similar to
sequence:INSDC:HS184254"
/note="Similar, but truncated at
the N-terminus, to Agrobacterium
tumefaciens (strain C58/ATCC
33970). ABC transporter, substrate
binding protein (AGR-L-861p).
Q8U7L1 (EMBL:HS184254) (540)
similarity:fasta;
with=UniProt:Q8U7L1
(EMBL:HS184254); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; ABC transporter,
substrate binding protein
(AGR-L-861p).; length=540; id
74.168; 511 aa overlap; query
1-509; subject 30-540"
/codon-start=1
/transl-table=11
/product="putative solute-binding
component of ABC transporter"
/protein-id="CAK05717.1"
/db-xref="GI:115254643"
/db-xref="GOA:Q1MMT5"
/db-xref="UniProtKB/TrEMBL:Q1MMT5"
/translation="MIKLSFAPSARLARRLSLSA
ALSAGLVMTAMTPAEAAKTTLNLG
MSVEPTGLDPTIAAPVAIGOVIVONVFEGLVTI

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QAGKIQPQLAKSWEISPDGLTYTF  
 KLQTGVKFHDGEAFDAASAKFSLDRAGADSVNP  
 QKRFFASIASIDTPDAETLVLHLS  
 APTGSLIYWLGWPASVMVAPKTAADDKTTTPVGTG  
 PFKFASWAKGDKVELARNADYWNK  
 DAAAKLDKVTFRFIADPQAQAAALKSGDLDAFPE  
 FAAPELMSSFDDGDARLVTRIGNTE  
 LKVVAGMNTAKKPFDDKRVQALMMAIDRKTVID  
 GAWSGLGTPIGSHYTPNDPGYQDM  
 TGVLPYDVEKAKALLAEAGYPNGFTFTTIKSPQMA  
 YAPRSAQVMQAMFAEIGVTMNIET  
 TEFPKWVQDIMKDRNFDMTIVAHAEPLDIDIYA  
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 DPAAQSAIYGAEQKILAEDVPALYLFVMPKLGWV  
 DKKLKGLWENEPISNVLSGVSWD E"

misc-feature complement(262917..264398) /locus-tag="RL0228"  
 /inference="protein  
 motif: Pfam:PF00496.8"  
 /note="Pfam match to entry  
 PF00496.8 SBP-bac-5"

sig-peptide complement(264326..264437) /locus-tag="RL0228"  
 /inference="protein  
 motif: SignalP-HMM:2.0"  
 /note="Signal peptide predicted  
 for RL0228 by SignalP 2.0 HMM  
 (Signal peptide probability 1.000)  
 with cleavage site probability  
 0.965 between residues 36 and 37"

gene complement(264588..265508) /locus-tag="RL0229"

CDS complement(264588..265508) /locus-tag="RL0229"  
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 sequence: INSDC:AE009372"  
 /note="Similar to Agrobacterium  
 tumefaciens (strain C58/ATCC  
 33970). Transcriptional regulator,  
 LysR family. Q8U7L2  
 (EMBL:AE009372) (332)  
 similarity: fasta;  
 with=UniProt:Q8U7L2  
 (EMBL:AE009372); Agrobacterium  
 tumefaciens (strain C58/ATCC  
 33970).; Transcriptional  
 regulator, LysR family.;  
 length=332; id 75.168; 298 aa  
 overlap; query 1-298; subject  
 33-330"  
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 transcriptional regulator"  
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 /db-xref="GOA:Q1MMT4"  
 /db-xref="UniProtKB/TrEMBL:Q1MMT4"  
 /translation="MQIRALMYFDELVRTNSMRQ  
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 APLVERSARGVKLTAAGELLAARAGRTLRELDHV  
 QQLIEDLKGLQRGRVSIYANGATV

		ANLLAPALAEFSLKYPKLRFTVTTITSARQAIDAV NSAEADIAVTLFAPPMSGTKVRLR SEIGYDLIATPQHFAAAHAEIPLRMLADYALALP DQSFGFRQAFDALFEKEGLSLDPV FVTSSLEMLKELVLSGAAVTLLPALTVRREIEAG QLLAIPLAGKTGIRTHVDLCVAPD RQLSFAATKLLDFIERFMRERTNRRRAETKD"
misc-feature	complement(264624..265253)	/locus-tag="RL0229"  /inference="protein motif: Pfam: PF03466.5" /note="Pfam match to entry PF03466.5 LysR-substrate"
misc-feature	complement(265323..265502)	/locus-tag="RL0229"  /inference="protein motif: Pfam: PF00126.10" /note="Pfam match to entry PF00126.10 HTH-1"
gene	complement(265565..266560)	/locus-tag="RL0230"
CDS	complement(265565..266560)	/locus-tag="RL0230"  /inference="similar to sequence: INSDC: AE017302" /inference="similar to sequence: INSDC: HS666251" /note="similarity: fasta; with=UniProt: Q72KS9 (EMBL: AE017302); Thermus thermophilus (strain HB27/ATCC BAA-163/DSM 7039).; Endo-type 6-aminohexanoate oligomer hydrolase.; length=330; id 42.724; 323 aa overlap; query 11-328; subject 12-324 similarity: fasta; with=UniProt: Q8UCD3 (EMBL: HS666251); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu2565.; length=334; id 72.755; 323 aa overlap; query 6-325; subject 6-328; putative peptidase" /codon-start=1 /transl-table=11 /product="endo-type 6-aminohexanoate oligomer hydrolase" /protein-id="CAK05719.1" /db-xref="GI:115254645" /db-xref="GOA:Q1MMT3" /db-xref="UniProtKB/TrEMBL:Q1MMT3" /translation="MPDLLNLITDIEGVSVGHAT DLVLGSGVTIVVFDEPVVASGTVL GGAPGGRDTGLLDPSMTVNAVDAFVLSGGSAFGL DAAGGVQAGLRELGRGFVGPVRI PIVPQAILMDLLNGGDKDWGLHSPYRDMGYTALQ AAAKGTFALGTTGAGTGATTATVK GGLGSASAVSSAGHRVAAIVAVNALGSATIGDGP HFWAAPFEKDAEFGGLGMPDVADH RMRLKGMNTPATTIGAVVTDAQLTKAEAHRLSLA GHDGFARALLPAHLPLDGDTVFAA"

STARHQRDDMASLMELCHLATIVMARAIARGVYA  
 ATALPVEGAQKAWRDYASSS"

misc-feature complement(265574..2665 /locus-tag="RL0230"  
 48)  
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 motif: Pfam: PF03576.3"  
 /note="Pfam match to entry  
 PF03576.3 Peptidase-S58"

gene complement(266793..2670 /locus-tag="RL0231"  
 68)

CDS complement(266793..2670 /locus-tag="RL0231"  
 68)  
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 sequence: INSDC: HS665250"  
 /note="similarity: fasta;  
 with=UniProt: Q8UCE1  
 (EMBL: HS665250); Agrobacterium  
 tumefaciens (strain C58/ATCC  
 33970).; Hypothetical protein  
 Atu2557 (AGR-C-4631p).; length=72;  
 id 71.429; 63 aa overlap; query  
 23-85; subject 6-68"  
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 /transl-table=11  
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 /db-xref="GI:115254646"  
 /db-xref="UniProtKB/TrEMBL: Q1MMT2"  
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 YRAAGVLSMKKQVIEYAGVPVGIVI  
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gene complement(267509..2704 /locus-tag="RL0232"  
 30)

CDS complement(267509..2704 /locus-tag="RL0232"  
 30)  
 /inference="similar to  
 sequence: INSDC: PCDGD"  
 /inference="similar to  
 sequence: INSDC: SME591791"  
 /note="C-terminus from codon 545  
 is similar to Burkholderia cepacia  
 (Pseudomonas cepacia). dgdA  
 DGDA-BURCE (EMBL: PCDGD) (  
 2,2-dialkylglycine decarboxylase  
 (EC 4.1.1.64) (DGD).), and entire  
 protein is similar to Rhizobium  
 meliloti (Sinorhizobium meliloti).  
 PUTATIVE AMINOTRANSFERASE PROTEIN  
 (EC 2.6.1.-). Q92MC9  
 (EMBL: SME591791) (( 975)  
 similarity: fasta;  
 with=UniProt: DGDA-BURCE  
 (EMBL: PCDGD); Burkholderia cepacia  
 (Pseudomonas cepacia).; dgdA;  
 2,2-dialkylglycine decarboxylase  
 (EC 4.1.1.64) (DGD).; length=432;  
 id 34.339; 431 aa overlap; query  
 549-970; subject 6-429  
 similarity: fasta;  
 with=UniProt: Q92MC9



(EMBL:SME591791); Rhizobium  
meliloti (Sinorhizobium  
meliloti).; PUTATIVE  
AMINOTRANSFERASE PROTEIN (EC  
2.6.1.-).; length=( 975; id  
64.928; 978 aa overlap; query  
1-973; subject 1-975"  
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VLTVRGQGYQVRLLEYLEGQGLTELTYLAPASVA  
ALGALCARLAQALADFNHPGLDRS  
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AIYPLSEEELKALWPLIVARAVILVASGEQQISV  
DPDNDYVRGNLDRERAIFDTAMSV  
PFDLMEAAILKAAGADVAAPETSGWLPLLPDIDP  
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MDWRL LARMATENGTAATRYGEYRLSRAGTARGQ  
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IGWKDQHLTLAGDNMTLHLDGLDLSVDDGAEIAA  
GDSLGTVFGEASSLGGLRVQLCSV  
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AAPPQIERGWKEHLFDVEGRAYLDMVNNVTILGH  
GHPRFAAAIGAQWLRNLNTNSRFHY  
AAITEFSERLAALSPDGLDAVFLVNSGSEANDLA  
LRLAQAHSGARNMLCLLEAYHGWS  
AASDAVSTSIADNPQAPTTRPDWVHTIVSPNTYR  
GDFRGPDTAADYLGMATPVLEAID  
AAGEGLAGFIAESVYGNAGGIPLPEGYLKELYAQ  
VRARGGLCIADEVQVGYARLGHYF  
WGFQQQGVVPDIITVAKGMGNHPLGAVITTREI  
AQSLEKEGTFFSSTGGSPVSCVAG  
MTVLDIMAEKQLQENARTVGDHLKARLAALIDRH  
PIAGAVHGMGLYLGLFVRDRRTL  
EPATEETAACDRLLLELGVIMQPTGDHQNVLKIK  
PPLCLSIDSADFFADMLEKVL EEG W"

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gene	complement(270544..271428)	/gene="purU"
CDS	complement(270544..271428)	/locus-tag="RL0233" /gene="purU"  /locus-tag="RL0233" /EC-number="3.5.1.10"

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/inference="similar to
sequence:INSDC:HS655252"
/note="similarity:fasta;
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(EMBL:C36871); Escherichia coli.;
purU; Formyltetrahydrofolate
deformylase (EC 3.5.1.10)
(Formyl-FH(4) hydrolase).;
length=280; id 37.993; 279 aa
overlap; query 5-281; subject
8-280 similarity:fasta;
with=UniProt:Q8UCL9
(EMBL:HS655252); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; purU;
Formyltetrahydrofolate deformylase
(AGR-C-4474p).; length=294; id
83.673; 294 aa overlap; query
1-294; subject 1-294"
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deformylase"
/protein-id="CAK05722.1"
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/db-xref="UniProtKB/TrEMBL:Q1MMT0"
/translation="MTSYVLTVSCKSTRGIVAAI
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FFTRVSFISEEGVPLAELKEGFEPICKRFAMDAE
IHDGNARMKVLLMVSFRFGHCLNDL
LYRWKIGALPIDIVGVVSNHFDYQKVVVNHDIPF
HHIKVTKENKLQAEQGIMDIVEQT
GTELIVLARYMQVLSAMCQKMSGKIINIHSFL
PSFKGANPYKQAYGRGVKLGATA
HYVTADLDEGP IIEQDTARITHAQSPDDYVSIGR
DVESQVLARAIHAHIHRTFLNGN
RTVVFPASPGGYASERMG"
misc-feature      complement(270640..2711 /gene="purU"
73)

/locus-tag="RL0233"
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motif: Pfam:PF00551.8"
/note="Pfam match to entry
PF00551.8 Formyl-trans-N"
misc-feature      complement(271186..2714 /gene="purU"
19)

/locus-tag="RL0233"
/inference="protein
motif: Pfam:PF01842.8"
/note="Pfam match to entry
PF01842.8 ACT"
gene              complement(271645..2726 /gene="exoZ"
64)

/locus-tag="RL0234"
CDS               complement(271645..2726 /gene="exoZ"
64)

/locus-tag="RL0234"
/inference="similar to

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/feature="10 probable transmembrane
helices predicted at aa 7-25,
35-57, 77-99, 130-152,159-176,
181-203, 208-227, 237-254, 261-283
and 298-320"
gene complement(272824..2740 /locus-tag="RL0235"
14)
CDS complement(272824..2740 /locus-tag="RL0235"
14)
/inference="similar to
sequence:INSDC:AE011898"
/inference="similar to
sequence:INSDC:XC22511"
/note="similarity:fasta;
with=UniProt:Q56771
(EMBL:XC22511); Xanthomonas
campestris.; gumE; GumE.;
length=432; id 28.571; 399 aa
overlap; query 1-384; subject
17-402 similarity:fasta;
with=UniProt:Q8PJF0
(EMBL:AE011898); Xanthomonas
axonopodis (pv. citri).; gumE;
GumE protein.; length=433; id
27.990; 393 aa overlap; query
6-384; subject 23-402"
/codon-start=1
/transl-table=11
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exopolysaccharide biosynthesis
protein"
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/db-xref="UniProtKB/TrEMBL:Q1MMS8"
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DYFANTRGLPLSYNTTGLFQNAL
GFPERFSFGIIDHRSSSIFLEQVSLANFCGVIAV
YLISMWEKLSRWDRLLMIGTAVLI
LVTNDTRTMLIFCFACIVGYFVFPKIPKNFNAL
MPLIVAAGFLVYVLKPNATGDNFT
GRINLTMKKIMELDPLAVLGLSVDRVAEFADSGY
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.272961,273019..273087,
273217..273273,
273292..273387,
273415..273483,
273616..273684,
273775..273843,
273877..273936,
273946..274014))
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motif:TMHMM:2.0"
/note="9 probable transmembrane
helices predicted at aa 35-57,

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		61-80, 92-114, 145-167, 212-234, 244-275, 282-300, 344-366 and 386-408"
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CDS	complement(274119..2752 01)	/inference="similar to sequence:INSDC:AF233448" /note="similarity:fasta; with=UniProt:Q9F0G8 (EMBL:AF233448); Rhizobium meliloti (Sinorhizobium meliloti).; endS; Endoglucanase precursor.; length=364; id 49.008; 353 aa overlap; query 10-359; subject 15-364" /codon-start=1 /transl-table=11 /product="putative carboxymethyl cellulase" /protein-id="CAK05725.1" /db-xref="GI:115254651" /db-xref="GOA:Q1MMS7" /db-xref="UniProtKB/TrEMBL:Q1MMS7" /translation="MLRFAAIARMPMKTTTRLTA LLLAALIPSPALAAEAPCYRGVN LSGGEYGERGGIYGTNYTYPSEDTIGYFAEKGMT IIRLPFRWERLQPALGGRLDEDEL KRIKDTIGLIRKHGMAVLLDPHNFGYYDKTQVGT APATDAAFGDFWARLAVEFANQDG VLFGLMNEPHDIKATDWLDAANAAIRSIRAVGAR NLILVPGTAWSGAGSWEKDVIGGA NGTVMLGVRDPLDFYAYEVHQYLDADSSGTHPTC EGAGA AVAAINGVTAWLKQNHKRG FLGEFGASADKDCMSGLTEIYATMSDNSDVWLGW SYWAAGDWWPANEPFNVQPRKGPE RPQMRLLAEVAKAGAGTCSAVKPAGK"
misc-feature	complement(274233..2750 78)	/locus-tag="RL0236"
		/inference="protein motif: Pfam:PF00150.7" /note="Pfam match to entry PF00150.7 Cellulase"
sig-peptide	complement(275096..2752 01)	/locus-tag="RL0236"
		/inference="protein motif: SignalP-HMM:2.0" /note="Signal peptide predicted for RL0236 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 1.000 between residues 34 and 35"
gene	275304..276911	/locus-tag="RL0237"
CDS	275304..276911	/locus-tag="RL0237" /inference="similar to sequence:INSDC:AE009744" /note="similarity:fasta; with=UniProt:Q8YAW9 (EMBL:AE009744); Brucella melitensis.; SUCCINOGLYCAN BIOSYNTHESIS TRANSPORT PROTEIN

		EXOP.; length=572; id 30.784; 536 aa overlap; query 5-507; subject 26-560" /codon-start=1 /transl-table=11 /product="putative exopolysaccharide related transporter" /protein-id="CAK05726.1" /db-xref="GI:115254652" /db-xref="GOA:Q1MMS6" /db-xref="UniProtKB/TrEMBL:Q1MMS6" /translation="MNQYDRNRVSRLPDWRSFEP SQTAPGVRVRSPVIRPDDFVRPS PEPAPPPFVPPASIAETRQYEPPAPPPPKPPVVD APPNAEPAAAPLLDLRSSIAAIW SRRLIVFGLALLGALAGGAVAPLIAQKFTAVSSL YFDPQRQIGLADAGAQSSGSPSEMI SALIDSQVQILTSGNVLRRVAEAMKLDQDPEFTG GRTDGAALIGTLQKALVITREAST YVVS LAATTNDPEKSARLANQVVTSTFTEEENSAS NGIYENTSSTLDGRLDDLRLQKVLE AEQAVETFRADNDMAATEGNLI SDQRLLSLNTLL VTAQEKTIQAKARADAVANLRVED IVAGNQAEGGVTSPLVSLRQQYATQAAAVGSLES QMGTRHPRLQAARSSLQSI SVEIR GELQRLATSARGEYEQAKAAEDSIAKELAVQKAL HASSSDKQVELNELQRKATAARDI YETVLKRSSQTSEEQNLNQSNIRVISPAEPPVKA DGPGKKILLVAGIIGGFLAGFVVG AGFAILAGLFGHPVIRSYFRKSSAAAA" /locus-tag="RL0237" /inference="protein motif: Pfam: PF02706.5" /note="Pfam match to entry PF02706.5 Wzz"
misc-feature	275571..276032	/locus-tag="RL0237" /inference="protein motif: Pfam: PF02706.5" /note="Pfam match to entry PF02706.5 Wzz"
misc-feature	order(275619..275687, 276792..276860)	/locus-tag="RL0237"  /inference="protein motif: TMHMM: 2.0" /note="2 probable transmembrane helices predicted at aa 106-128 and 497-519"
gene	277070..277402	/locus-tag="RL0238"
CDS	277070..277402	/locus-tag="RL0238" /inference="similar to sequence: INSDC: AE008995" /note="similarity: fasta; with=UniProt: Q8UIT0 (EMBL: AE008995); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0212.; length=128; id 34.722; 72 aa overlap; query 41-108; subject 48-119" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05727.1" /db-xref="GI:115254653" /db-xref="UniProtKB/TrEMBL:Q1MMS5"

		/translation="MRLLMMLLISLAAVPGLAPA SAFAVDWTKSVDSGVQPLYPYKGL PGVKAQPDKKEEESYNCRTEIVQIRRRYDEIFRS GGMPTLMYVCERDGFVTTGGKVPL RGHYQPVPR" /locus-tag="RL0238" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0238 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.996 between residues 24 and 25"
sig-peptide	277070..277139	
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CDS	complement(277814..278572)	/inference="similar to sequence:INSDC:SSD901" /note="similarity:fasta; with=UniProt:P72897 (EMBL:SSD901); Synechocystis sp. (strain PCC 6803).; Slr1619 protein.; length=249; id 45.267; 243 aa overlap; query 10-246; subject 7-244" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05728.1" /db-xref="GI:115254654" /db-xref="UniProtKB/TrEMBL:Q1MMS4" /translation="MTTKDDRLEFEAHKREMSLA LGKDEASFQQSLNTLIGLDFDYS YLWSWMGVPIIQLPVDILATQEVIWETKPDVIE TGIARGGSLIFMASILAAMGNDA KVVGVDDIDIRAHNRESIETHPMSSRIKMIQGGSV DDDVIVAVKAEIPPSARVMVVLDS DHSYEHVLAECRAYGPLVTEGCVLVVADTFIGHL TEEQAFTKRSKVWLRGNEPLKAVT DYLAETDRFEVDPVLNGKLVLS SSPGGYCVCRKA "
misc-feature	complement(277823..278572)	/locus-tag="RL0239"
		/inference="protein motif:Pfam:PF04989.2" /note="Pfam match to entry PF04989.2 CmcI"
gene	complement(278605..279753)	/locus-tag="RL0240"
CDS	complement(278605..279753)	/inference="similar to sequence:INSDC:AF047478" /inference="similar to sequence:INSDC:SSD901" /note="similarity:fasta; with=UniProt:O68392 (EMBL:AF047478); Brucella melitensis.; perA; Perosamine synthetase.; length=367; id 35.484; 341 aa overlap; query

		19-359; subject 17-352 similarity:fasta; with=UniProt:P72893 (EMBL:SSD901); Synechocystis sp. (strain PCC 6803).; rfbE; Perosamine synthetase.; length=378; id 73.829; 363 aa overlap; query 3-365; subject 4-366" /codon-start=1 /transl-table=11 /product="putative perosamine synthetase" /protein-id="CAK05729.1" /db-xref="GI:115254655" /db-xref="UniProtKB/TrEMBL:Q1MMS3" /translation="MTNRIFYTKPSITQLETDYA TDAAATGWGAHCYDYINRFERDFK TYLGSGFAIATSSCTGAMHMGALAALGVGEGDEVI LADTNWVATVSPIVHLGAKPVFVD VLPDSWCIDPSEVERHITPKTKAIIATHLYGNLC DMDALLEIGQRTGIPVIEDAAEAV GSVWNGRRAGSMGTFGTFSFHGKTTLTTGEGGMF VTNDAALSERVLTLNHNHGRARGQT KQFWPDEIGFKYKMSNIQAAIGCAQLERIEELVA RKREILAAVMVRLSALPGISMNPE YSGTINGAWMPTAVFHPSTGTTREIMQQAFEAAAN IDARVFFYPLSSLSMFEDRPENVN AWSIPGRAINLPSYHDMSEADIDRVAATLLDVAG GRIYHNRTALRQSV"
misc-feature	complement (278662..2797 26)	/locus-tag="RL0240"  /inference="protein motif:Pfam:PF01041.7" /note="Pfam match to entry PF01041.7 DegT-DnrJ-EryC1"
gene	280053..280805	/locus-tag="RL0241"
CDS	280053..280805	/locus-tag="RL0241" /inference="similar to sequence:INSDC:SSD901" /note="similarity:fasta; with=UniProt:P72897 (EMBL:SSD901); Synechocystis sp. (strain PCC 6803).; Slr1619 protein.; length=249; id 43.145; 248 aa overlap; query 7-246; subject 8-246" /codon-start=1 /transl-table=11 /product="onserved hypothetical protein" /protein-id="CAK05730.1" /db-xref="GI:115254656" /db-xref="UniProtKB/TrEMBL:Q1MMS2" /translation="MTTKDDRQEFANKREMSLA LGRDTDVFRQTLDTLVSLDKYDYS YLWSWGMPIIQMPADVMATQEWIATKPDVIVE TGVARGGSMIFQAAMLQLIGKGV VGVDIDIRAHNRQAIESHPMAHRVELIEGPSTSA EIMAKVKASIEGASVMVILSDH SKAHVLDELARNYAPLVTGQYLVVADTILGRYEP SQVPTKRKSVLLPGDEPLVALNDY LQETDRFELDTIINGKLVLS SSPGGYLRCVRS "



misc-feature	280101..280799	/locus-tag="RL0241" /inference="protein motif: Pfam: PF04989.2" /note="Pfam match to entry PF04989.2 CmcI"
gene	280888..281466	/gene="wbbJ"
CDS	280888..281466	/locus-tag="pRL0241A" /gene="wbbJ" /locus-tag="pRL0241A" /EC-number="2.3.1.-" /inference="similar to sequence: INSDC: AE004113" /inference="similar to sequence: INSDC: HS968215" /note="similarity: fasta; with=UniProt: WBBJ-ECOLI (EMBL: HS968215); Escherichia coli.; wbbJ; Putative lipopolysaccharide biosynthesis O-acetyl transferase wbbJ (EC 2.3.1.-).; length=196; id 25.455; 165 aa overlap; query 27-185; subject 40-195 similarity: fasta; with=UniProt: Q06962 (EMBL: AE004113); Vibrio cholerae.; rfbO; RfbO protein (Acetyltransferase RfbO, CysE/LacA/LpxA/NodL family).; length=188; id 45.109; 184 aa overlap; query 4-187; subject 3-186" /codon-start=1 /transl-table=11 /product="putative lipopolysaccharide biosynthesis O-acetyl transferase" /protein-id="CAK05731.1" /db-xref="GI:115254657" /db-xref="GOA:Q1MMS1" /db-xref="UniProtKB/TrEMBL:Q1MMS1" /translation="MHLGSTFYDETELRLPFRH LGANVKIKRTAGLFFVENISIMDD ARIDDFTIIVASREHVEIGCNVHIASQCYISGSD GFVMEDFSGLAPGVKIYTSSDDYT GEKMTNPTLPRHLIGGPAGKVVLRLKHVIIGSNSV VLPKVITIEEGSSVGSLSLVNKSLP AWGVYAGIPVRRRLDRSQNILILEKELGASRA"
gene	complement(281701..282939)	/locus-tag="RL0242"
CDS	complement(281701..282939)	/locus-tag="RL0242"  /inference="similar to sequence: INSDC: AE008792" /inference="similar to sequence: INSDC: SSD901" /note="similarity: fasta; with=UniProt: RFBV-SALTY (EMBL: AE008792); Salmonella typhimurium.; rfbV; O antigen biosynthesis abequosyltransferase rfbV (EC 2.4.1.-).; length=333; id 32.386; 176 aa overlap; query

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6-159; subject 3-170
similarity:fasta;
with=UniProt:P72899 (EMBL:SSD901);
Synechocystis sp. (strain PCC
6803).; Slr1063 protein.;
length=689; id 30.180; 222 aa
overlap; query 6-225; subject
9-220"
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KFYNVEEDRKFP HGSFGDVFQYIC
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HFLDQGAVSFLQRPFYRSIVNSAI
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AVAFRFWAERKNFIKAYELYTRIMWGGMLNHPEI
RNFRERLPLMVAIQTLVSEVNSAI
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LGYPNLVLFHEHDL SRHIIM"
misc-feature      complement(282400..2829 /locus-tag="RL0242"
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                  /note="Pfam match to entry
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gene              complement(282936..2834 /locus-tag="RL0243"
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39)
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                  meliloti).; ExpA8 (Putative
                  dTDP-4-dehydrorhamnose
                  3,5-epimerase protein) (EC
                  5.1.3.13).; length=187; id 44.898;
                  147 aa overlap; query 1-145;
                  subject 13-159 similarity:fasta;
                  with=UniProt:Q8YT94
                  (EMBL:AP003591); Anabaena sp.
                  (strain PCC 7120).; rfbC;
                  DTDP-4-dehydrorhamnose
                  3,5-epimerase.; length=189; id
                  47.134; 157 aa overlap; query
                  1-157; subject 14-170"
                  /codon-start=1

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misc-feature	complement(282948..283427)	/locus-tag="RL0243"  /inference="protein motif: Pfam:PF00908.7" /note="Pfam match to entry PF00908.7 dTDP-sugar-isom"
gene	complement(283475..284710)	/locus-tag="RL0244"
CDS	complement(283475..284710)	/locus-tag="RL0244"  /inference="similar to sequence:INSDC:AF170880" /inference="similar to sequence:INSDC:RME591985" /note="similarity:fasta; with=UniProt:Q9L9E7 (EMBL:AF170880); Streptomyces sphaeroides.; NovU.; length=420; id 37.778; 405 aa overlap; query 6-410; subject 11-414 similarity:fasta; with=UniProt:Q92U91 (EMBL:RME591985); Rhizobium meliloti (Sinorhizobium meliloti).; Putative NDP-hexose 3-C-methyltransferase protein.; length=410; id 55.231; 411 aa overlap; query 3-410; subject 2-410" /codon-start=1 /transl-table=11 /product="putative methyltransferase" /protein-id="CAK05734.1" /db-xref="GI:115254660" /db-xref="GOA:Q1MMR8" /db-xref="UniProtKB/TrEMBL:Q1MMR8" /translation="MTAHNCRFCNAPLKH RHFVDL GSTPLANAYLTEEQLKLPEPSYPL RAFVCTECWLQADAFVPPEDIFSHYAYFSSYSD GWVEHARQFTIMARERFGLDATSQ VIEVASNDGYLLKHFEAGVPVLGIEPAENVAEV ARQIGVPTEARFFGKETAADLVSR GLAADIVIGNNVLAHVPDINDFVGGLSAVLKPDG VVSVEFPHLLRLMENIQFDTVYHE HFYYLSLLAVEKVF <del>AAHGLK</del> VF <del>DVEEL</del> PTHGGSL RVLACRATSMVHAIGHGLAKVRAD EAAAGFDKVETYEAFOSRVAPIKDGLLAFLTEA

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with=UniProt:RFBG-SALTY
(EMBL:AE008792); Salmonella
typhimurium.; rfbG;
OrderedLocusNames=STM2091;
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4.2.1.45). CDP-glucose
4,6-dehydratase (EC 4.2.1.45).;
length=359; id 45.714; 350 aa
overlap; query 8-352; subject
5-353 similarity:fasta;
with=UniProt:Q92U92
(EMBL:RME591985); Rhizobium
meliloti (Sinorhizobium
meliloti).; Putative CDP-glucose
4,6-dehydratase protein (EC
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347 aa overlap; query 8-352;
subject 8-352"
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KVYANNNGSGVPFVETDMLGGKDPY
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IGGGDWSKDRLIPDFIRAFESSQP
ILLRYPEAIRPWQHVLEPLGGYLAFAEALTLAGE
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CDS       complement(285762..2865 /gene="ddhA"
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/EC-number="2.7.7.33"
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sequence:INSDC:AE016923"

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overlap; query 1-256; subject
5-260 similarity:fasta;
with=UniProt:Q7NR91
(EMBL:AE016923); Chromobacterium
violaceum.; ddhA;
Glucose-1-phosphate
cytidylyltransferase (EC
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256 aa overlap; query 1-256;
subject 1-256"
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32)

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/inference="protein
motif: Pfam:PF00483.9"
/note="Pfam match to entry
PF00483.9 NTP-transferase"
gene            complement(286621..2870 /locus-tag="RL0247"
04)
CDS             complement(286621..2870 /locus-tag="RL0247"
04)

/note="no significant database
hits"
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74)

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CDS	complement(287084..287374)	/locus-tag="RL0248" /note="no significant database hits" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAK05738.1" /db-xref="GI:115254664" /db-xref="UniProtKB/TrEMBL:Q1MMR4" /translation="MIRYATSAASNPPPPKAREV SAAEPPVEMSRTKPVIEVASAGAA LAAYPLLPSGESDELGSDTLPKTTKPPRRAATKR KPKVAEADDAPLQLSLEA"
gene	complement(287614..287700)	/gene="tRNA-Leu"
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sig-peptide	287869..287935	/locus-tag="RL0249" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0249 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.698 between residues 23 and 24"
gene	complement(288300..288662)	/locus-tag="RL0250"
CDS	complement(288300..288662)	/inference="similar to sequence:INSDC:SME591783" /note="similarity:fasta; with=UniProt:Q92SU7 (EMBL:SME591783); Rhizobium

		meliloti (Sinorhizobium meliloti).; Hypothetical protein SMc00345.; length=93; id 82.796; 93 aa overlap; query 24-116; subject 1-93" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05740.1" /db-xref="GI:115254666" /db-xref="GOA:Q1MMR2" /db-xref="UniProtKB/TrEMBL:Q1MMR2" /translation="MLCEGDCAHAPQALNLSKRK DIAMTEKARVTILYCTQCNWLLRA SWMAQELLHTFSDSLGEVALIPATGGNFEIRVNG DLIWERKRDGGFPGPRELKQVRVD IVEPGRDLGHVDRASLES" /locus-tag="RL0250"
misc-feature	complement(288309..2886 17)	/inference="protein motif:Pfam:PF05169.2" /note="Pfam match to entry PF05169.2 Seleno-W-rel" /locus-tag="RL0251"
gene	288797..289573	/locus-tag="RL0251" /inference="similar to sequence:INSDC:AB177545" /inference="similar to sequence:INSDC:AE007963" /note="similarity:fasta; with=UniProt:Q60GF4 (EMBL:AB177545); Comamonas acidovorans (Pseudomonas acidovorans).; ORF7NB; Glutamine amidotransferase.; length=256; id 29.464; 224 aa overlap; query 30-239; subject 28-236 similarity:fasta; with=UniProt:Q7D1W7 (EMBL:AE007963); Agrobacterium tumefaciens (strain C58/ATCC 33970).; AGR-C-389p.; length=254; id 55.603; 232 aa overlap; query 14-245; subject 23-254" /codon-start=1 /transl-table=11 /product="putative glutamine amidotransferase" /protein-id="CAK05741.1" /db-xref="GI:115254667" /db-xref="GOA:Q1MMR1" /db-xref="UniProtKB/TrEMBL:Q1MMR1" /translation="MVSSRDRPYQEEPVRVAVIE NMRNTGLGALAAALDEAGAEIEWF RVWRDGILPKDISGHDALVVLGGEQSALDDETHP YLPVLRLARRFGDAGKAVLGICL GSQILARAYGADNHLGIAREFGWHGIGVTAEGRA DPLLSPLGGEFTIFEWHADTFSLP EGAVRLASSPVAENQAFRIGRAVYGTQFHFEEANS AVVAQWKAIEFPDTIARIAPGWLEN HAELAAARHAGAADAAGLAIARAWVSLIEQEEVEM
CDS	288797..289573	

misc-feature	288857..289396	LSQASA" /locus-tag="RL0251" /inference="protein motif: Pfam: PF00117.10" /note="Pfam match to entry PF00117.10 GATase"
gene	289585..290133	/gene="nodL" /locus-tag="RL0252"
CDS	289585..290133	/gene="nodL" /locus-tag="RL0252" /EC-number="2.3.1.-" /inference="similar to sequence: INSDC: AE007232" /inference="similar to sequence: INSDC: AE007968" /note="similarity: fasta; with=UniProt: NODL-RHIME (EMBL: AE007232); Rhizobium meliloti (Sinorhizobium meliloti).; nodL; Nodulation protein L (EC 2.3.1.-).; length=183; id 48.370; 184 aa overlap; query 1-182; subject 1-182 similarity: fasta; with=UniProt: Q8UIJ1 (EMBL: AE007968); Agrobacterium tumefaciens (strain C58/ATCC 33970).; nodL; Nodulation protein L (AGR-C-527p).; length=179; id 70.391; 179 aa overlap; query 2-180; subject 1-179" /codon-start=1 /transl-table=11 /product="putative nodulation protein" /protein-id="CAK05742.1" /db-xref="GI:115254668" /db-xref="GOA:Q1MMR0" /db-xref="UniProtKB/TrEMBL:Q1MMR0" /translation="MLASERDKMAAGEWYCCLLDD ELDLLRRQARLAVHAHNTLPADER GAVAPALRALFAQAAPDIFIEAPFHCSYGINITL GERVYFNAGCTVLD SGRVTIGDRS MFGPGVQIYCAEHHKEPALRSTGIEIARPVTIGS DVWIGGSAILGGITIGDGAIVGA GAVVTRDVPAGATVVG NPARIR"
misc-feature	289807..289860	/gene="nodL" /locus-tag="RL0252" /inference="protein motif: Pfam: PF00132.9" /note="Pfam match to entry PF00132.9 Hexapep"
misc-feature	289867..289920	/gene="nodL" /locus-tag="RL0252" /inference="protein motif: Pfam: PF00132.9" /note="Pfam match to entry PF00132.9 Hexapep"
misc-feature	289975..290028	/gene="nodL" /locus-tag="RL0252" /inference="protein motif: Pfam: PF00132.9"



misc-feature	290029..290082	/note="Pfam match to entry PF00132.9 Hexapep" /gene="nodL" /locus-tag="RL0252" /inference="protein motif: Pfam: PF00132.9" /note="Pfam match to entry PF00132.9 Hexapep1"
gene	290133..290669	/gene="gfa" /locus-tag="RL0253"
CDS	290133..290669	/gene="gfa" /locus-tag="RL0253" /inference="similar to sequence: INSDC: PD34346" /inference="similar to sequence: INSDC: SME591789" /note="Similar to Paracoccus denitrificans. Gfa GFA-PARDE (EMBL: PD34346) (Glutathione-dependent formaldehyde-activating enzyme (EC 4.4.-.-).), and similar, but extended at the N-terminus, to Rhizobium meliloti (Sinorhizobium meliloti). Hypothetical protein SMC04177. Q92K68 (EMBL: SME591789) (153) similarity: fasta; with=UniProt: GFA-PARDE (EMBL: PD34346); Paracoccus denitrificans.; gfa; Glutathione-dependent formaldehyde-activating enzyme (EC 4.4.-.-).; length=193; id 25.175; 143 aa overlap; query 40-173; subject 30-163 similarity: fasta; with=UniProt: Q92K68 (EMBL: SME591789); Rhizobium meliloti (Sinorhizobium meliloti).; Hypothetical protein SMC04177.; length=153; id 76.712; 146 aa overlap; query 29-174; subject 1-146" /codon-start=1 /transl-table=11 /product="putative glutathione-dependent formaldehyde-activating enzyme" /protein-id="CAK05743.1" /db-xref="GI:115254669" /db-xref="GOA:Q1MMQ9" /db-xref="UniProtKB/TrEMBL:Q1MMQ9" /translation="MPANGRDDLAISTASKAPLD QKANREDIMSERTLPMEGGCRCGR VRLKISAPPLLTMACTGCTGCQKMTSSGYSLSAAI PSEGFVETQGEPIVIGGLHGVTKHY FCPHCMSWMFTRPEGMDWCNLRVTMLDDPSWFT PFIETWTSEKLSFAETGAVHSYEA LPEMEAYEGLVKEYMGRG" /gene="gfa" /locus-tag="RL0253" /inference="protein motif: Pfam: PF04828.3"
misc-feature	290301..290588	

		/note="Pfam match to entry PF04828.3 DUF636"
gene	complement(290983..2928 15)	/gene="lepA"
CDS	complement(290983..2928 15)	/locus-tag="RL0254" /gene="lepA"  /locus-tag="RL0254" /inference="similar to sequence:INSDC:HS034224" /inference="similar to sequence:INSDC:SME591783" /note="similarity:fasta; with=UniProt:LEPA-ECOLI (EMBL:HS034224); Escherichia coli.; lepA; GTP-binding protein lepA.; length=599; id 56.928; 599 aa overlap; query 12-610; subject 1-597 similarity:fasta; with=UniProt:LEPA-RHIME (EMBL:SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; lepA; GTP-binding protein lepA.; length=608; id 93.894; 606 aa overlap; query 5-610; subject 3-608" /codon-start=1 /transl-table=11 /product="putative GTP-binding protein" /protein-id="CAK05744.1" /db-xref="GI:115254670" /db-xref="GOA:Q1MMQ8" /db-xref="UniProtKB/TrEMBL:Q1MMQ8" /translation="MARMSTNSTTPLSHIRNFSI VAHIDHGKSTLADRLIQTTGGLAE REMSEQVLDNMDIERERGITIKAQTVRLHYQANN GEKYILNLIIDTPGHVDFAYEVSR LSACEGSLLVVDASQGVEAQTLANVYQAIDNNHE IVTVLNKIDLPAAEPDRIKEQIEE VIGIDASEAVLISAKTGLGIPDVLEAIVHKLPAP KSPGGDKAPLKALLVDSWYDAYLG VMVLVRVIDGVLTGQTVRMMGTDAKYQVERVGV LTPKMVNIDRLGPGEIGFITASIK EVADTRVGDTITEDKRPTAQALPGFKPAQPVVFC GLFPVDAADFEDLRAAMGKLRLND ASFSFEMESSAALGFGFRCGFLGLLHLEIIQERL ERFDLDLIATAPSVVYKMFMTDG TERELHNPADMPDVVKISEIHEPWIRATILTPDD YLGILKLCQDRRGIQIELTYVGT RAMLTYDLPLNEVVVDFYDRLKSISKGYASFDT LTDHREGNLVKMSILVNGEVVDAL SMMVHRTAAEKGRDMCEKLKELIPKHMFKIPIQ AAIGGNVIARETISALRKDVTAKC YGGDATRKRLLDKQKAGKKRMRQFGKVEIPQEA FIAALKMGDE"
misc-feature	complement(290992..2913 18)	/gene="lepA"  /locus-tag="RL0254" /inference="protein motif:Pfam:PF06421.1" /note="Pfam match to entry

misc-feature	complement(291319..291585)	PF06421.1 LepA-C" /gene="lepA" /locus-tag="RL0254" /inference="protein motif: Pfam: PF00679.10" /note="Pfam match to entry PF00679.10 EFG-C"
misc-feature	complement(291952..292164)	/gene="lepA" /locus-tag="RL0254" /inference="protein motif: Pfam: PF03144.8" /note="Pfam match to entry PF03144.8 GTP-EFTU-D2"
misc-feature	complement(292231..292779)	/gene="lepA" /locus-tag="RL0254" /inference="protein motif: Pfam: PF00009.10" /note="Pfam match to entry PF00009.10 GTP-EFTU"
gene	complement(292892..293593)	/locus-tag="RL0255"
CDS	complement(292892..293593)	/locus-tag="RL0255" /inference="similar to sequence: INSDC: A39184" /inference="similar to sequence: INSDC: AE006856" /note="similarity: fasta; with=UniProt: TENA-BACSU (EMBL: A39184); Bacillus subtilis.; tenA; Transcriptional activator tenA.; length=236; id 33.663; 202 aa overlap; query 34-231; subject 22-218 similarity: fasta; with=UniProt: Q97VM4 (EMBL: AE006856); Sulfolobus solfataricus.; tenA-2; Transcriptional activator (TenA-2).; length=tenA-2; id 37.559; 213 aa overlap; query 20-232; subject 9-215" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="CAK05745.1" /db-xref="GI:115254671" /db-xref="UniProtKB/TrEMBL: Q1MMQ7" /translation="MMDASTQSTD TTGSFTAAAW DRIAPIMAEIEALPLLQRLSDGTL PPEVFRHYILQDALYLKHYARCLAIVA AKAPDNA QVLRFLGSAQKAITVEQGLHAGFL TQFGITSANVTSAEPSPAGFAYTNFLLATAYHSS YAVALSSILPCFWIYWHVGEAIKN RPVIEGNAFQAWINTYGD PQFAAGAREVIALTDM AARAAS PVERAQMTDVFIRASQYE WMFWDSAWRQETWPV"
misc-feature	complement(292910..293551)	/locus-tag="RL0255"

gene	293730..294308	/inference="protein motif: Pfam: PF03070.4" /note="Pfam match to entry PF03070.4 TENA-THI-4" /locus-tag="RL0256"
CDS	293730..294308	/locus-tag="RL0256" /inference="similar to sequence: INSDC: AE008997" /note="similarity: fasta; with=UniProt: Q8UIP8 (EMBL: AE008997); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Transcriptional regulator.; length=193; id 69.271; 192 aa overlap; query 5-192; subject 2-193" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="CAK05746.1" /db-xref="GI: 115254672" /db-xref="GOA: Q1MMQ6" /db-xref="UniProtKB/TrEMBL: Q1MMQ6" /translation="MDWKMEPELEQAIGIRIRTL RQEKALTLDDLAASGVSRAMISR IERAEASPTASLLARICAALGLSLSAFFAEEGQA SPLARRQEQQVWRDPETGYIRRSV SPPGTPSDVDIVEVEFPPGARVSFPPHASAHGMT QHIWLFIDGELEMTAGEAVYRLRPG DCLFMPVGEHGVFHNPGNAPARYCVVLNRGGR"
misc-feature	293778..293942	/locus-tag="RL0256" /inference="protein motif: Pfam: PF01381.9" /note="Pfam match to entry PF01381.9 HTH-3"
gene	294333..294851	/locus-tag="RL0257"
CDS	294333..294851	/locus-tag="RL0257" /inference="similar to sequence: INSDC: AE007964" /inference="similar to sequence: INSDC: PSTTRG" /note="similarity: fasta; with=UniProt: TTR-PSESZ (EMBL: PSTTRG); Pseudomonas syringae (pv. tabaci).; ttr; Acetyltransferase (EC 2.3.1.-) (Tabtoxin resistance protein).; length=EC 2.3.1.-; id 39.412; 170 aa overlap; query 4-171; subject 6-173 similarity: fasta; with=UniProt: Q8UIP7 (EMBL: AE007964); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Acetyltransferase (AGR-C-420p).; length=172; id 70.175; 171 aa overlap; query 1-171; subject 1-171" /codon-start=1 /transl-table=11 /product="putative acetyltransferase"

		/protein-id="CAK05747.1" /db-xref="GI:115254673" /db-xref="GOA:Q1MMQ5" /db-xref="UniProtKB/TrEMBL:Q1MMQ5" /translation="MPGIRILSAEEARAAVPALS EVLVDCVAGGASVGFMQPYGPDDA EPYWRDVADAVATGANLLLVAELDGRIVGTVQVG AAQMPNQPHRGDLKLLVHRSARG KGLARLLMDAAEERAAGRKTLLVLDLTATGSDAE AIYPRLGWQRVGVIPDYALWPEGG FCATTLFYKRLA"
misc-feature	294519..294767	/locus-tag="RL0257" /inference="protein motif: Pfam: PF00583.9" /note="Pfam match to entry PF00583.9 Acetyltransf-1"
gene	complement(294867..295478)	/locus-tag="RL0258"
CDS	complement(294867..295478)	/locus-tag="RL0258"
		/inference="similar to sequence: INSDC: OCA82447" /inference="similar to sequence: INSDC: SME591790" /note="similarity: fasta; with=UniProt: Q6LBD3 (EMBL: OCA82447); Oligotropha carboxidovorans (Pseudomonas carboxydovorans).; Hydrolase of HAD-superfamily.; length=236; id 26.425; 193 aa overlap; query 2-180; subject 4-186 similarity: fasta; with=UniProt: Q92NB5 (EMBL: SME591790); Rhizobium meliloti (Sinorhizobium meliloti).; Hypothetical protein SMc01745.; length=211; id 50.521; 192 aa overlap; query 1-192; subject 4-195" /codon-start=1 /transl-table=11 /product="putative haloacid dehydrogenase hydrolase" /protein-id="CAK05748.1" /db-xref="GI:115254674" /db-xref="GOA:Q1MMQ4" /db-xref="UniProtKB/TrEMBL:Q1MMQ4" /translation="MKVLMVDVDGVLIHGRPTDG LPHFTYLERDLGLRFDLLQQEFFQ THWGDIIIGRAALEPRLAGVLAKIAPHLAETLI DYWFENDSRLDRNLLEELAGLRQS GITLLLATNQEHRRARYLMEQIGLSAHFDDIIYS AALGHSKSPDFFRATERAGVLP GEIAFIDDMAVNIEAARQFGWNAAQWTAGATLGG ALPVFARPT"
misc-feature	complement(294912..295478)	/locus-tag="RL0258" /inference="protein motif: Pfam: PF00702.10" /note="Pfam match to entry PF00702.10 Hydrolase"

gene	295612..296637	/locus-tag="RL0259"
CDS	295612..296637	/locus-tag="RL0259"
		/inference="similar to sequence:INSDC:HS85823" /note="similarity:fasta; with=UniProt:APHA-MYCRA (EMBL:HS85823); Mycoplana ramosa (Mycoplana bullata).; aphA; Acetylpolyamine aminohydrolase.; length=341; id 71.386; 339 aa overlap; query 1-339; subject 1-339" /codon-start=1 /transl-table=11 /product="putative acetylpolyamine aminohydrolase" /protein-id="CAK05749.1" /db-xref="GI:115254675" /db-xref="GOA:Q1MMQ3" /db-xref="UniProtKB/TrEMBL:Q1MMQ3" /translation="MRVIYSEDHKLRLDARTELHA GQLVTPFEAPFRAEWILAAVKQAG FTDVVAPDAHGLETARKVHDPAYLDFLATVWDRW VAAGFTGEAIANSFAVRRTSQRVP DNIVGAIGHYANAADTSITKGSYEAAIASMRCAI TGADWLNAGNRFAFALCRPPGHHA GIDLFGGYCFINNSGVAAQRLLDHGARKVAVLDV DFHHGNGTQDLFYHRGDVFTASLH GDPMQAFPPYFLGHADEEGEGEGTGANRNYPMPFG TPWDVWSSALADALTRIKAFGAEA IVVALGVDTFERDPISFFSLTSDDFTRMGAMIAS AGLPVLACMEGGYGVPEIGLNVAN VLKGLEA"
misc-feature	295690..296634	/locus-tag="RL0259" /inference="protein motif:Pfam:PF00850.9" /note="Pfam match to entry PF00850.9 Hist-deacetyl"
gene	296647..297222	/locus-tag="RL0260"
CDS	296647..297222	/locus-tag="RL0260" /inference="similar to sequence:INSDC:AE008281" /inference="similar to sequence:INSDC:AF449411" /note="similarity:fasta; with=UniProt:RECX-MYXXA (EMBL:AF449411); Myxococcus xanthus.; Regulatory protein recX.; length=187; id 35.849; 159 aa overlap; query 17-168; subject 25-183 similarity:fasta; with=UniProt:RECX-AGRT5 (EMBL:AE008281); Agrobacterium tumefaciens (strain C58/ATCC 33970).; recX; Regulatory protein recX.; length=230; id 68.452; 168 aa overlap; query 11-178; subject 58-225" /codon-start=1 /transl-table=11 /product="putative transcriptional regulatory protein" /protein-id="CAK05750.1"

		/db-xref="GI:115254676"
		/db-xref="GOA:Q1MMQ2"
		/db-xref="UniProtKB/TrEMBL:Q1MMQ2"
		/translation="MTDETVPSDIPTSRMLSWAR NSTVYRLERRMMTEKQLFDAIARK AKEKFAGISAAQLKAVADFAVKFAYDNKVLDDHA YAEVSTRSAVRGGKSKRAIAQKLA AKGVSSDKVEAALEEADDLYAAAI FARKRAFGPF RRVELDEKRKAKELSAFARNGFSF DIGRKVFDMSFEDAEEIIVAGRSAAPQHQRS"
misc-feature	296818..297174	/locus-tag="RL0260" /inference="protein motif: Pfam: PF02631.5" /note="Pfam match to entry PF02631.5 RecX"
gene	297295..298206	/locus-tag="RL0261"
CDS	297295..298206	/locus-tag="RL0261" /inference="similar to sequence: INSDC: C90740" /inference="similar to sequence: INSDC: SC0939119" /note="similarity: fasta; with=UniProt: YBIF-ECOLI (EMBL: C90740); Escherichia coli O157: H7.; ybiF; Hypothetical transport protein ybiF.; length=295; id 36.630; 273 aa overlap; query 32-302; subject 14-285 similarity: fasta; with=UniProt: Q9K3X0 (EMBL: SC0939119); Streptomyces coelicolor.; Putative integral membrane protein.; length=295; id 40.441; 272 aa overlap; query 27-296; subject 11-280" /codon-start=1 /transl-table=11 /product="putative transmembrane protein" /protein-id="CAK05751.1" /db-xref="GI:115254677" /db-xref="GOA:Q1MMQ1" /db-xref="UniProtKB/TrEMBL:Q1MMQ1" /translation="MDIKNIETGTDGAALIAQPG ISPTSGGLAAGVAMCLMSMSSIQF GAALSSSAIATYGVAGATWLRFAAIIILAAVVR PSVLRYSQAQWQATLLLGTTTAAM TLCFFAAIQRLPLGLAIAIDFLGPLSVAVFGYGL TWRLTWPLIAAAGILFLAHDGEGW VGNSSGVLFALGSVGVAVYILLTKKVGAFAFKGL EGLSMSLIVAGLVATPFGLAETGG AFTAQGLVEVLGLAILVPLL PYALEMVALRRMPS ASFGILMSLEPALGALAGFLILAQ PMTALQMLGTALVVAASAGATASAAKT"
misc-feature	order(297352..297420, 297457..297525, 297553..297621, 297640..297708, 297775..297843, 297880..297936, 297964..298032, 298051..298119,	/locus-tag="RL0261"

	298129..298197)	/inference="protein motif:TMHMM:2.0" /note="9 probable transmembrane helices predicted at aa 20-42, 55-77, 87-109, 116-138,161-183, 196-214, 224-246, 253-275 and 279-301"
misc-feature	297817..298188	/locus-tag="RL0261" /inference="protein motif:Pfam:PF00892.8" /note="Pfam match to entry PF00892.8 DUF6"
gene	complement(298251..298718)	/locus-tag="RL0262"
CDS	complement(298251..298718)	/locus-tag="RL0262"
		/inference="similar to sequence:INSDC:SME591791" /note="similarity:fasta; with=UniProt:Q92MN5 (EMBL:SME591791); Rhizobium meliloti (Sinorhizobium meliloti).; Hypothetical protein SMC02351.; length=155; id 78.431; 153 aa overlap; query 1-153; subject 1-153" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05752.1" /db-xref="GI:115254678" /db-xref="GOA:Q1MMQ0" /db-xref="UniProtKB/TrEMBL:Q1MMQ0" /translation="MDNDIQGRPAHVAAIRERAE AEMREMGVDAAFIDRLVETFYGRV LAHPDLGPVFDARLSGRWPEHMAKMKSFWSAVAF RSGAYGGKPVQAHTGVQNLTPLDF PKWLSLFAATLDDIAPTPEAKAWFMATAERIAKS LILSLFYNPALDDPARKPA"
gene	298892..299875	/locus-tag="RL0263"
CDS	298892..299875	/locus-tag="RL0263" /inference="similar to sequence:INSDC:SME591783" /note="similarity:fasta; with=UniProt:Q92KS6 (EMBL:SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; HYPOTHETICAL TRANSMEMBRANE PROTEIN.; length=327; id 78.834; 326 aa overlap; query 1-326; subject 1-326" /codon-start=1 /transl-table=11 /product="putative transmembrane protein" /protein-id="CAK05753.1" /db-xref="GI:115254679" /db-xref="GOA:Q1MMP9" /db-xref="UniProtKB/TrEMBL:Q1MMP9"



		/translation="MLARFFRSSKRSFDSLSEQE ILALGIASEEDDARIYLAYADRLR REFPASAKVFEDMAEVEDTHRKSLIEIHRQRFGE RIPLIRREHVEGFYERKPDWLRAN LSLDAMRRETEAMEEQAYRFYVEAAKRTSDASTR QLLGDLALAEQGHEDIARMLGDKH TPEDVKHDEDATVHRQFVLTYVQPGLAGLMDGSV STLAPIFAAAFATQDTWQTFVLVGL SASVGAGISMGFTEAAHDDGKISGRGSPIKRGLA CGIMTALGGLGHALPYLIPHFWTA TITAAVVVFELWAIAFIQNRYMETPFLRAAFQV VLGGLVLGAGILIGNG" /locus-tag="RL0263" /inference="protein" motif: Pfam: PF01988.8" /note="Pfam match to entry PF01988.8 DUF125"
misc-feature	299432..299872	
misc-feature	order(299693..299761, 299798..299866)	/locus-tag="RL0263"  /inference="protein" motif: TMHMM: 2.0" /note="2 probable transmembrane helices predicted at aa 268-290 and 303-325"
gene	complement(300040..300639)	/locus-tag="RL0264"
CDS	complement(300040..300639)	/locus-tag="RL0264"  /inference="similar to sequence: INSDC: C97389" /note="similarity: fasta; with=UniProt: Q8UIP1 (EMBL: C97389); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0252 (AGR-C-433p).; length=204; id 58.376; 197 aa overlap; query 4-199; subject 8-204" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05754.1" /db-xref="GI: 115254680" /db-xref="UniProtKB/TrEMBL: Q1MMP8" /translation="MRIKGIFVAMMAMFAMATAA IPAPSRNASMVTGNATSQPIGHYD FCQIHRSECGADRNAGPVAMNPGKWSLVRSVNAT ANRTITPMTDKIYKGDEVWAYPT TAGDCEDFALLKRRMLIQRGFPAADLLMTVVRKP DGEHGAHLTLRTAEGDFVLDNLAA DVKPWFGTPYSFVKRQSSYNAGRWVTIENGRDVL VGALR"
misc-feature	complement(300043..300606)	/locus-tag="RL0264"  /inference="protein" motif: Pfam: PF06035.1" /note="Pfam match to entry PF06035.1 DUF920"
misc-feature	complement(300568..300627)	/locus-tag="RL0264"  /inference="protein"

		motif:TMHMM:2.0"
		/note="1 probable transmembrane
		helix predicted at aa 5-24"
sig-peptide	complement(300579..300639)	/locus-tag="RL0264"
		/inference="protein
		motif:SignalP-HMM:2.0"
		/note="Signal peptide predicted
		for RL0264 by SignalP 2.0 HMM
		(Signal peptide probability 1.000)
		with cleavage site probability
		0.560 between residues 19 and 20"
gene	complement(300805..301629)	/locus-tag="RL0265"
CDS	complement(300805..301629)	/locus-tag="RL0265"
		/inference="similar to
		sequence:INSDC:AE008997"
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		VAPDRVILVGSSMGGWIALRLAQELARQGGPKLA
		GMVLIAPAPDFTSELIEPNLKAKE
		RKSLAERGYFEERSQYSPEPNIYTRALIEDGRKN
		RVLDGIIETGCPVHILQGMKDADV
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gene	301757..302344	/gene="infC"
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		O157:H7.; infC; Translation
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		length=180; id 58.537; 164 aa
		overlap; query 33-195; subject
		14-177 similarity:fasta;
		with=UniProt:IF3-RHIME
		(EMBL:SME591783); Rhizobium
		meliloti (Sinorhizobium

		meliloti).; infC; Translation initiation factor IF-3.; length=177; id 85.393; 178 aa overlap; query 18-195; subject 1-177" /codon-start=1 /transl-table=11 /product="putative translation initiation factor" /protein-id="CAK05756.1" /db-xref="GI:115254682" /db-xref="GOA:Q1MMP6" /db-xref="UniProtKB/TrEMBL:Q1MMP6" /translation="MGARCCNVPKQREENTTIRR PFKTDAPVKDGPNSNREIRIPKVQ LIGADGENMGVVPTDQALRMAEEAGLDLVEISPN VEPPVCKILDGKLYANQKAAE ARKKQKIVEVKEIKMRPNIDTHDYEVMKAMGRF FDEGDKVKVTLKFRGREMAHQELG MKLLQQVKADTIEFAKVEAEPKLEGRQMMMLAP K"
misc-feature	301841..302068	/gene="infC" /locus-tag="RL0266" /inference="protein motif: Pfam: PF05198.3" /note="Pfam match to entry PF05198.3 IF3-N"
misc-feature	302081..302341	/gene="infC" /locus-tag="RL0266" /inference="protein motif: Pfam: PF00707.9" /note="Pfam match to entry PF00707.9 IF3-C"
gene	302656..302859	/gene="rpmI" /locus-tag="RL0267"
CDS	302656..302859	/gene="rpmI" /locus-tag="RL0267" /inference="similar to sequence: INSDC: SME591783" /inference="similar to sequence: INSDC: TTH224858" /note="similarity: fasta; with=UniProt: RL35-THETH (EMBL: TTH224858); Thermus thermophilus.; rpmI; 50S ribosomal protein L35.; length=65; id 52.381; 63 aa overlap; query 2-64; subject 1-62 similarity: fasta; with=UniProt: RL35-RHIME (EMBL: SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; rpmI; 50S ribosomal protein L35.; length=67; id 95.522; 67 aa overlap; query 1-67; subject 1-67" /codon-start=1 /transl-table=11 /product="putative 50S ribosomal protein L35" /protein-id="CAK05757.1" /db-xref="GI:115254683" /db-xref="GOA:Q1MMP5"

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misc-feature	302665..302841	
gene	302898..303302	/gene="rplT" /locus-tag="RL0268"
CDS	302898..303302	/gene="rplT" /locus-tag="RL0268" /inference="similar to sequence: INSDC: AE016864" /inference="similar to sequence: INSDC: SME591783" /note="similarity: fasta; with=UniProt: RL20-PSESM (EMBL: AE016864); Pseudomonas syringae (pv. syringae).; rplT; 50S ribosomal protein L20.; length=118; id 60.684; 117 aa overlap; query 1-117; subject 1-117 similarity: fasta; with=UniProt: RL20-RHIME (EMBL: SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; rplT; 50S ribosomal protein L20.; length=134; id 93.284; 134 aa overlap; query 1-134; subject 1-134" /codon-start=1 /transl-table=11 /product="putative 50S ribosomal protein L20" /protein-id="CAK05758.1" /db-xref="GI:115254684" /db-xref="GOA:Q1MMP4" /db-xref="UniProtKB/TrEMBL:Q1MMP4" /translation="MARVKRGVTSKAKHKKVLKA AKGFYGRKNTIRTAKAAVDRSKQ YAYRDRKVNKRNFRLWIQRINAAVREFGLTYGR FIDGLNKAGIEVDRKVLSDMAIHE PEAFGALVSAKKALEYLKEAGTANEFEGAVK"
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gene	303453..304535	/gene="pheS" /locus-tag="RL0269"
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		with=UniProt:SYFA-ECOLI (EMBL:B64930); Escherichia coli.; pheS; Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20) (Phenylalanine--tRNA ligase alpha chain) (PheRS).; length=327; id 51.453; 344 aa overlap; query 1-344; subject 1-326 similarity:fasta; with=UniProt:SYFA-RHIME (EMBL:SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; pheS; Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20) (Phenylalanine--tRNA ligase alpha chain) (PheRS).; length=360; id 87.778; 360 aa overlap; query 1-360; subject 1-360" /codon-start=1 /transl-table=11 /product="putative phenylalanyl-tRNA synthetase alpha chain" /protein-id="CAK05759.1" /db-xref="GI:115254685" /db-xref="GOA:Q1MMP3" /db-xref="UniProtKB/TrEMBL:Q1MMP3" /translation="MSDIDQLNTSLLAEIAAADD ETALEAVRVSA LGKKGSVSELLKT LGAMTPEERQSKGAAINVLKNAVTEALTARKTTL RQAAIDARLQAETVDVSLPVRSSP AERGRIHPISQIVDEITAIFADMGFSIAEGPDIE TDYYNFTALNFPEGHPAREMHDTF FFNPDENGERKVLRTHTSPVQVRTMEAQTPPIRI IIPGKTYRQDSDATHSPMFHQVEG LVVDKKANVANLRWVLEEFCKTFFEVDVSVTMRFR PSFFPFTEPSFEVDIQCDRSGPIV KFGEGTDWMEILGCGMVHPNVRLRYGGLDLPDEYQG FAWGMGLDRIAMLKYGMPDLRDF NADVRWMTHYGFRPLDMPTLFGGLSA" /gene="pheS" /locus-tag="RL0269" /inference="protein motif: Pfam:PF02912.6" /note="Pfam match to entry PF02912.6 Phe-tRNA-synt-N"
misc-feature	303498..303716	
misc-feature	303780..304445	/gene="pheS" /locus-tag="RL0269" /inference="protein motif: Pfam:PF01409.8" /note="Pfam match to entry PF01409.8 tRNA-synt-2d"
gene	304552..306975	/gene="pheT"
CDS	304552..306975	/locus-tag="RL0270" /gene="pheT" /locus-tag="RL0270" /EC-number="6.1.1.20" /inference="similar to sequence: INSDC:B97390" /inference="similar to sequence: INSDC:I41284"

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(EMBL:I41284); Escherichia coli.;
pheT; Phenylalanyl-tRNA synthetase
beta chain (EC 6.1.1.20)
(Phenylalanine-- tRNA ligase beta
chain) (PheRS).; length=795; id
36.965; 817 aa overlap; query
1-806; subject 1-794
similarity:fasta;
with=UniProt:SYFB-AGRT5
(EMBL:B97390); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; pheT; Phenylalanyl-tRNA
synthetase beta chain (EC
6.1.1.20) (Phenylalanine-- tRNA
ligase beta chain) (PheRS).;
length=807; id 84.015; 807 aa
overlap; query 1-807; subject
1-807"
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misc-feature	305755..305961	
misc-feature	306688..306969	
gene	complement(307030..307389)	/inference="similar to sequence: INSDC: SME591783" /note="similarity: fasta; with=UniProt: Q92SS8 (EMBL: SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; Hypothetical protein SMC00367.; length=119; id 62.712; 118 aa overlap; query 1-118; subject 1-118" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05761.1" /db-xref="GI:115254687" /db-xref="UniProtKB/TrEMBL: Q1MMP1" /translation="MSDRQAVEQTVHLYVEGMAF ANEAAALKKAFHPKSSIIGHYENAV EWLTRDEFIAAILQEEPAPPGTQPYMDIQSVDVE GDAASVKVTDDFAGMRFTDYLSSL KIDGRWTIVSKLFLHHR"
CDS	complement(307030..307389)	/locus-tag="RL0271"
gene	complement(307497..308492)	/locus-tag="RL0272"
CDS	complement(307497..308492)	/inference="similar to sequence: INSDC: AP003005" /note="similarity: fasta; with=UniProt: Q98CQ3 (EMBL: AP003005); Rhizobium loti (Mesorhizobium loti).; Oxidoreductase, aldo/keto reductase family.; length=332; id 71.818; 330 aa overlap; query 1-330; subject 2-331" /codon-start=1 /transl-table=11

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misc-feature	complement(307557..308477)	/locus-tag="RL0272"  /inference="protein motif: Pfam:PF00248.9" /note="Pfam match to entry PF00248.9 Aldo-ket-red"
misc-feature	complement(308409..308477)	/locus-tag="RL0272"  /inference="protein motif: TMHMM:2.0" /note="1 probable transmembrane helix predicted at aa 26-48"
gene	308617..309525	/locus-tag="RL0273"
CDS	308617..309525	/locus-tag="RL0273" /inference="similar to sequence: INSDC:SME591783" /note="similarity: fasta; with=UniProt:Q92SS5 (EMBL:SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE TRANSCRIPTION REGULATOR PROTEIN.; length=296; id 72.542; 295 aa overlap; query 1-295; subject 1-295" /codon-start=1 /transl-table=11 /product="putative LysR family transcriptional regulator" /protein-id="CAK05763.1" /db-xref="GI:115254689" /db-xref="GOA:Q1MMN9" /db-xref="UniProtKB/TrEMBL:Q1MMN9" /translation="MNRTQLSQLAVLAHVSEHRS FRAAAKELLVAPSAISHAISLEE SLGVRLARTTTRSVAPTEEGRLLLERLRPALEEI DIALEAVRDTRAKPAGNLRITAPR FASDLLLAPRLGDFLNLYPDITLEIANEDGFTDI VKEGFDAGIRLEESLEADMIARV SPDLTTVIAASPEYFEHHPKPEHPRDLVHHRCIK RRFTNGSIYRWEFEKDGQELVSV DGPLIVSEDRALALLAALNGAGLAYLFDMRVYDEL AGGTLVRVLEDWCAPYSGPFLYYP TRRQMRPALRAFIIDFFRYSEQDTGGR"
sig-peptide	308617..308689	/locus-tag="RL0273"



		/inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0273 by SignalP 2.0 HMM (Signal peptide probability 0.758) with cleavage site probability 0.691 between residues 25 and 26"
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misc-feature	308881..309507	/locus-tag="RL0273" /inference="protein motif:Pfam:PF03466.5" /note="Pfam match to entry PF03466.5 LysR-substrate"
gene	complement(309571..310068)	/locus-tag="RL0274"
CDS	complement(309571..310068)	/locus-tag="RL0274"
		/inference="similar to sequence:INSDC:SME591783" /note="similarity:fasta; with=UniProt:Q92SS4 (EMBL:SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; Hypothetical protein SMc00371.; length=163; id 77.160; 162 aa overlap; query 1-162; subject 1-162" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05764.1" /db-xref="GI:115254690" /db-xref="UniProtKB/TrEMBL:Q1MMN8" /translation="MAKEKTLEDLFYDTLKDIIYF AERQILRALPKMARAAQSPKLKKG FEKHREETEGQVERLQQVFELIGKRAQGKTCEAI QGIIAEGEEIMEEFKGTVALDAGL ISAAQAVEHYEIIARYGTLKTWAATLGLKEVVGLL DQTLQQETATDKTLSQLATTAANQ KAKAA"
misc-feature	complement(309580..310053)	/locus-tag="RL0274"
		/inference="protein motif:Pfam:PF05974.1" /note="Pfam match to entry PF05974.1 DUF892"
gene	310215..310832	/locus-tag="RL0275"
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IWDMRDFDGCMAAVCIAVPWMVDHYRVESDWQR
LAWWIHDHLPYASLCFFPKLWAFN
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gene      complement(310822..3112 /locus-tag="RL0276"
65)
CDS       complement(310822..3112 /locus-tag="RL0276"
65)

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33970).; Acetyltransferase
(AGR-C-449p).; length=147; id
57.143; 147 aa overlap; query
1-147; subject 1-147"
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acetyltransferase"
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90)

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id 68.038; 316 aa overlap; query

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		KALIVTKVGSMDGQKTLKETIYLKAVEDSLRRL
		QTDYIDVYLSHWPDEDTTPEETLG
		AYAKLKQQGKIRAIGCSNYDAKLLQASFDAAEKA
		GLPRYDVLQPEYNLYERSSSFEGPL
		ADLCVKEDIGVITYFSLAAGFLTGKYRSKSDTQG
		RAREGRVSKYLDDKGLRILAALDK
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misc-feature	complement(311283..312209)	/locus-tag="RL0277"
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		sequence: INSDC: SME591783"
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		sequence: INSDC: SP10405"
		/note="similarity: fasta;
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		(EMBL: SP10405); Streptomyces
		purpurascens.; rdmF; RdmF.;
		length=346; id 28.354; 328 aa
		overlap; query 2-324; subject
		10-329 similarity: fasta;
		with=UniProt: Q92SS0
		(EMBL: SME591783); Rhizobium
		meliloti (Sinorhizobium
		meliloti).; PUTATIVE
		OXIDOREDUCTASE PROTEIN.;
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		DIDDVIAARDNRNVVTEAYMITYSPVWQKVRSL
		IDEGAIGSLRHVQGAFTYFNRPDA
		NMRNVPELGGGGLPDIGVYPVMGTRFSTGKEPLW
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		DFELSFYISTQMANRQVMVFHGTEGYIEVKSPFN ANRWGPTEEIELADRSHSESRIFRF QDSRQYKRQVEAFARAVKNGKEEIVTLENSKLNQ KVIDAIYRASEKDGWEAV"
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CDS	complement(313495..313872)	/locus-tag="RL0279"  /inference="similar to sequence: INSDC:B97391" /note="similarity: fasta; with=UniProt:Q8UIM6 (EMBL:B97391); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0267 (AGR-C-459p).; length=117; id 31.356; 118 aa overlap; query 3-120; subject 2-112" /codon-start=1 /transl-table=11 /product="putative transmembrane protein" /protein-id="CAK05769.1" /db-xref="GI:115254695" /db-xref="GOA:Q1MMN3" /db-xref="UniProtKB/TrEMBL:Q1MMN3" /translation="MRKLIHFIAIAGGIGFLVDAG ILSALLALTPLGPFLARLVIAIAFA MAATWAFNRSETFDRSGRSLAAEGFRYGSVGVT ALVNYGLYSALLLSLPALQPLAAM VIASIASMIFSFFGYSRFVFRAE"
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gene	complement(313869..314876)	/locus-tag="RL0280"
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/inference="similar to
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/note="N-terminus to codon 240 is
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actinomycescomitans. DNA for
glycosyltransferase, lytic
transglycosylase, dTDP-4-rhamnose
reductase, complete cds. 005377
(EMBL:AAAB2668) (234), and entire
protein is similar to Anabaena sp.
(strain PCC 7120). A110042
protein. Q8Z0P8 (EMBL:AP003581)
(315) similarity:fasta;
with=UniProt:005377
(EMBL:AAAB2668);
actinomycescomitans).; DNA for
glycosyltransferase, lytic
transglycosylase, dTDP-4-rhamnose
reductase, complete cds.;
length=234; id 25.688; 218 aa
overlap; query 9-220; subject
1-213 similarity:fasta;
with=UniProt:Q8Z0P8
(EMBL:AP003581); Anabaena sp.
(strain PCC 7120).; A110042
protein.; length=315; id 54.054;
296 aa overlap; query 11-306;
subject 11-306"
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SRRFVKSFPAVSGGFEIETEMSVHASRLKLPVSE
LELDYGRRPEGSHSKLSTFRDGAK
ILWMFAMLMKETRPFAFFSAISATFMLASLGFMA
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[illegible]

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/note="similarity:fasta;
with=UniProt:EX7L-ECOLI
(EMBL:CEK129H2R); Escherichia
coli.; xseA; Exodeoxyribonuclease
VII large subunit (EC 3.1.11.6)
(Exonuclease VII large subunit).;
length=456; id 34.990; 483 aa
overlap; query 14-495; subject
8-438 similarity:fasta;
with=UniProt:EX7L-AGRT5
(EMBL:AE007966); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; xseA; Probable
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1-526; subject 1-532"
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gene	complement(319773..320273)	/locus-tag="RL0284"
CDS	complement(319773..320273)	/locus-tag="RL0284"  /inference="similar to sequence:INSDC:AE008999" /note="similarity:fasta; with=UniProt:Q8UIM1 (EMBL:AE008999); Agrobacterium tumefaciens (strain C58/ATCC 33970).; pecS; Transcriptional regulator, MarR family.; length=168; id 77.500; 160 aa overlap; query 7-166; subject 8-167" /codon-start=1 /transl-table=11 /product="putative MarR family



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/note="Pfam match to entry  
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LOCUS (LOC): AP008934 GenBank (R)  
GenBank ACC. NO. (GBN): AP008934  
GenBank VERSION (VER): AP008934.1 GI:72493824  
CAS REGISTRY NO. (RN): 864028-20-6  
SEQUENCE LENGTH (SQL): 2516575  
MOLECULE TYPE (CI): DNA; circular  
DIVISION CODE (CI): Bacteria  
DATE (DATE): 26 Dec 2007  
DEFINITION (DEF): Staphylococcus saprophyticus subsp. saprophyticus ATCC  
15305 DNA, complete genome.  
SOURCE: Staphylococcus saprophyticus subsp. saprophyticus ATCC  
15305  
ORGANISM (ORGN): Staphylococcus saprophyticus subsp. saprophyticus ATCC  
15305  
Bacteria; Firmicutes; Bacillales; Staphylococcus  
PROJECT (PJID): GenomeProject:15596  
COMMENT:  
This work was done in collaboration with Makoto Kuroda, Miyuki  
Kumano, Kazuya Morikawa, Masato Higashide, Atsushi Maruyama, Yumiko  
Inoue, Kimio Matoba, Toshiko Ohta (University of Tsukuba), Hideki  
Hirakawa, Satoru Kuhara (Kyushu University), and supported by the  
Research for the Future Program of the Japan Society for the  
Promotion of Science.  
REFERENCE: 1  
AUTHOR (AU): Kuroda,M.; Yamashita,A.; Hirakawa,H.; Kumano,M.;  
Morikawa,K.; Higashide,M.; Maruyama,A.; Inose,Y.;  
Matoba,K.; Toh,H.; Kuhara,S.; Hattori,M.; Ohta,T.  
TITLE (TI): Whole genome sequence of Staphylococcus saprophyticus  
reveals the pathogenesis of uncomplicated urinary tract  
infection  
JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 102 (37), 13272-13277  
(2005)  
OTHER SOURCE (OS): CA 143:280290  
REFERENCE: 2 (bases 1 to 2516575)  
AUTHOR (AU): Hattori,M.; Yamashita,A.; Toh,H.; Oshima,K.; Shiba,T.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (11-MAR-2005) Contact:Masahira Hattori  
Graduate School of Frontier Sciences, University of  
Tokyo; 5-1-5 Kashiwanoha, Kashiwa, Chiba 277-8561,  
Japan

## FEATURES (FEAT):

Feature Key	Location	Qualifier
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CDS	509..1876	/locus-tag="SSP0001" /note="similar to gi 27466919 ref NP-763556.1  [Staphylococcus epidermidis ATCC 12228], percent identity 80 in 455 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="chromosomal replication initiator protein" /protein-id="BAE17146.1" /db-xref="GI:72493825" /translation="MSEQEIWEKVLTLAQEKVSS ASYQTFLKDTKLFLQNEQAIVVT DDDFVANWLKMNYAEIIKAALYEAIGHEIAPVFY TEELKSLHTSEQKEENQPEQPAK KYTPGVDEAVIGGEQFNTHNTFETFVIGPGRNRP HAASLAVAEAPAKAYNPLFIYGGV GLGKTHLMHAIGHYVLDNNPDAKVIYTSSEKFTN EFIKSIRDNKTERFREKYRNIDVL LIDDIQFIQNKEQTQEEFFHTFNELHQANKQIVI SSDRPPKEIAKLEDRLRSRFEWGL IVDITPPDYETRMALQKKIGEENLNIPTEALTY IANQIQSNIRELEGALTRVLAFSK LQGQPITTELTAELKDIIQAPKSKKITIQDIQK IVGQYYSVRIEDFSAKKRTKSIAY PRQIAMYLSRELTDPSLPKIGEEFGGRDHTTVIH AHEKIVKDIQNDPTFKQEVENLEK EIRNQ"
gene	2124..3254	/locus-tag="SSP0002"
CDS	2124..3254	/locus-tag="SSP0002" /note="similar to gi 27466920 ref NP-763557.1  [Staphylococcus epidermidis ATCC 12228], percent identity 93 in 376 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="DNA polymerase III beta subunit" /protein-id="BAE17147.1" /db-xref="GI:72493826" /translation="MEFTIRRDYFINQLNDTLKA ISPRTTLPILTGIKIEVKNNNEVIL TGSDSEISIEITIPKQVDGEDIIDIVETGSVVL GRFFVDIIKKLPGKEVKLSTNEQF QTLITSGHSEFNLSGLDPDQYPLLPQVSRDDAIQ LSVKVLKNVIAQTNFAVSTSETRP VLTGVNWLIIQENELICTATDSHRLAVRKVALEDD SENKNVVIIPGKALSELNKMIMSDSE EDIDIFFASNQVLFKVGNNVFISRLLEGHYPDTS RLFPENYEIKLGIDNGEFYHAIDR

gene	3815..4039	ASLLAREGGNNVIKLSTGNELVELSSTSPEIGTV
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gene	4036..5151	/locus-tag="SSP0004"
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		NNYLKQLQYGQKTDSTMLEVLNQQFAEYALKITL
		RREHFINELESLAKPIHSGITNER
		ETLSLNYLPSIKLENKDKSETERLEEVLTILNDN
		MEREKDRGVCLYGPHRDDLGFNVN
		GMDAQTYGSQGGQRTTALSIKLAEIELMNIEVGE
		YPILLDDVLSELDDSRQSHLLST
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7134..9827

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YVYKDRKVYHQGYKKGV PQFDLKV  
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QRTRELAFLNKGISITLRDERGEE  
VREDTYHYEGGIKSYVEMLNENKQPLHEEPIYVH  
QTKDDIEVEIALQYNKG FATNLLT  
YANNIHTYEGGTHEEGFKRALS RVLNSYGLNSKI  
IKEDKERLSGEDTREG LTAIVSIK  
HGDPQFEGQTKTKLGNSEVRQIVDKLFS ELFERF  
LYEHPQVGRIVVEKGIMASHARLA  
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RDLNKDTIDFIDNYDGNEREPSVL  
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gene	12929..14212	/locus-tag="SSP0009"
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gene	14528..15229	/locus-tag="SSP0010"
CDS	14528..15229	/locus-tag="SSP0010" /note="similar to gi 27466927 ref NP-763564.1  [Staphylococcus epidermidis ATCC 12228], percent identity 75 in 228 aa, BLASTP E(): 2e-98" /codon-start=1 /transl-table=11 /product="putative branched-chain amino acid permease" /protein-id="BAE17155.1" /db-xref="GI:72493834" /translation="MENEAHVTFKQGVKACIPTL LGYAGVLSFGIVAVASGFSLLEI ILLCLLVYAGAAQFIICALVIAGTPISAIVLTAF IVNSRMFLLSMTLAPSYKDYSLLN RIGLATLVTDTEFGVAVTPHLKGEKINDRWLHGL NITAYVFWTIACIIGALFGKYIHD PDVLGLDFAITAMFIFLAVSQFESIRRSKVKIYL VLIICVIVMMLGLSLFMPSYLAII LASTITAALGVVMER"
gene	15226..15555	/locus-tag="SSP0011"
CDS	15226..15555	/locus-tag="SSP0011" /note="similar to gi 27466928 ref NP-763565.1  [Staphylococcus epidermidis ATCC 12228], percent identity 61 in 109 aa, BLASTP E(): 3e-34" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17156.1" /db-xref="GI:72493835" /translation="MTTIIHMLTIIILCGIVTWL TRIIPFVMISKVHLSERVVKWLSF IPITLFTALIIDGVLVQQEGVMGYTINMPFLITM IPTIVVAIVSRSLTITILSGIIIM ALLRWVF"
gene	15827..16795	/locus-tag="SSP0012"
CDS	15827..16795	/locus-tag="SSP0012"

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gene	17076..17987	/locus-tag="SSP0013"
CDS	17076..17987	/locus-tag="SSP0013"
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gene	18002..19969	/locus-tag="SSP0014"
CDS	18002..19969	/locus-tag="SSP0014"
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CDS

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19966..20412

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ENEYHYRVRYSEKEHVLFFDITK  
EVYTNELYESSKPIIATLFLDNYDEITQNMNDTQ  
KSEINSMVTRVISRWATEHNIYFK  
RYSSDQFVAYLNQNILNEIEATNFSILSQLREKS  
VGYRAQLTLSIGVGEGSENIDLG  
ELSQSGLDLALGRGGDQVAIKHINGNVRFYGGKT  
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ELKDRFITSDEAWDIMTSKTTLVVVDTHKPEMVI  
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SSPLLVYMEPYASSTAELVTELLEYQPTEQRLTR  
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aa, BLASTP E(): 7e-70"  
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gene  
CDS

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20443..21852

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LELDTILNDAERRILELSSSTRES  
GFKDIRDVLGDVYENAE LL DQNSGQTPGIPTGYR  
DL DQMTAGFNRNDLIILAARPSVG  
KTAFALNIAQKVATHEDHFSVGIFSLEMGADQLA



		TRMICSSGNVDSNRLRTGMMTEED WNRFTIAVGKLSRTKIFIDTPGIRITDIRSKCR RLKQEHGLDMIVIDYLQLISGSGS RFSDNRQQEVSEISRTLKAIARELECPVIALSQL SRGVEQRQDKRPMMSDIRESGSIE QDADIVAFLYRDDYYNRGEDEDDDDDSNYEPQTN DDNGEIEIIIIAKQRNGPTGTVKLH FMKQYNKFTDIDYAHADFG"
gene	22148..23431	/locus-tag="SSP0017"
CDS	22148..23431	/locus-tag="SSP0017" /note="similar to gi 57285312 gb AAW37406.1  [Staphylococcus aureus subsp. aureus COL], percent identity 89 in 427 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="adenylosuccinate synthase" /protein-id="BAE17162.1" /db-xref="GI:72493841" /translation="MSSIVVVGTTQWGDEGKGKIT DFLAEQADVIARFSGGNNAGHTIK FGGETYKLHLVPSGIFYKEKLAVIGNGVVVDPA LLKELDALNERGISTDNLRISNRA QVILPYHIKQDEYEEERRGDNKIGTTKKGIGPAY VDKAQRIGIRVADLLDKETFEKLL KDNIEYKGAYFEGMFGKACPTFEEIFETYYAAGQ RLAQFVTDITAKVLDDAFVADEKVL FEGAQGVMLDIDHGTYPFVTSSNPVAGNVTVG VGPTFVSKVIGVCKAYTSRVGDGP FPTLFDGHHIREVGREYGTGTTGRPRRVGWFD SVVLRHSRRASGITDLSINSIDVL TGLKEVKICTAYELDGKEITEYPANLKDLQRCKP IFETLPGWTEVDVTGCRSLEELPNN ARRYLERISELCDVKISIFSVGPDRNQTNLLKSL W"
gene	complement(23521..24732)	/locus-tag="SSP0018"
CDS	complement(23521..24732)	/locus-tag="SSP0018" /note="similar to gi 42781882 ref NP-979129.1  [Bacillus cereus ATCC 10987], percent identity 41 in 398 aa, BLASTP E(): 1e-85" /codon-start=1 /transl-table=11 /product="putative glycosyltransferase" /protein-id="BAE17163.1" /db-xref="GI:72493842" /translation="MAKVLFINSIGSIGHLNPTIA VCKELVARGEVVYYIGDQYQDKL KDTGVEIRTLPTDEIIQRFTAYGSGNLFHVVNGL LNTADVILPKILEDTKNEHYDYLI SDSMFSFGNLIAQKLHIPTISSITSFAHTAETFE AALNYNAQALSETEMNDVEDTFNH LQQHIQTITYGVEVNSRYETMNNPGDFNIAYILEK FQINPELFDZAHYRFVGPVSMQPP STDFMSQVDQSRPIVYVSLGTVFNQNIFFNQCF AALKDLDVSVIVSIGEANNAADF"

		TVPDNVLLKSYVPQTELLQHTALFLTHAGMNSTN EALLMDVPLLAFPQNADQPLVAQQ IENINVGQQLNSETVTTEDLKAKVVEMLQNRATY QAAIKKIKQTQALDQPGYVTAVDQ ILTFRDHHINH"
tRNA	25017..25091	/product="tRNA-Glu" /note="SSPtRNA01"
tRNA	25098..25170	/product="tRNA-Asp" /note="SSPtRNA02"
gene	25365..25823	/locus-tag="SSP0019"
CDS	25365..25823	/locus-tag="SSP0019" /note="similar to gi 20089628 ref NP-615703.1  [Methanosarcina acetivorans C2A], percent identity 29 in 105 aa, BLASTP E(): 2e-05" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="BAE17164.1" /db-xref="GI:72493843" /translation="MTNHKHIEETDLINLISDRH HDLRQKVEYMTAQQLPQVHFGSSE WYLIMI IKYDQPTFAELTHKINLTRQAIHKAVKQ LEQKQVVQIESVPNNKKEKRVTLT EFGIMCYEKYIKNKQHIIIEHIGQVIGASEVAHLE QLLQADWQLENDKPDE" /locus-tag="SSP0020"
gene	26277..27683	/locus-tag="SSP0020"
CDS	26277..27683	/locus-tag="SSP0020" /note="similar to gi 16077336 ref NP-388149.1  [Bacillus subtilis subsp. subtilis str. 168], percent identity 45 in 456 aa, BLASTP E(): e-117" /codon-start=1 /transl-table=11 /product="putative permease of the major facilitator superfamily" /protein-id="BAE17165.1" /db-xref="GI:72493844" /translation="MATQVNVKSPKMFALVLMIG GFMGLFSETALNMALTDIMADFKV SAATVQWLTTGYLLVMACLVPASSYLIKWFSTKT LIVSGILLSLLGVVIGALAPNFGL LLLGRLIQALGTGILLPIMVTVLMLIFPIEKRG VMGIMGLVITAGPALGPTLSGVII SASSWHYIFWISAVLYLVVLGLAFTNTENVEIS KPKIDILSICLSTIGFAGLIFALS SMAEAAFTNVIVWLPLVIGILALIIIFVVRQFKID SPMLNLNVFKYPMFVLGAAMVFIT ILCILSTGILLPLYLKGALLFSSVIAGLTLLPGN AVNLVLSPVVGSLFDRFGARYFGI IGYLLMFI AAMTFALII SASTPVWAIILTFMVLF FGITMVMMPAQTNALNQLPHDLYA DGSATITTTLIQVGGSAGTAIAITLYTTAMKSFGA ANPNVSQEIIILSHGVQFTFFFFITA LTVIGFILSLFVKKQKSV" /locus-tag="SSP0021"
gene	28100..28801	/locus-tag="SSP0021"
CDS	28100..28801	/locus-tag="SSP0021" /note="similar to gi 27466936 ref NP-763573.1

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gene	28814..30646	/locus-tag="SSP0022"
CDS	28814..30646	/locus-tag="SSP0022"
		/note="similar to gi 57285314 gb AAW37408.1  [Staphylococcus aureus subsp. aureus COL], percent identity 87 in 608 aa, BLASTP E(): 0.0"
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		/transl-table=11
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		/protein-id="BAE17167.1"
		/db-xref="GI:72493846"
		/translation="MKWLKHFQSLHTKLIVIVYVL LIIIGMQIIGLYFTNSLEKELTQT FKNNISQYAKQIEINIEKVYDEDNAINAQKEVQN LLNEYANRQEIEEIRFIDKDQIIM ATSKQSTRSLINQKANDNSIQKALSLSGEINSHTV LKDYGNGKQRVVYNLPVKTSNDG TIGDVYIEADINDVYNQLSNINQIFIVGTGISLL ITVILGFFIARTITKPIITDMRNQT VEMSKGNYTQRVKIYGNDEIGELALAFNNLSKRV QEAQANTESEKRRLDSVITHMSDG IIAIDRRGRVRIVNDMALTMGMTMKEDIIGDHML KVLKLEEDFSLDEIQENNDSFLLD INENEGIIARVNFSTIVQETGFVTGYIAVLHDVT EQQQVERERREFVANVSHELRTPL TSMNSYIEALES GAWKDGELAPQFLSVTREETER MIRLVNDLLQLSKMDNESEQITKE IVDFNMFINKI INRHEMSAKDTTFVREVPTETIF TEIDPDKMTQVFDNVITNAMKYSR GDKRVEFHVKQNALYNRMTIRVKDNGIGIPINKV DKIFDRFYRVDKARTRKMGGTGLG LAISKEIVEAHNGRIWANSVEGQGTSIFITLPCE VLEDGDWDAE"
gene	30636..31976	/locus-tag="SSP0023"
CDS	30636..31976	/locus-tag="SSP0023"
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		/transl-table=11
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		QMHSNHNLIIPDLTDEFLILDFS YDMPLATYLGQ
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		APKAPEAMKSYHTIYNRISVDTMNSILFNDSVVV
		RSTKSGTATYNNNTGVANYNDETE
		KYRYTNLSEDENRSTNMQDSIPSTYDYINNHHGGF
		TDDYRLFNIDNKN GELTYQMFLNG
		RPTFNDEYLNNIKVSWGDKGVFSYARALLKANVT
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		PQWYVQYNGEW RAYEDGRLE"
gene	31977..32759	/locus-tag="SSP0024"
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		FEQTYHDYPIMNNNKARLEFNINN
		DGKATSYKQTAMKSIAPSEGANNDDKKQVNSAKSA
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gene	33192..33983	/locus-tag="SSP0025"
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		12228], percent identity 91 in 263
		aa, BLASTP E(): e-138"
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		NPYETKSLAGFDIESFNVSHDAIDPQFYIFHNHY
		KKFTILTDTGYVSDRMKGMIQGS
		AFVFESNHDVDMLRMCGYPWKTQ RILSDMGHVS

gene	34583..35062	NEDAGRAMTDVITGSTKRIYLSHL
CDS	34583..35062	SQDNNMKDLARMSVGQVLNENDIDTEKEVLLCDT DKANATPIYTL" /locus-tag="SSP0026" /locus-tag="SSP0026" /note="similar to gi 27466941 ref NP-763578.1  [Staphylococcus epidermidis ATCC 12228], percent identity 86 in 159 aa, BLASTP E(): 3e-75" /codon-start=1 /transl-table=11 /product="hypothetical protein orfX" /protein-id="BAE17171.1" /db-xref="GI:72493850" /translation="MKITILTVGKLKEYWKQAI AEYEKRLSAYSKIEIIEVPDEKAP ENMSDKEVEQVKEKEGQRLAKVKQQSTVITLEI KGNMLTSEGLAKEIESRMTRGQSD FTFIIGGSNGLHKDVLDRSDYALSFSKMTFPHQM MRVILIEQVYRAFKIMRGEAYHK" /locus-tag="SSP0027" /locus-tag="SSP0027" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17172.1" /db-xref="GI:72493851" /translation="MDSGYHLPHNAVVEEFEFM LSLLDVSKEYYIYEDLKALFFEEM VKNGLFKFKHGRMYERIKNSINMKEIYFKVYNGK ATYDDIKKLYYTDSEKKPSKNFNQ NWNIEIIRDYLEFMAFLGVLPTYKKGKNRENDKKH YISDTLIKYKNGTLLLSDIILGMK FRNASKDYSNFEYDITLRPFVVAIKILQLAKEL GVLEV DGA V L C G L V K L Q N N E S L K D MSNIDFSNRNNNNWTKKQIKEFGRLTFMKQWLN IVLEIPLVNTRNIKFDITNFDINN YDFYHESIFIGETYNHLEITPQIANIIICPEKCN DEEVLSILKDAKLINENKQNAHIN FDTDLPSRELVEADRLFKSKSKIEFELDEVQIQ EFSMSNENFDIGFQIAKSSDGTAY ENFIYQQLLNTFENSKVRQLGSQFTGQRLSDTVI DCVVYHHQMKSRIKIIVECKAGKA IKSFDERKEINNVQNTLKLANINDYDGVWYIITD SNQIPTQTHGGYRSSNNSYSFEEK LLTLQFDIQMSTGKPTIVTAFSYEMFMKFLSDIK EINGIITSQSTKHFWVWSKKFVNK AYISVQA" /locus-tag="SSP0028" /locus-tag="SSP0028" /note="similar to gi 57015737 gb EAL52527.1  [Campylobacter upsaliensis RM3195], percent identity 31 in 267 aa, BLASTP E(): 1e-30" /codon-start=1 /transl-table=11 /product="putative DNA modification methylase" /protein-id="BAE17173.1" /db-xref="GI:72493852"
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gene	36942..37721	
CDS	36942..37721	

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gene	37714..38757	/locus-tag="SSP0029"
CDS	37714..38757	/locus-tag="SSP0029" /note="similar to gi 13542247 ref NP-111935.1  [Thermoplasma volcanium GSS1], percent identity 27 in 379 aa, BLASTP E(): 6e-27" /codon-start=1 /transl-table=11 /product="putative modification methylase" /protein-id="BAE17174.1" /db-xref="GI:72493853" /translation="MSNIYSYHAKFHESIPNEYI NKYSQEFETILDPFCGSGTTLKES LKLGRNAIGIDVSPAILSSKVNTNFYDKNKLKR VYDYILKQFNSNISINVIKFPDYE RWYTEENHLQLSKLKNIIDNIEENSYPREFFLLCF LSISNKSNNRRKTWNIGYLADNVL PDLDSKFVAIDSFQKVSKEIENIDFEELYKLGN RSIHIEKKDINTAKLDCKVDMVMT SPPYPFAVD FIRYHRLSMYWLQENIEQLTRQEIG ARNKRNNKGNLSLFFNEIEKSFIN IMRVVRTDGYWAMTIADTTNRNKVKIPFIDWTINL FYEHGWILVEDRIRELQQQTMAQK RIPEEHILVFKKI"
gene	complement(38843..39355)	/locus-tag="SSP0030"
CDS	complement(38843..39355)	/locus-tag="SSP0030" /note="similar to gi 22652813 gb AAN03831.1  [Enterococcus faecalis], percent identity 29 in 167 aa, BLASTP E(): 2e-15" /codon-start=1 /transl-table=11 /product="putative replication protein RepA" /protein-id="BAE17175.1" /db-xref="GI:72493854" /translation="MNRTLQILLKRQKSLNFSVY SEFESKQLSMFNDDKTMIDFEGKK LSITLNPDFVYLLNNFDENSICFMSDFTNLKSI YSKHLYRLFTEYQDESTYTFSIEA FREFLDINSKYPHMKDIDKPVLRMIKEELNQFYQ YFEYKKVLEMPQRVTEIKFNFIKV KNSCTNYISH"
gene	complement(39676..40182)	/locus-tag="SSP0031"
CDS	complement(39676..40182)	/locus-tag="SSP0031"

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/feature "note" {
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	)	
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CDS	complement(43065..44414	/locus-tag="SSP0036"
	)	
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CDS       complement(46830..48257 /locus-tag="SSP0039"
)
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[Staphylococcus aureus], percent
identity 87 in 476 aa, BLASTP E():

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CDS	50166..51905	

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CDS	55110..56750	/locus-tag="SSP0044" /locus-tag="SSP0044" /note="similar to gi 49257044 dbj BAD24833.1  [Staphylococcus aureus], percent identity 81 in 547 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17189.1" /db-xref="GI:72493868" /translation="MNHILETLIKLLKVGME AID RKGLIAILTSSIGNDEMDDSEQAV MVYNELIDKLQLNIPKDVDRPNISYFQIQKKP NDTILVEMMISIFHIKRFDS ELFV FKDKGWQKVNEDELQGLISKMIQVLLVDYKPSLS ILKNVVVGLQNSIDVEELVENKQY IGCGHNMFNLD AFEVVGNSIKIFPATRLNLELVK SDVITEKTPPHFNRYM LEFANFDS DLQYFLFQHIAVLLTANTKYRRALLLYGGAKNGK SVFINLVRSFFYSEDIVSKALNEL QGRFDKESLVGKKLMASDEIGESRIQEKIVNDLK KLVSVEPVHVDRKKGKTQVETTLDL KLAFGTNARLNFP SAHAKALERRIAVIPCEYYVE KADPDLIEKLQDEKKEIFLYLYMYV YKQIVKNDIEY LQNDRVTEISHDWLNFGYEFVSS KSASIANQKACINLLRKLIEIKPG SRIKVSELNKVINEEIKVSSQVIKQLIQANFDTQ TKLYNGYDYWIDLGWKEADKKEIH DISKKDNIISLDKNENITDDETLDEENLDFDWED FDDE"
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gene	56975..58657	/locus-tag="SSP0046"
CDS	56975..58657	/locus-tag="SSP0046" /note="similar to gi 49257045 dbj BAD24834.1  [Staphylococcus aureus], percent identity 95 in 537 aa, BLASTP E(): 0.0" /codon-start=1

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CDS	59190..59501	
gene	59517..60023	
CDS	59517..60023	

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CDS	complement(60680..61915	/locus-tag="SSP0052"
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[Staphylococcus aureus subsp.
aureus COL], percent identity 85
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CDS      complement(63578..66370 /locus-tag="SSP0054"
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		VDEAHSRGKLEEV IQDYNLNFGTN
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		IQAYSRTNRVEKETKPF GKIVNYRDLKQNTDNAL
		KLFSQTEDTDRVLMRDYDEYKAEF
		VDALAELKAVALKPQDMDQVQDENEKKAFVEAFR
		LVSKLVLR LKAFDEFDFTKANIGM
		NEQEFEDYKSKYFAIYDEVKPKRGEVEKVSILND
		IDFEIEILRNDRINVS YIMDLVRQ
		IDLKDKAEQQNRNDQIRRM LDNADDPTLRLKRDL
		LREFIDDVIPELSEEDNIDEAYIL
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		GQNTDNNNKKDNDQTQERDKKSDE
		TEKQSNDEVAENNQNTKNQSQGESNAAEATNEAN
		SQNSRTITIDEAKSIAFNSEDILN
		FTQNKDELIYNKDKSNNDEIFIETPFGGINESVK
		HHAIIDKNTGKIIKTGGAITSPDG
		PIKAENGYIDKDIYNSTTDFYNTYVYKKGMPFEF
		TATSDVPEQKYKELSNIVGNYWQK
		EQGYDNESNQSTSNNNQSQNEKENNQTS DNSKQS
		TKKDAKVDQNRENIETNNDESNQK
		QNNEEQQENSNEEASQNEEREDPNQQIEQPSSD
		KQNPDAAQENNNQNN DENTDGNNY
		ENEQSQDVESKSS ENDKETSNAS"
gene	67735..68484	/locus-tag="SSP0056"
CDS	67735..68484	/locus-tag="SSP0056"
		/note="similar to
		gi 55820776 ref YP-139218.1
		[Streptococcus thermophilus LMG
		18311], percent identity 51 in 251
		aa, BLASTP E(): 1e-62"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="BAE17201.1"
		/db-xref="GI:72493880"
		/translation="MVSVTQRISQIKQPRGGYLN



gene	68526..69032	RKSFEVKQLEPETLIDTKYENIAP QTIGLVVDYLTRMVINQDKEKSFAISLTGAKLAG ELQTAESLLKDINDNDDLSIIKAC QLVNYDMVYRAGSMPKEFKIPDQDTINNIKSLIN RSLSFFNQIGEVKMDGFTFEGGYT SIIDTGDGDFLTEDTLWDFKVSQQLPQKNSTLQL VIYYLMGKASQNPTFENIRYIGIY NPRFNQIYKYDMTQADSEMIETIQKCVIGYD"
CDS	68526..69032	/locus-tag="SSP0057" /locus-tag="SSP0057" /note="similar to gi 17227189 ref NP-478355.1  [Staphylococcus aureus], percent identity 56 in 157 aa, BLASTP E(): 1e-39" /codon-start=1 /transl-table=11 /product="truncated hypothetical protein" /protein-id="BAE17202.1" /db-xref="GI:72493881" /translation="MKKTITSLAVATLLLSASGV VKAENKEDWDEPVFIKADLEGQ DLQQTENDLGVDNDYETYNVNVNDVSNYIPNSSN LSYIYSSATIEHKKWGKGV DVKID TPDNITKVTSEQYQNAAITAGIKNAEIHIAVPEP VTGEGALAGIYKAYEEKGNLILK IFKIQTKK"
gene	69029..69502	/locus-tag="SSP0058"
CDS	69029..69502	/locus-tag="SSP0058" /note="similar to gi 17227189 ref NP-478355.1  [Staphylococcus aureus], percent identity 52 in 149 aa, BLASTP E(): 5e-37" /codon-start=1 /transl-table=11 /product="truncated conserved hypothetical protein" /protein-id="BAE17203.1" /db-xref="GI:72493882" /translation="MNDLGTISEENKKGKGYSDE ALNASIADIKEQLADIKQNQDKQI TQQQVEDTVNKVLDERGLSEILSNNQIQMINNNM VNVANSNALTS DPKAFKQNAKDVL KNIEKNSDDLNLNKGKDKAKDLNTEENRNLLQRLW DGIVEIIQSIIQFFSNLLNKL"
gene	69784..70647	/locus-tag="SSP0059"
CDS	69784..70647	/locus-tag="SSP0059" /note="similar to gi 57285193 gb AAW37287.1  [Staphylococcus aureus subsp. aureus COL], percent identity 76 in 284 aa, BLASTP E(): e-122" /codon-start=1 /transl-table=11 /product="UTP-glucose-1-phosphate uridylyltransferase" /protein-id="BAE17204.1" /db-xref="GI:72493883" /translation="MKIKKAIIPAAGLGTRFLPA TKAMPKEMLPILDKPTIQYIVEEA VAAGIEDIIIVTGKHKRAIEDHFDNQKELEMILE"

gene	71017..71685	EKGKSDLLQSVKYSSNLANMFYVR
CDS	71017..71685	QKEQKGLGHAIWTARQFIGNEPFAVLLGDDIVQA
		DTPAIKQLMNQYETTGKSIIGVQQ
		VNEIETHRYGIVDPEESYNELFSVNKFVEKPEIG
		TAPSNLAIMGYVLKPDIFDYLER
		QEIGRGGEIQLTDAIEHLNSEDVCYAYNFEGERY
		DVGEKIGFVKTTIQFALKDDYMKK
		EITEFIKSINK"
		/locus-tag="SSP0060"
		/locus-tag="SSP0060"
		/note="similar to
		gi 506697 gb AAA64640.1
		[Staphylococcus aureus], percent
		identity 62 in 221 aa, BLASTP E():
		2e-72"
		/codon-start=1
		/transl-table=11
		/product="capsular polysaccharide
		biosynthesis protein"
		/protein-id="BAE17205.1"
		/db-xref="GI:72493884"
		/translation="MEETIDLNKLFAILKKNMKY
		LIILPIVFLVLSMMMTFLFITPKY
		SSSTQVLVNQKETDSQMQAQVQSDLQLVNTYSE
		IIKSPRILDKVSKNLKGKYSSEEI
		AGMLTVSNQAESQILNIAVENESREAAGKVANEI
		ANVFSKDVNKIMNVDNVSILSKAD
		YYGSKDSPKPLINAVGVFLGLIVALIIIFLKEI
		LDKRIKTEEDVEELLDLPLVLGVIQ RFDY"
gene	71701..72393	/locus-tag="SSP0061"
CDS	71701..72393	/locus-tag="SSP0061"
		/note="similar to
		gi 506698 gb AAA64641.1
		[Staphylococcus aureus], percent
		identity 65 in 229 aa, BLASTP E():
		2e-80"
		/codon-start=1
		/transl-table=11
		/product="capsular polysaccharide
		synthesis protein"
		/protein-id="BAE17206.1"
		/db-xref="GI:72493885"
		/translation="MAKKIDTEITTLITHKKPKA
		VVSEKFRGIRSNILFSTADAEIQT
		LLIASDKPSSGKSTVSANIAVTYAQAGFKTLLID
		GDMRKPTQHYIFNKNNIKGLSNVI
		INKSTFEDAVYSTEVLNLDVLTSGPIPPNPSELI
		GSSNMMDLFEELKQRYDFILIDTP
		PVNTVTDAQLFGELTKNAVYIIDVETNNKESVKK
		GKNLLEKSGTKILGAVLNKAQLDK
		SSSSYYYYGEES"
gene	72393..73157	/locus-tag="SSP0062"
CDS	72393..73157	/locus-tag="SSP0062"
		/note="similar to
		gi 49484857 ref YP-042081.1
		[Staphylococcus aureus subsp.
		aureus MRSA252], percent identity
		54 in 251 aa, BLASTP E(): 1e-76"
		/codon-start=1
		/transl-table=11
		/product="capsular polysaccharide
		biosynthesis protein"

gene	73181..75016	/protein-id="BAE17207.1"
CDS	73181..75016	/db-xref="GI:72493886"
		/translation="MIDVHNHLLIGVDDGPQSVE ETISLLEQAKKQGITGIVVTPHHL HPKYDNIFADVEWGINKLQHNQQIKDLEIQLYAG QEIRITDQILDDLEQHKVKGINGS KYLIELPSNSVPHYTKNLLYEIQTKGFVPIIAH PERNKAIKNNINLLYELINNGALS QITASSLTGELGKNIQKLSIQILEHNLVHFVASD AHHSESRPFSLDALFSTPKLKNIE SVISMLLDNNEAMIQDKSVVTGRPIEFKRNKFFG LF"
		/locus-tag="SSP0063"
		/locus-tag="SSP0063"
		/note="similar to gi 506700 gb AAA64643.1  [Staphylococcus aureus], percent identity 73 in 599 aa, BLASTP E(): 0.0"
		/codon-start=1
		/transl-table=11
		/product="capsular polysaccharide biosynthesis protein"
		/protein-id="BAE17208.1"
		/db-xref="GI:72493887"
		/translation="MKYISIKQRFMMLLFIDSII VTFSVFLGYYILEPFFKGYSINVL ILSSLILLISHHVFAQIFDLYHRAWAYASVSELI LIVKSVTSSIVATGIIVPIFTQQA PFLRLYFITWMMHLLLLIGGSRLSWRIYRKTFISK EGKKKPTLIVGGGRGGSLLIRQMM NTPYMGMEPVLVDDDSNKQKMSIASGVKVQGCI KDIPELVKKFNKKIIIIAIP TLSQ QRLREINKLCEGTNVEVFKMPNIENVMGSGEIEVN KLKKVEVEDLLGRDPVELDMASIS KELTHKTI LVTGAGGSIGSEICRQVCKFTPDRIM LLGHGENSIYHIHQELIGLYKEEI EVIPIIADVQDKERMKKVMQAYKPYVVYHAAAHK HVPLMEYNPQEAIAKNNVLGTRNTA EAAKLAEVSKFVMVSTDKAVNPPNVMGASKRVAE MVIQSMNNETSKTDFVAVRFGNVL GSRGSVIPLFKKQIEAGGPVTVTHPGMTRYFMTI PEASRLVLQAGALATGGEIFVLDM GKPVKIVDLAKNLIRLSGYKEEDIGIEFSGIRSG EKLFEELLNKDEIHPEQVYEKIYR GKVQKIEKEELYNKIDDFLINESVRDEIIFFVNN NKTGEEKCKMD"
gene	75001..75765	/locus-tag="SSP0064"
CDS	75001..75765	/locus-tag="SSP0064"
		/note="similar to gi 56964929 ref YP-176660.1  [Bacillus clausii KSM-K16], percent identity 38 in 248 aa, BLASTP E(): 2e-45"
		/codon-start=1
		/transl-table=11
		/product="putative glycosyltransferase"
		/protein-id="BAE17209.1"
		/db-xref="GI:72493888"
		/translation="MQNGLVSVIMPLYNNEDYIE KSILSVINQTYENWEILIINDKSV"

gene	75762..76850	DSSKEIATKYSDIYSNIKLINLKINNGVANARNI GINNARGEYMAFLDSDDEWLPQKL EKQINFMNKNDYNFTCTYYGKMDSSENSVLPTVIK PKYSLNYNQILKNNIGNSTAIINV KKLGKFTVPLIKRNDYALWLKVIKKAKKVHTLE EVLSYHRLHSNSLSKKLDLIKYH YLVYRNYENLSIVKTISLIIYWSVKTIYKMIRSK IL"
CDS	75762..76850	/locus-tag="SSP0065" /locus-tag="SSP0065" /note="similar to gi 28211867 ref NP-782811.1  [Clostridium tetani E88], percent identity 28 in 273 aa, BLASTP E(): 9e-22" /codon-start=1 /transl-table=11 /product="putative glycosyl transferase" /protein-id="BAE17210.1" /db-xref="GI:72493889" /translation="MCTLHLCSIFGDAFFQNF IK SINENNESEVFYPRKNGYTYNNNQ AFVHSLELYNGIDRYLYYTKQKKCINEIERYYKL NEFSIIHAHTLYTDGYQAYILNKK YNIPYIVTVRSTDINIFYKYRKDLYFIARNIIKN SKGIVFLSKSYLTRTEKLFNINLK SKSNIITNGIDDFISNIYNKPKYNDNTKTILTV GYISKRNQLKICKAINKLNKRGY SIKYVIIIGKSLDKKILRKILKYSFVEYKEFMDKN TLIKEYRKADIFAMASLHETFGLT YLEALSQNTPVLYTKSEGFDQLFNDGEVGYSVNP LSTLDISEKIEKILQEKYRYDQVY LKVQQFEWQDIGRKYKLLYQNLGQAHDR"
gene	76840..78051	/locus-tag="SSP0066"
CDS	76840..78051	/locus-tag="SSP0066" /note="similar to gi 57285349 gb AAW37443.1  [Staphylococcus aureus subsp. aureus COL], percent identity 29 in 404 aa, BLASTP E(): 5e-47" /codon-start=1 /transl-table=11 /product="capsular polysaccharide synthesis protein" /protein-id="BAE17211.1" /db-xref="GI:72493890" /translation="MTGKIKSKNYIKFLQDVLIN VLSSTLLAMSLQLIIFPFLSSGIS TTEFGTLIAIYGVNNLIVNFLGNSLNNIRLINRQ SVEGYNLIYYIINTLSVILVLISI NILSINIGAINLILFCIFTFLANNRNYFMVNYRL KLQYNKILKLNILIIILGYFLGLLL YMHTDLWSIIIFLSGEIFAVIYMFITNALIINVSK DEFKFNKAITLDFIKLSFSNFINN FLNYLDRFLIIPILGAASMGIIYFAASAISKIIIM ILTPINNVLLSHITNLDMNIKRRR LILLYLITLLFIFPLYFIINSFSNFLVDILYINL ADEAKKLIPITIGILFNIVTNLL NNFLLKKYPITYQTIIQFVYGTVYLMMLAILLSTN FGLKGFAYSLVIANITKYLHVLI VLFVKQNKEKN"

gene	78051..79217	/locus-tag="SSP0067"
CDS	78051..79217	/locus-tag="SSP0067" /note="similar to gi 2499141 sp Q48453 YC07-KLEPN [Klebsiella pneumoniae], percent identity 23 in 354 aa, BLASTP E(): 3e-09" /codon-start=1 /transl-table=11 /product="putative glycosyl transferase" /protein-id="BAE17212.1" /db-xref="GI:72493891" /translation="MKKVLVFSKTRGFFNHLFNT KFNGWMISSLNNSYEKFTMKKKIL SLVGRSTILDIIGYIHTIKTVTNKADIYATYNRF LEANVPYIIYLENPTALFHYKLKR YSTKMGRNLTKLINDKNLKAVICMSEACREGFI KLYGPPIIERDDLIIEQIYPLITEE KLQIDTRHNDNKKFSLLFIAQGGKGFISKGGIEVV NTFIQLEKKIKNIELNIITSSNDI PPKILLKINNSSENINLIEFGISYDELKKYYIESN VLIHLTRQDSFGLTILEAMKYGTP VITTKLYSIPELIKENKNGYLTEPSYWFFNQENL PNPVWNNRRNTIFSKKSDKSKEK FLYDKIIYLYENREDYNQLKDTAYRNSKEKPFSE EFIINKWENLLNKIEMRKEK"
gene	79372..80376	/locus-tag="SSP0068"
CDS	79372..80376	/locus-tag="SSP0068" /note="similar to gi 45533027 ref ZP-00184022.1  [Exiguobacterium sp. 255-15], percent identity 62 in 330 aa, BLASTP E(): e-116" /codon-start=1 /transl-table=11 /product="putative UDP-glucose 6-dehydrogenase" /protein-id="BAE17213.1" /db-xref="GI:72493892" /translation="MNYNSLNIRFSNNLESSLED AEYIIIIATPTDYDENNNYFDTSTV EEVIEKCIKMNDNATIIKSTVPVEYTKKIKEKY NKKNIIFSPEFLREGNALYDNLYP TRIIVGEKSDKGKEIAELFRKGALNNNAKILLTN STEAEAIKLFSENTYLAMRVVSFFNE LDMYAEINDLNSKDIIEGVSLDSRIGEHYNNPSF GYGGYCLPKDTKQLKANYKNIPNN IISAVVDSNNTRKKFITNQIMSKNPKTVGIYRLT MKTNSDNFRYSSIQDIMHNLNEKT ELIIYEPTYKEDTFENIKVEHDLKKFKNTSDIIL SNRYEKDLEDVLNKVYTRDIFKRD"
gene	complement(80430..81650)	/locus-tag="SSP0069"
CDS	complement(80430..81650)	/locus-tag="SSP0069"  /note="similar to gi 42784434 ref NP-981681.1  [Bacillus cereus ATCC 10987], percent identity 22 in 384 aa, BLASTP E(): 2e-17" /codon-start=1

		<pre> /transl-table=11 /product="putative polysaccharide polymerase" /protein-id="BAE17214.1" /db-xref="GI:72493893" /translation="MKTYTKLIFSKEILFVFLFY AGFYKSVVPFSGAIDITIALLFAS ISITLYDTIKDGYLYKQSLVSIIIFIFFIVYIFI SYFYSPSADSLTKSLHFSLTSGWA FIGSFLIIKSNNFNVFKGIIILALISSIFGLK EYFNNTIHTQLNVFGSDYLALGRL LGISILILLANILLIKQSITNKIFTSMITLFLLL ILIVSGGRAPLLFLIITILIFLLF QVNLNNKTLKYNKLLPSFIVFLITVVLIFFSNL AIFETFKTRLLFLTTSQSGGGASAS GRIDRFKIAFDMFKDSPYKGDIDFSKYGMAN DYPHNIFLEIAAELGIIGILIFSI ILIYSLYNLHLNFQKDKQNKLLYWKILLIFIYTL LNANISGDIIGNKILFASLGFMIA FSNIYRHNLSINKN" </pre>
gene	81821..82378	/locus-tag="SSP0070"
CDS	81821..82378	<pre> /locus-tag="SSP0070" /note="similar to gi 16579852 gb AAL26667.1  [Staphylococcus aureus], percent identity 74 in 185 aa, BLASTP E(): 7e-78" /codon-start=1 /transl-table=11 /product="capsular polysaccharide synthesis protein" /protein-id="BAE17215.1" /db-xref="GI:72493894" /translation="MKRVFDLFTSIVVLGFLSPF LFLVSIAIKLESKGPIVFKQKRPG INNKFNIYKFRSMKVETPDVATDKIDANIYITK SGRFIRKTSIDELPQLFNVIKQDM SVVGPRPALYNQYDLIAKRTNESVHTVVKPGLTGL AQVMGRDDITDDQKVQYDKYYVEN QTFILDMFIIYKTIRNTITSEGVKH" </pre>
gene	82573..82917	/locus-tag="SSP0071"
CDS	82573..82917	<pre> /locus-tag="SSP0071" /note="partial similar to gi 49485038 ref YP-042259.1  [Staphylococcus aureus subsp. aureus MSSA476], percent identity 52 in 109 aa, BLASTP E(): 2e-24" /codon-start=1 /transl-table=11 /product="truncated capsular polysaccharide synthesis protein" /protein-id="BAE17216.1" /db-xref="GI:72493895" /translation="MVNYMNVNYYLTKEIAEKAK SEGVNQFIFFSIMSVFGLDGEVVK QVIISKKTLTKPKTSYGLSKIRAEEMLDEIQSNE FKVALLRSSMIYGESAPGNFSKLI KLSKHFTSISSN" </pre>
gene	83048..83251	/locus-tag="SSP0072"
CDS	83048..83251	<pre> /locus-tag="SSP0072" /note="partial" /codon-start=1 </pre>

		/transl-table=11 /product="truncated capsular polysaccharide synthesis protein" /protein-id="BAE17217.1" /db-xref="GI:72493896" /translation="MRELQNKKKSISIKLPNKLK LFGKLSIFNKLYGNLVYSKDIDEV NYNDDFITETEAYIKTLKHKSRF" /locus-tag="SSP0073" /locus-tag="SSP0073" /note="similar to gi 16129122 ref NP-415677.1  [Escherichia coli K12], percent identity 50 in 74 aa, BLASTP E(): 2e-13" /codon-start=1 /transl-table=11 /product="putative restriction endonuclease" /protein-id="BAE17218.1" /db-xref="GI:72493897" /translation="MSELLKRKDLMQLLKINDGT FRNWKKAGMPIVKAQNEEFFDLEQ VKRWHKKVTEGIDNLIIDKKYDNNTISDVFKCSQ QGGMRRSHLTNTLVLF SNHKNDVY RDHTVIDDEGNETLHYTGMGQKGDQDIEHGQNK LNHSEDL SIKVYLFESFISGEHIF RGEVRLYDKPYTTEQNDRMVWVFPLTFNNSEYYI PGNISDEKYREQANLINKLSDNDI YERAIKVKQVGRKEAVTKVYARNIHVAAHVKNRS NGYCDLCNKPAFPKDRNGRAYLEC HHVDWLANGGKDSIDNAVALDPNCHRMHELDL SDVKFLKDRNLNYYQSKNL" /locus-tag="SSP0074" /locus-tag="SSP0074" /note="similar to gi 49482343 ref YP-039567.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 58 in 1069 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17219.1" /db-xref="GI:72493898" /translation="MANLVNDTLSAWLLVESLQP GEVKYDKGSTLPKSNFQNEQQKQ LQSFDDYYDIWNDERYTIAEQSQKYGKRIFRLYR NCFYYKEIDKEIQNIFNDNTEVFN PNEKRCYGYTFQTDENGKVITDSLHIMPIMSALK EIRNNKSANIEQIFNDSKRKFQQR FNEIIADEPINKDKLRDLATYRDFFAVLISETN GIFKHVFVIEYVKNSESPDPNFNS FFIGDIERARKDPNQTLKAYIEGINGEKRIEVE NKEIFDEFLHPANLPDGRWPSQIE HKLYLMQQLAVNQITSSKEHISTVNGPPGTGKTT LLKDIFAHLVVERAKAFAALDEPR DAFENFKIHETDTSPIKVLKEEFSKFKMVVASSN NGAVENISKDLPKMEEVARDHEGK VFPDYELSYNKAIDELKSFSSTIASRLIGEPAWGL FSGVFGKGDNINKVMNQIFNNGSN
gene	84032..85018	
CDS	84032..85018	
gene	85137..88361	
CDS	85137..88361	

		NSDSKFDDPHASFVKLLQNEKNSLSYKQLMKKWR DCTKDFGKELKKVKELKELSVEAY NKYKENEKLLNKEKELESEIEMLKESLNQNRNDL SSKNSELEDVKNNFQYIEQQIETI DEMIQTYNPNNIFKKMKSWLNQTTTNNLDCKED KIKLLEEKKSYPHTKINDLQKCIKE ISNNNKDFEQKIKNNEEKINECNIKLTEYNQYKS DSNVTFPDSDFWNKNKYEKQVEN LWNSNELQYHRGLLFLKAMELQKLILIANNGPVY YAMQDFKARNSYLDAPIRVTNAW NVMHLIFPVSTTFASFASMYRGLPKDFIDYLF DEAGQALPQAAVGALYRSKRVI GDPIQIEPVVTMEDNLIANIRKGYNIHERLLSKE SSVQTVADFANKYGYWKTQTDGDA KKHWIGIPLWVHRRCLKPMFTIANQIAYDNKMVL PKTITDIGKTGWYDVKGNSVQRQF VKEQGDVKVIALLNKNDWKQSIENGNEPSVYVISP FTEVKKQIQLLARRELIQTVSDDT KKVSDWIKNSIGTVHTFQGEAKKVYFVIGTDNN QDGAVNWSCAKPNLLNVAVTRAKK EFYIIGDKERIKSKPYYSVINLESNIEYLDEAIE GGRDTNKKFN"
gene	89179..89601	/locus-tag="SSP0075"
CDS	89179..89601	/locus-tag="SSP0075" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17220.1" /db-xref="GI:72493899" /translation="MMINIILLSEIEEILTHLYE ERQKIDQQFAKEDMLNVEVFQQLF EVLEPYSETIRLLLGHNGDSSFEMKIKNEIGKRF INLGELHHVSKVREDLVKEYLYVI LIKTFQYWSANKDSIDVREVASTMRDIQLKGIRK TIGL"
gene	complement(89858..91264)	/locus-tag="SSP0076"
CDS	complement(89858..91264)	/locus-tag="SSP0076"  /note="similar to gi 56964863 ref YP-176594.1  [Bacillus clausii KSM-K16], percent identity 28 in 502 aa, BLASTP E(): 2e-44" /codon-start=1 /transl-table=11 /product="putative glycosyl transferase" /protein-id="BAE17221.1" /db-xref="GI:72493900" /translation="MKVIKSNKVTNKFKVSILIS TYNKEKFIENTLNNILAQTMNKND FELIIVDDCSTDNTLDIISKKIESFSNYQFVQLD ENSGTPAKPRNLSIDLKSGKYIMF VDGDDWLPDALENLYTLLKSNKTDYATGLTKYV YSDRIARSGVALSKIAYNKIGLKN FRKSFYHLAPAGRMMKSSVIKNNIRFPFEMIFGE DLQFFAEVFFNTKNISTTQDVVYC ANRYDENISLVKSEASTVLNRIKWQNEAYRYLT KYKNNKIFANLLYRIINKDILEGK FYKKGFIKEIDTLLPVFQDILNTIDNDFNSLDYA DTLNLQHALTLIKNGDKKEIIDFV



gene	92039..92248	NFYLKKEKPLYLSDKYYYVYKENKYKKRMHII
CDS	92039..92248	LQKIIKKDENIFLKLYSKNSSELKY LEIKNRKDPTNYTVLEIKKHLFKTGEYTVQFKAN ELSKGKLALTVLDKDLNGAAIKSG MQFDFYETVNGNLGYIKK" /locus-tag="SSP0077" /locus-tag="SSP0077" /note="similar to gi 15894750 ref NP-348099.1  [Clostridium acetobutylicum ATCC 824], percent identity 34 in 66 aa, BLASTP E(): 6e-05" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17222.1" /db-xref="GI:72493901" /translation="MNQKGLKLKHLQKRTTIEY IPTINTLSEQDIYDVIFVTMKYSD FYNVPTLAENKSQNIIFVGNNMCH" /locus-tag="SSP0078" /locus-tag="SSP0078" /note="similar to gi 25010861 ref NP-735256.1  [Streptococcus agalactiae NEM316], percent identity 42 in 243 aa, BLASTP E(): 2e-42" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17223.1" /db-xref="GI:72493902" /translation="MQKRND FIVK LLEKASI QNG MRVLDVGCATGEVTQIVANKVGDQ GEVIGVDMNQDMLHMAEENNQFENVKYIKGDIYN LPKDIGKFDAIVGRRVLMYLPGAY EALNVLKGHLKPNGIFCFQESDAINGGVGADNLP MHQKAIQLVWKTVESEGDIHIGQ KLYILFQKVGVPVEFISEAVIQTSDDNDLKWLI DIMATRMKERQVVKSSFSIEQFLN DLTNESEKHHS AFIRDMAFGICGKI" /locus-tag="SSP0079" /locus-tag="SSP0079" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17224.1" /db-xref="GI:72493903" /translation="MKDLCSLAGLNYRLQKLSNI FIKPMNWHLKFLIVVMRIMTNYLI ITALYRFICLAYLILCLAIRSRNKMMHLTSINES SPPKSSVKLIHYFMSMLMWPI LGT INFMLPTLT TYKGGEVHEVALLD SVLGIGMAI IG VLFSKFIS KWMHLLFILSIVITI SWYVLEDILLFKLVLMLLFGLTFGGARI IFRKMI VTTYASHTVKHIYSLGNALGLPIL ALCIYLSILNLFVWLPSFILLIVLLFLLKIGHH ERISSHEKSPN" /locus-tag="SSP0080"
gene	92485..93216	
CDS	92485..93216	
gene	complement(93543..94334)	
CDS	complement(93543..94334)	
gene	complement(94318..95466)	

CDS	complement(94318..95466 /locus-tag="SSP0080"	
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gene	complement(95886..97382 /locus-tag="SSP0081"	
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gene	98147..99811	/locus-tag="SSP0082"
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gene	complement(102564..103196)	/locus-tag="SSP0085"
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gene	103656..104042	/locus-tag="SSP0086"
CDS	103656..104042	/locus-tag="SSP0086" /note="similar to gi 57285035 gb AAW37129.1  [Staphylococcus aureus subsp. aureus COL], percent identity 57 in 125 aa, BLASTP E(): 6e-37" /codon-start=1 /transl-table=11 /product="putative truncated permease of the major facilitator superfamily" /protein-id="BAE17231.1" /db-xref="GI:72493910" /translation="MNFVVNFLVNLNMYLLIVLI AGYAQSQFNASDSSAGLVAGLFIV GSLMGRFVMGKYINSLGPRKVLLIGTVLFTITSV

gene	104039..104836	FYFVESSLFLIIVRIINGFSFGL
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		12228], percent identity 47 in 246
		aa, BLASTP E(): 2e-67"
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		TSIIFQAICFLVTAFSHSAWMLLI
		GGALLGLGYGNITSTSQSVSVEVVPKEKIARATS
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		VVLSQTFIIALIGTVIGLVLTIIITGAFLPSAVPI
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gene	106172..106834	/locus-tag="SSP0089"
CDS	106172..106834	/locus-tag="SSP0089"
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		QFKLLAKQKKDVLSQTEYKQLMSQLNLEAIENKL
		PSEISGGQKQRVAIAKALYTQPSI
		ILADEPTASLDTQNAMEVMEILKAQTSEKNKTCI
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		12228], percent identity 44 in 121
		aa, BLASTP E(): 1e-24"
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gene	107587..108891	/locus-tag="SSP0091"
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		str. 168], percent identity 49 in
		432 aa, BLASTP E(): e-123"
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gene	complement(109057..109785)	/locus-tag="SSP0092"
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CDS	109992..110858	
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gene	complement(113511..114047)	/locus-tag="SSP0096"
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gene      complement(114929..1160 /locus-tag="SSP0098"
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gene      complement(116129..1163 /locus-tag="SSP0099"
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gene      complement(116343..1168 /locus-tag="SSP0100"
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CDS       complement(116343..1168 /locus-tag="SSP0100"
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/note="similar to

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gene	complement(118073..118918)	/locus-tag="SSP0103"
CDS	complement(118073..118918)	/locus-tag="SSP0103"

gene	119102..120490	/note="similar to gi 2462704 emb CAA74935.1  [Staphylococcus xylosus], percent identity 78 in 276 aa, BLASTP E(): e-128" /codon-start=1 /transl-table=11 /product="Lactose operon transcription activator" /protein-id="BAE17248.1" /db-xref="GI:72493927" /translation="MQVLWKKFQKKLIDANLAEC GIEVGVPNVGYSYNVFQQAVLHIV TQGEGIFTYNNETHHLKAGDMFLLERGMEVEYKP SFSNPWTYYWVGINGKQILTYLSR SSIVDTHVLINKNTKDIQSIIKKICNLSQTIQSN NSHDILIMQHIYQLVYALQDKFPA HFSVQVDIVNEDIQYAVEYINSNYQKDITIVDVA KSVNISRSHLFKLFKRNLCSPKE YLTYIRMYHASQLLINTNLLINEISSKIGYKDP LFSKNFTKHFEISASEYRTCFVSH QTNTD"
CDS	119102..120490	/locus-tag="SSP0104" /locus-tag="SSP0104" /note="similar to gi 2462705 emb CAA74936.1  [Staphylococcus xylosus], percent identity 88 in 462 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="lactose permease" /protein-id="BAE17249.1" /db-xref="GI:72493928" /translation="MDRHLTGKQKFAFGFGAIGK DAIFNIVGVFLMFYITDIVGLSPA FVGVMFLFVARIWDAINDPIMGMIVDNTRNNFGKF KTWLSIGTLANAIVTILLFTNFDL PQTAMYVYISILYISWGMTYTMMDIPYWSWLPNL THNPREREEVSVIPRFFASLAAFT VGTFGLYFIHQLDVFGNGSDSVGIFIFAIICSA VFIITIGVTVFKVPEDKELEQQIG IKVNFKDIGRILFKNKELLAIMGVLLTFNLCLQT LNGSIIYYFKYVVNAEHLFSIFNS MILCEMVGLLLLPRFIKWVGRTKAFNTAVSFIIL GLLIILIAGFIAPKSTLLIILGAG ILRIGSGFMIGITTVSLADVIDYGEVKFGQRNES IITSTNTFLTASQAVAALIVGVG LSILGYTPNESQSLVTINGLRIMIIIAPLL FVCL TAFLYHKAFNLKGDFLTDIEKTLQ FKRQREHRERIK"
gene	120502..123480	/locus-tag="SSP0105"
CDS	120502..123480	/locus-tag="SSP0105" /note="similar to gi 2462706 emb CAA74937.1  [Staphylococcus xylosus], percent identity 65 in 991 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="beta-D-galactosidase" /protein-id="BAE17250.1" /db-xref="GI:72493929"

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PYVPRENPCGRYKRSFEINDYNEQSDYHLNFEGV  
DSAFYIWINEQFVGYSQIAHSISE  
FDITPYVQKGINSIEVIVLKYSDBGTYFENQDMFR  
HSGIFRDVYILKRSKSRVDDFKIE  
TTINHESNNGKINF TLQKHHLGNNINLVLYNPKG  
LEIDRAIVSKHHQFVIDNPQLWSS  
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TDQYGFYVMSEADLETHGVVRLYG  
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WCDHSIQVGIKEGKPIFRYGGDFG  
EALHDGNFCVDGIVSPDRIPHEGYEYFKHEHRPL  
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YSGYNNIQTTLVTNYKIIEDESNIS  
LVFEINIESEAVPPVLKGS LTWTVYQDGKVNVDY  
NLEKDNNAPFLPRFGLLITLPSTY  
EQINY YGNGPMSSYQDKGIATYLD MFETT VTNN  
DVHIKPQEAGSHNQTTIMNITNNE  
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gene complement(123703..1254 /locus-tag="SSP0106"  
48)  
CDS complement(123703..1254 /locus-tag="SSP0106"  
48)

/note="similar to  
gi|53612285|ref|ZP-00091282.2|  
[Azotobacter vinelandii], percent  
identity 42 in 370 aa, BLASTP E():  
3e-67"  
/codon-start=1  
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KDGKKALRPVPVLGMLQPDGITAYEYNGETYLLI  
ANEGDAQDYDGYSEEV RVKDIKDD  
IKLDAKY YEGYTQAE LDKLVANGLFDDDLGRLK  
VTTSHKFRDKNGKYNALVSFSGRS  
FSILKGS DLSMVDNGSDIEQRIKDILPGRFNAN  
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QYLYDEENKDISPEGITFVSSDS

		PTGKPMLMVSFELSGTTSTFELNEIDETFDQTHP DGQNDTDNAQQSNNSEHDDTDET KGEYNTDVETQDDEEDTVATQDNDSVTSVTNIED NVNIENIGKSPAINQTTDIDNSDNL NSENIVAVHHGPTHLLNNNATLNNISKISRSFVNEA SNHTLKMSDANTRLNHNQYQLATK KTNQINHQKIINMNSPIATNTEIEHPEAKNEGNH SINKQQLPNTGQSQNHAPLWSSLI LGVALLLIGRKQKSK"
gene	125625..126572	/locus-tag="SSP0107"
CDS	125625..126572	/locus-tag="SSP0107" /note="similar to gi 27467395 ref NP-764032.1  [Staphylococcus epidermidis ATCC 12228], percent identity 60 in 315 aa, BLASTP E(): e-110" /codon-start=1 /transl-table=11 /product="putative glucosyl transferase" /protein-id="BAE17252.1" /db-xref="GI:72493931" /translation="MIRILIPCFNEASVLEQTYA KLTEIMQRDSISNNYKYELLFIDD GSKDRTLAIKALAQRDHAVKFISFSRNF GKESA MYAGLCASTEAEALVILDGDLQHP PTLIPQMIAHYRDGEDQVVAKRDRGTGEHVIRKTV SQLYYAVINKIVDVLLEDGVGDFR LLSQRAIREVVNLGEYNRFSKGLFAWIGFEPKVI EYENVVRADGESKWTFSLLNYGI DGLISFNNKPLRAILYFGLFVCAMSFLYILFNFI YTVSYGVSTPGYFTTIVAVLFLGG VQLTSLGVIGEYIGRIYYEVKQRPLYIIRQTNLS DCEVD"
gene	126574..128076	/locus-tag="SSP0108"
CDS	126574..128076	/locus-tag="SSP0108" /note="similar to gi 57284748 gb AAW36842.1  [Staphylococcus aureus subsp. aureus COL], percent identity 40 in 492 aa, BLASTP E(): e-117" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17253.1" /db-xref="GI:72493932" /translation="MRALHINKIHLILTGLFIFY ILMAIFTPLTHDDWDWYSQYGIQM LQEHFANLNGRYLGNLFEIVAVRFDWFRWLAYAV FSMLIIWVISQFVKHKQTSIICLA AFILMVTMPNEIYKQTYGWFAFYNYVPATLCVL FILWFIVTVLFYRN SHKPSTNIIF YCVCFGGQFFIENATLFNTLIIAIALVLHIYFYK KAYPKFVVGWFI SALGTIIMFLNP NYRKIFFEGSDYQQVSSDTGIVDKVYKTVTTILP DWIFFNQIVIIITIIVGILLVMLYK TRQMTKTYTSRYWFIVCGLTLLPIYYFFIFKQFE LQHFMITLTNLTNTMVCFI FLCA LILAIHTVISQKEVRYTLYLLIASIILVCGPLII VSPIGPRNFYTVYAIYVVILLILL AQLEVFN RKSEKWITGLAIFCAVMYLGVFYNIHA ANEARISQLKEAVHADSKQRIYSM"

gene	128404..128592	EKLPPFEHYLHHATPTS AKYQTLFNEYEGLPKDTK VKYVPYGSISNQKQSK"
CDS	128404..128592	/locus-tag="SSP0109" /locus-tag="SSP0109" /codon-start=1 /transl-table=11 /product="truncated hypothetical protein" /protein-id="BAE17254.1" /db-xref="GI:72493933" /translation="MSEKEIEDHELEQLNKEIEA ELNAYDADKEFQKEKKQFLTLTFI CKLIIVLLMLMGLVKLFI"
gene	128626..130131	/locus-tag="SSP0110"
CDS	128626..130131	/locus-tag="SSP0110" /note="similar to gi 15925638 ref NP-373172.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 59 in 502 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="putative glycosyltransferase" /protein-id="BAE17255.1" /db-xref="GI:72493934" /translation="MTIYNINFGIGWASSGVEYA QRYRAQLLRKCNETIKFVFLDFIK NENIQTLTENIGFKNEEIIWLYQYFTDIKIAPTS VTVDEIIKPLYSEITKVENQGKTR KIHFNHNSNYLVCYLKNEDSDVVD RVEYISRGKL LRDYYSYVRVLSEYFAPEDNSAK LYMRSFYNE DGSIA YNEYVNDEESMFVFEDNILY GKQAL IACFLEKLHLTDK DMLIVD RSKD I GQTVLQNKGPARGVVIHAEHYNESTTND TYILWNNHYEYVFMNAHEIDFFIT ATDIQNQLLAQQFEK NYHRKPKIYTIPVGS LSTL VKPNRRKPYSIITASRLATEKHVD WLVKAVLKAKASVPEITFDIY GEGGQRQLLSKLI QENHAEDYITLKGHVNLNQVYQDY ELFLSGSTSEG FGLTLMEAIGSGLGMIGFDVNYG NPTFIKHQKNGYLIPIDL NEDKES EIIDHLAEGIVNYFDNDTSRFNQASYEIAENFTQ PVVVQKWN NLI SEVLYD"
gene	130124..131449	/locus-tag="SSP0111"
CDS	130124..131449	/locus-tag="SSP0111" /note="similar to gi 49487426 ref YP-044647.1  [Staphylococcus aureus subsp. aureus MSSA476], percent identity 40 in 443 aa, BLASTP E(): 3e-97" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17256.1" /db-xref="GI:72493935" /translation="MINLFDVFDKKAILLYKSFK HAGKQRKTIVIEENGFLPDDILTP YAFFANNPETTSQPLFFNEVPIPRFWTIEGNNNT AFIKNLDEVKARI IYKANYKHRIV ERVEWLNKR GHTQYIDY YNKVGKRYAQVVL DANS

		QKSILKRYFNYNNEVMMVENFVTN DIMLTKWKNKAYFFHSKIQFVNFYLEVAQLESENF MINSLSISSAVLNGLSEYGNDISF WQGDITPEIMKHMENALAKEKRNFKIILPSPSAY EKVIELIDEQYKNRIFQSGYVYRF VKENRHSNQVLTLTNSDQIPHLEEIVQAHPNLEF HVAALTEMSMKLLSLNKYDNNVLY PNAKRQKFISLYKSCDIYLDINKGNEILDAVRAA FDYNLVILGYNETHSHNKDVTPENN LFEEVQFEILSSILRDIVAEPHLDQRLRQQWQQ ASSISKAEFIRSLAQ"
gene	complement(131950..1324 17)	/locus-tag="SSP0112"
CDS	complement(131950..1324 17)	/locus-tag="SSP0112"
		/note="similar to gi 42519880 ref NP-965810.1  [Lactobacillus johnsonii NCC 533], percent identity 39 in 148 aa, BLASTP E(): 5e-27" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="BAE17257.1" /db-xref="GI:72493936" /translation="MNFGTQIKMIRKENQLTQE QFGNQLNISRQTVSTWENNRYLPDI EMLVEIAKTFNLSLDDLILGNSVVKDKLVNDTKF VKRIRLSILSMIFILIAIVSALLF TSLPSHVSQDGVLPQEPWFLVILAFFSLLTGLIIG MVNLVLIFINYYKYARRRK"
gene	132621..132848	/locus-tag="SSP0113"
CDS	132621..132848	/locus-tag="SSP0113"
		/codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17258.1" /db-xref="GI:72493937" /translation="MNKKLFFASIISIVLGASLG ISFLLIPSYVNENGILKEPWYLVE SGFSFVIIGGLLMFFAIGGYLCHYFENKIHK"
gene	133062..133826	/locus-tag="SSP0114"
CDS	133062..133826	/locus-tag="SSP0114"
		/note="similar to gi 15614707 ref NP-243010.1  [Bacillus halodurans C-125], percent identity 67 in 254 aa, BLASTP E(): 5e-97" /codon-start=1 /transl-table=11 /product="putative oxidoreductase" /protein-id="BAE17259.1" /db-xref="GI:72493938" /translation="MNGKVMVMTGGSSGMGKAMA QKFAEAGAKVVITGRSLERLEAAK EEIEQYEGQILCIDMDVRDPERVQYTVDKTVETF GKIDGLVNNAAGNFLCAAEDLSYN GWHSVIDIVLNGTWHCTQAVGKEWIKNGQRGRII NMVATYAWRAGIGVIHSASAKAGV LSMTRTLAVEWGSKYGINVNAIAPGPIDNTGGSG KLSLSEEAKQQTLDSPLERMGQP"

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gene      complement(134063..1345 /locus-tag="SSP0115"
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CDS       complement(134063..1345 /locus-tag="SSP0115"
69)
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          [Staphylococcus caprae], percent
          identity 57 in 159 aa, BLASTP E():
          5e-48"
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          /protein-id="BAE17260.1"
          /db-xref="GI:72493939"
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          ENLHQFLFDFIFNIDEKYIRLYLQ
          LSYALFQFKDEFLQHIKNIHQILD TNIANYYNSI
          EISVNKDEFTTMILMFLESWYLVN ASFIDMEQ"
gene      complement(134975..1352 /locus-tag="SSP0116"
11)
CDS       complement(134975..1352 /locus-tag="SSP0116"
11)
          /note="partial similar to
          gi|15925659|ref|NP-373193.1|
          [Staphylococcus aureus subsp.
          aureus Mu50], percent identity 60
          in 78 aa, BLASTP E(): 6e-24"
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gene      135869..136585          /locus-tag="SSP0117"
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          [Staphylococcus epidermidis ATCC
          12228], percent identity 62 in 239
          aa, BLASTP E(): 1e-72"
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          QPQQTEQASTEQPAQEAAAPQTEETQQPQQEATTQ
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CDS	137123..137872	QDAAAVKLYNTAGASQWVTA"
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		/note="similar to
		gi 27468612 ref NP-765249.1
		[Staphylococcus epidermidis ATCC
		12228], percent identity 54 in 250
		aa, BLASTP E(): 2e-66"
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		/transl-table=11
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		QQTAEQPQQVEQPQQTEQASTEQPAQEAAPQTEA
		TQQPQQEATTQSASSSNESSSNESS
		SSSEASESSSSGVNAHLQQIAQRESGGDIHATNP
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gene	138190..138768	/locus-tag="SSP0119"
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		Copenhageni str. Fiocruz L1-130],
		percent identity 40 in 191 aa,
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		/protein-id="BAE17264.1"
		/db-xref="GI:72493943"
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		SKLVKDHVEEEEINKLKQQEGGDIVVLGSPRFAHY
		LMQLNLVDEYKITISPTLIGKGLP
		LFQNIHDKVDLKLKSETFESGALGLNYQVLN"
gene	complement(138876..1397	/locus-tag="SSP0120"
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CDS	complement(138876..1397	/locus-tag="SSP0120"
	72)	
		/note="similar to
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		[Clostridium acetobutylicum ATCC
		824], percent identity 46 in 295
		aa, BLASTP E(): 2e-73"
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gene	139985..140254	GDAQQLIFNIFNFRFMAINAGPYFVKNPSSISFTV
CDS	139985..140254	LFKKSEIELLETVYNKLVENGKAI
		MPLNQYDFSERYGWVQDQYDVSWQLLVTNDPITH
		RIEPTLLFMNENVGRAEEAIHFYN
		KVFKNSEPGDKFYYPEGLEPNKTSQLAHARFKIE
		NQWFTCMD SAYDYG YQFN EGISLM
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		HVLKKNKVLYR"
gene	140316..140741	/locus-tag="SSP0122"
CDS	140316..140741	/locus-tag="SSP0122"
		/note="similar to
		gi 15673115 ref NP-267289.1
		[Lactococcus lactis subsp. lactis
		Il1403], percent identity 31 in
		143 aa, BLASTP E(): 4e-05"
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		KNPFA"
gene	140907..142493	/locus-tag="SSP0123"
CDS	140907..142493	/locus-tag="SSP0123"
		/note="similar to
		gi 50123306 ref YP-052473.1
		[Erwinia carotovora subsp.
		atroseptica SCRI1043], percent
		identity 41 in 536 aa, BLASTP E():
		e-112"
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		FSYISGTFSPLLPALAGSMLKALLEILKSLNWI
		NDKGATFAILNATSNGVFYFLPIF
		IGMSASKKLVNPNYIGGVIAASLLEPSFTNLLKS
		EENLTFIGLPLVVTDFASTVFPLL

gene	142496..142759	IAIAIYAPLERLLKRWVPKVLQFLVPMLSLIIM VPLTVLVFGPFSEYVSSGIGIDYM PGFSRILTGVI IASFWPFLVVLGVHWGLVPIMID NFAHGGDIFIAITAASVFAQIGIA FGVVLRSRRNKDLRSLSIGTTLSGLLAGVTEPIL YGLILWYKRLIPIVLVSGAIGGAI IAIFDVRVTTFVLNNLFIIPVFKPIYGYILGIAI ALIIGTILTFVFGFEAKNSEKPLE AKENTNNLQEGASTMIFAPLSGEIVKLENAPDPV FSTEAMGKGIAIEPENDTVYAPFD GVVETIFNTKHAIGFEVMKG"
CDS	142496..142759	/locus-tag="SSP0124" /locus-tag="SSP0124" /note="similar to gi 46907267 ref YP-013656.1  [Listeria monocytogenes str. 4b F2365], percent identity 41 in 82 aa, BLASTP E(): 2e-12" /codon-start=1 /transl-table=11 /product="putative phosphotransferase system IIA component" /protein-id="BAE17269.1" /db-xref="GI:72493948" /translation="MIIHIGLETVQLKGEHFDVF VEENQKISQGEPLIKFNKAIKKE GYKLITPVVITNSENIEKIKFNESLSITHGQKLM ELKYIKRGV"
gene	142763..144193	/locus-tag="SSP0125"
CDS	142763..144193	/locus-tag="SSP0125" /note="similar to gi 16802364 ref NP-463849.1  [Listeria monocytogenes EGD-e], percent identity 61 in 469 aa, BLASTP E(): e-176" /codon-start=1 /transl-table=11 /product="beta-glucosidase" /protein-id="BAE17270.1" /db-xref="GI:72493949" /translation="MLNQTSSAFPNDFLWGGGLA ANQVEGAARIDGKGLSTADALSQG VFNPVYDPPEQYMKKDAIDFYHKYKEDIKLF LGFKVLRISISWPRIFPNGDELEP NEKGLAFYDHDVIDELKKYNSEPLITLSHYEMPLY LVEKFNGWESRNVITYFEHFAETV FRRYKNKVKYWITFNEINMILHAPFNGGGIQQDL NEIDKSTLYQAIHHQFVASASVVK IGHEINSDFQIGCMIAGTPTYPLTSNPDDVIAAM NKDREIYFFADVHVGRGYPSYMDR YFKENHIDIHITEEDRNILKNTVDFISFSYYMSN CATVNP GDIEQSKGNIMNIIKNPY LSESEWGPVDPQGLRYILNQFYDQYQLPLFIVE NGLGAKDRLVKSEDGNYTVIDDYR IDYLNHNLIEVEKALKDGVDIIGYTAWGPIDIVS NSTGEFRKRYGFIYVNRDYNFEGT FERYRKKSFYWYQNVIKTNGNSLISK"
gene	144396..145187	/locus-tag="SSP0126"
CDS	144396..145187	/locus-tag="SSP0126" /note="similar to gi 23468715 ref ZP-00124050.1

		[Pseudomonas syringae pv. syringae B728a], percent identity 37 in 261 aa, BLASTP E(): 3e-52" /codon-start=1 /transl-table=11 /product="putative arginase" /protein-id="BAE17271.1" /db-xref="GI:72493950" /translation="MGAHLLNWLIPNDSNQEAFF IKVEEPDEDALELENGVYGQSQII NNVKQAQDILNQEQPKVVTLGNCMVSPAPFDY LNQKYGDELGIVWIDTHHPDISYPK DITNEHAMVVANLLGEGDSELSKLVKAPLKTNQF LHVGLQELLDFEAENLEKLNFDYK VQGTESYNYEEIQQWIKENNFSKIAIHFDIDVLD PNEFRATYFAEPHIESFPAAAGQM SLSHLNDILKGISENNDIVGFTVAEYMPWDEINL KNTLKDNLNIFH"
gene	complement(145234..1461 84)	/locus-tag="SSP0127"
CDS	complement(145234..1461 84)	/locus-tag="SSP0127"  /note="similar to gi 15925679 ref NP-373213.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 78 in 314 aa, BLASTP E(): e-149" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17272.1" /db-xref="GI:72493951" /translation="MDYRVLLYYKYTTIDDPFLF ATEHLAFCKDLELKGRIIVSTEGI NGTVSGTVEATDKYMEALKNDARFQGITFKVDEA EGHAFKKMHVRPRQEIVALDLEDD VNPRELGTGNLSPKEFREALLSDDTVVIDARNDY EYDLGHFRGAVRPDITFRDLDPDW IKENKEQFMDKKIVTYCTGGIRCEKFSGYLLKEG FEDVSQLEGGIATYGKDPETKGEF WDGKMYVFDERISVEVNHVDKTVVGKEWFDGTPC ERYINCSNPECNKQILVSEENEAR YLGACSHCAKHENNRVYVKKHNISDEEKAKRLEN FKELVK"
gene	complement(146472..1466 93)	/locus-tag="SSP0128"
CDS	complement(146472..1466 93)	/locus-tag="SSP0128"  /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17273.1" /db-xref="GI:72493952" /translation="MPKVEERMLEDIENKETRSE SNLSSEKEMQQNAFERLGKDVVII ETLSIMNIIIFAISTISLIGALIFTNKKKS"
gene	146840..147310	/locus-tag="SSP0129"
CDS	146840..147310	/locus-tag="SSP0129"  /note="similar to gi 28900156 ref NP-799811.1  [Vibrio parahaemolyticus RIMD

		2210633], percent identity 65 in 156 aa, BLASTP E(): 2e-56" /codon-start=1 /transl-table=11 /product="putative peptide methionine sulfoxide reductase" /protein-id="BAE17274.1" /db-xref="GI:72493953" /translation="METVYLAGGCLWGVQAFVKT LPGVINTEGGRANGITDTLHGEYD GYVEVIKTEFDPQKVSVDLMGYLFEIIDPYSVN KQGQDVGLRVRTGLYSEDEKHLKE AQQFIDGIEDHHLIATEVLPLTNYVRSAAENQDR LSRFPDDYCHLPKELVYKYK"
gene	complement(147380..1475 11)	/locus-tag="SSP0130"
CDS	complement(147380..1475 11)	/locus-tag="SSP0130"
		/note="similar to gi 1778752 gb AAB49287.1  [Staphylococcus lugdunensis], percent identity 61 in 42 aa, BLASTP E(): 8e-08" /codon-start=1 /transl-table=11 /product="putative antibacterial peptide" /protein-id="BAE17275.1" /db-xref="GI:72493954" /translation="MTGIVEAIGNAVNVGLAHDW ATMGVSIADVLAAGVDSVLGFFK"
gene	147786..148286	/locus-tag="SSP0131"
CDS	147786..148286	/locus-tag="SSP0131"
		/note="similar to gi 27467176 ref NP-763813.1  [Staphylococcus epidermidis ATCC 12228], percent identity 26 in 171 aa, BLASTP E(): 1e-10" /codon-start=1 /transl-table=11 /product="immunodominant antigen" /protein-id="BAE17276.1" /db-xref="GI:72493955" /translation="MNQLVKVTLATGLALSAMVA TTSSMTSNSTFIAHGSSENIDYQVN GYTTDANDFILEPSFIEAVKNNNFVINGYNITGN EQQESSMIDIYDQIIAKTGEQTAS MVDFEVKKGAVSKEALIEQYGQPIEKPFEQAQGF DYRYHIGDNIVQYIVEDGYVKDVQ INAENE"
gene	complement(148353..1489 19)	/locus-tag="SSP0132"
CDS	complement(148353..1489 19)	/locus-tag="SSP0132"
		/note="similar to gi 27467011 ref NP-763648.1  [Staphylococcus epidermidis ATCC 12228], percent identity 57 in 177 aa, BLASTP E(): 4e-55" /codon-start=1 /transl-table=11 /product="transcriptional regulator"

		/protein-id="BAE17277.1" /db-xref="GI:72493956" /translation="MNEEMMTDSRILKTKRNTRK ALITLLKHKKYDDISVKDICEVAG ISRGTFYLYHKDFDLVEQYQFEITKEGSKRVQS LLQSERHLLYYHIINFWNNEAELL LLLISNNGSPDVQNQLKKTLLQYNAEKNVFPYTKK SHFSEKERHYFVVFLSNAIFGIIQ EWNNGQQETPEELSTIIHKIIPDSLLG"
gene	149059..149787	/locus-tag="SSP0133"
CDS	149059..149787	/locus-tag="SSP0133"
		/note="similar to gi 27467012 ref NP-763649.1  [Staphylococcus epidermidis ATCC 12228], percent identity 80 in 242 aa, BLASTP E(): e-107" /codon-start=1 /transl-table=11 /product="ABC-type multidrug transport system ATPase component" /protein-id="BAE17278.1" /db-xref="GI:72493957" /translation="MSELVAKLTNATKYYGKKKV LDHIDIELSSGKILGLIGPSGSGK TTTIKCLMGMEKLDEGHAQIFDTEIPDRKILNEI GYMQSDALYESLTAHENLVFFGN LMGLKGEKCLKQAIATNMKLVNLEGELNKIVNTFS GGMKRRLSLAITLLANPNLIILDE PTVGIDPSLRDIWKQLKHLTKKGKSVIVTTHVM GEAERCDYIGLIVEGRLFIMGTPQ ELKDKFGVDSIEEVFIKAEAEVQS"
gene	149784..150878	/locus-tag="SSP0134"
CDS	149784..150878	/locus-tag="SSP0134"
		/note="similar to gi 27467013 ref NP-763650.1  [Staphylococcus epidermidis ATCC 12228], percent identity 77 in 364 aa, BLASTP E(): e-164" /codon-start=1 /transl-table=11 /product="ABC-type multidrug transport system permease component" /protein-id="BAE17279.1" /db-xref="GI:72493958" /translation="MRFKAVFIRVIKELLRDKRT LALMLFAPILVLTLLYFVFDTNSE TDLKIGIDDNVPQKIVNALPSDKVDIEKIKSPDS IKDTIVNTKLDSYITKNGSNLEVT YANEDPSKTGSTKQLLGSIAIQQNKMQDMMKIVEK IPNNMKQKNAQQDENVKLDNHYLY GDEDSTYFDKMFPIIGFFVFLFVFLISGIGLLR ERTNGTLERLLATSVKRSEIVFGY LAGYGLFAILQTLLIVFYAILILNIEVAGSIWWV LLINILIALAALAMGIFVSTFANS EFQMIQFIPIVAIPQVFFSGIIPLENIADWVSVI GYLFPLRYAGDALTNIMIKSQGFE FIWFDIGILFVFIFVFTVLNIVGLKRYRKV"
gene	151261..158211	/locus-tag="SSP0135"
CDS	151261..158211	/locus-tag="SSP0135"
		/note="similar to gi 15991793 gb AAL13053.1

[Streptococcus gordonii], percent  
identity 57 in 1543 aa, BLASTP  
E(): 0.0"  
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protein"  
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SIRKFTNGIASVLIGSTILLGAVI  
DKEADAAEQQPTSEVYGQTDNNYKSESNSNSVQ  
HDEERTNIINDNDEANYSNHSEIP  
IHDKSSEYDQKPINEQDTSNHHETHLNQNATENH  
VKEESKEVSTEEESIEDRKTEEST  
TEESKAVEEANKENTTEKNDEGSLDLEKEKDTYK  
DEKDNKGKKNELESHNHRIENKVE  
DNVYKNNKETNLESKNENVNKDDKVNTSSSTSIE  
KPEDNATRSNLINSVNHSLKQLDN  
AKNNTKQSLLENYYQTHTNATASDAKKAIEKLN  
IDFTKQNSDQLIALLLIELANQMD  
KDKVQANVPASKRAETNNESLSIETNTTNIIEKTL  
AKPSTSKFRSANTRATNVVNYAAN  
QSGRNVNHLVFANTSYEILGGGKKYNQVFMTMDG  
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GKYIHPGTSRKPYRVNNIHDANGRTIAIGSYDSA  
TNTAKYTFTNYVDIYNNVRGSFSL  
LSWPFKELVTTDKQSVPGITVAGEDYTQNVIFN  
YGNRTVPVISDINYLTKDFAEFTT  
YINQNRAFNTGSKVRLSGQGFKFTSPDEIEVYKV  
LNNSQFRDSFSPDYANLTQVRNPK  
IIINS DG SATVDLGDIGTLGYIIRSKPNTLPDFS  
GIGVLKSEYTFNNKNQRDTRAHA  
SSIQFVRAELAGFGGGYVWFDKNNDGVQNDSN  
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ITGHYNFDNLTNGNYLVEFVMPEGYIPTQANSTV  
DDKDSDVVFENGRIYIAHVTIKAD  
NMTIDAGLVSDTTSESLSESLSTESLSQSLSLSHS  
LSLSESESTSQSLSLSTSESLSQS  
LSLSASESLSESESLSESESLSESESLSASESL  
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TGNECHKHGLIPLLTALGGIILLR  
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gene complement(158256..1590 /locus-tag="SSP0136"  
08)

CDS complement(158256..1590 /locus-tag="SSP0136"  
08)

/note="similar to  
gi|27467999|ref|NP-764636.1|  
[Staphylococcus epidermidis ATCC  
12228], percent identity 32 in 250  
aa, BLASTP E(): 3e-36"  
/codon-start=1  
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/product="conserved hypothetical  
protein"  
/protein-id="BAE17281.1"  
/db-xref="GI:72493960"  
/translation="MLIKNIFTTVSSRNSAIIFY  
AIALYPFLYLITLILPTNFMQIGG  
ETNSLSGLEFYFVILLAQSQFAVPLILMTYFVSY  
LFFEEYESGRLIFYKDISRIRLYN  
SKLVALFSMYIIYYVILFVSSEILYFTYIHQYDY  
ASGAFLSNVHETNYSTILCIVGIF  
CITLIAICFSVMLSMKLSTGFDILSVIVLLMFMV  
IAPMIHGLKYLFPNGYDHAITPSD  
LLTKLGLMILTTLYSVICYLVLKMFKKLEY"

gene complement(159013..1598 /locus-tag="SSP0137"  
94)

CDS complement(159013..1598 /locus-tag="SSP0137"  
94)

/note="similar to  
gi|27468000|ref|NP-764637.1|  
[Staphylococcus epidermidis ATCC  
12228], percent identity 40 in 286  
aa, BLASTP E(): 2e-53"  
/codon-start=1



		/transl-table=11 /product="ABC-type multidrug transport system ATPase component" /protein-id="BAE17282.1" /db-xref="GI:72493961" /translation="MLKIDDLTKRFGADFNVID GVSLTINRGEVVGLIGKNGAGKTT LMKMIAKTKRPTSGAIFLNGIDIFQHHNLIKNVG IMIDTVHFKHFSAKKNLTYYLKVN HKTQYLKNIDNILDVGLLHTYGGKVKDFSFGMK QRLSLAMCLVDEPEIAIMDEPFVG LDPDGVNTLIHSLRTWASKKGTALLISSHQLNEL AEVCDRFVLLKEGKLQNIDFNKEQ LIKIVVKEQIYPEHRQELLNLFSTIKDIEEKAVI MQSGSEEEYNEIINYLVKYYTLENT INEQDNLYQYFDEFERK" /locus-tag="SSP0138" /locus-tag="SSP0138" /note="partial similar to gi 53771566 ref ZP-00355727.1  [Exiguobacterium sp. 255-15], percent identity 35 in 254 aa, BLASTP E(): 2e-41" /codon-start=1 /transl-table=11 /product="truncated conserved hypothetical protein" /protein-id="BAE17283.1" /db-xref="GI:72493962" /translation="MFNEFKFIFRNKMLIIALIA IAAIPLLYVALFVGSMWSPYDKTD QLKISIVNQDQSAKLNGEKVTIGDDVVDKLDND KFDFQEVSKKEAFNQLEKGKSVGT IIIPKDASSNATTLDDKNPKKIKIETQVNPSSY TGSQSAQKAIDTVTNSIKDNIRTN YLDQLFASAKKSQSGFKDTSNALGDMSDAESQLI DGNQQVTDGLKQLAPTVGQPAQQL ISGNQQVTDGLNQQLQNNNDQLKAQIDQSVEQQDG VAFEGDNEKALNNVTNVNENNATE ADKYGETIVPYMASVSLFVGAVSFSAIYPLRKML TKDVTSLKQAFGKLLLYLVQGAVS ALLMSSWAIFALNMSIDNIGKFIIVGLLWAI TVTTFLSLLLDRIGLFISMVLLIL QLSASEGMFPIELSAQFFRWIHPFSPMSYAIQGY REAIFTNAGHFNFVGVVALLVGII VIMMILQYLVLWLNKRQRLPFSIEFK" /locus-tag="SSP0139" /locus-tag="SSP0139" /note="similar to gi 46113687 ref ZP-00183301.2  [Exiguobacterium sp. 255-15], percent identity 26 in 133 aa, BLASTP E(): 3e-09" /codon-start=1 /transl-table=11 /product="transcriptional regulator" /protein-id="BAE17284.1" /db-xref="GI:72493963" /translation="MENVDKTIEEAITKFQIVML HLNKEIVEIVKETGLSNLLSREQI DAMRIKNEGKVTINELAGLQNIKTAASKRIAK
gene	160295..161728	
CDS	160295..161728	
gene	161751..162203	
CDS	161751..162203	

		LEEMGYVQRAYSDNKRIKLIMLSD EGETFLQRATAVMTEAVKDRLGNKFTAEVHHFV EQLTHIVNAFKAHK"
gene	162475..163101	/locus-tag="SSP0140"
CDS	162475..163101	/locus-tag="SSP0140" /note="similar to gi 27469109 ref NP-765746.1  [Staphylococcus epidermidis ATCC 12228], percent identity 33 in 171 aa, BLASTP E(): 3e-19" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17285.1" /db-xref="GI:72493964" /translation="MKRTIERVLTWIGIVLQILG VVLMAVLIPMMGNGEVKEAFISQM MQEDSSFTYEDGNTIFSTFSGLLTTGLVLGIILL IIALIAVFLISKPKVAGVLLIIA GVISFLGNWINAVLWLVAGIMLLVRKPKEPIYDK EEDDDVNPYIKDGSQVNERNNSFI LSEEQKENEQETIKDAYSQSKDDNKTDLDNLDDL DERSKKLKEDPYKY"
gene	163286..163393	/locus-tag="SSP0141"
CDS	163286..163393	/locus-tag="SSP0141" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17286.1" /db-xref="GI:72493965" /translation="MMMALGMLLPVLVVGFITMS ILEERKRNRRNKKKDK"
gene	163828..164751	/locus-tag="SSP0142"
CDS	163828..164751	/locus-tag="SSP0142" /note="similar to gi 30020265 ref NP-831896.1  [Bacillus cereus ATCC 14579], percent identity 41 in 304 aa, BLASTP E(): 6e-64" /codon-start=1 /transl-table=11 /product="putative permease" /protein-id="BAE17287.1" /db-xref="GI:72493966" /translation="MSEMLYILQTVLLPIFIMIF LGYILQKKFTLDLNTLAKLNIYVF VPGFIFVKFYKTHFALSLLFYIIFFVIYMFVLF LIGKLLSMFRKTDKGETTTLTNSL MFFNSGNYGVPVNDLVFKGDPLAMSVQVIVLSLQ NIFTFSYGVFAIQSLHIGKLKALL GYFKMPVLYALLLAIILNYNHIPIPEFIWTPANY VADAMIAIALMLGAQISNIKFSL KWSKSYAYVFIRLIIGPLIALVIKIMGIEGIIA QTLFIASAMPTSVNSSVIAQEYDN HPELAAELVFLSTLLSAITVVIVIVIYMSKILF"
gene	complement(164873..165190)	/locus-tag="SSP0143"
CDS	complement(164873..165190)	/locus-tag="SSP0143" /codon-start=1 /transl-table=11

gene	165391..167241	/product="hypothetical protein"
CDS	165391..167241	/protein-id="BAE17288.1"
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		/translation="MFVAEVAFSTNKEHEQQLYN KVKKTTQSELHNVAGLKSSEVWTKS KSDDVEYVVVSKWDEKKDFQNWVARPSHVEEHKA MHKKSKNGEADKPPFQKTLRQYTV VEF"
		/locus-tag="SSP0144"
		/locus-tag="SSP0144"
		/note="similar to gi 15925607 ref NP-373141.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 79 in 612 aa, BLASTP E(): 0.0"
		/codon-start=1
		/transl-table=11
		/product="anaerobic ribonucleoside-triphosphate reductase"
		/protein-id="BAE17289.1"
		/db-xref="GI:72493968"
		/translation="MNKLEKNLKHLLITKDPTVVN ENANKDSATFSTMRDLTAGVVS YALDYLLPKHVAQAHEAGDIHFHDLDYHPFQPLT NCCLIDAESMLSHGFQIGNATVTS PKSIQTASAQLVQIIANVSSSQYGGCTIDRVDEL LSKYAKFNEMKHRQIAEKFVHESV IDTYVDERVTQDIGDAIESLEYEINTLYTSNGQT PFVTLGFGGLGTDYRSRKIQEAILS TRIKGLGKDRTAIFPKLVFSIKRGVNLNESDPN YDIKQLALECSTKRMYPDILNYDK TVELLGDFKAPMGCRSFLPAWKDKDGHYENNGRC NLGVVTLNVPRIALESKGDMEAFW KIFHQRMALIMHDALVYRIERIAQATPENAPILYQ NGAFKHRLKETDDIMTLFKGQRAT LSIGYIGLYEAATVFYGPHWERLSKAKAFTLDIL KSMKAYQLKWTEQYDIWFSIYSTP SESLTDRFCRLDREQFGEIADITDKGYQNSFHY DVRKDVTPFEKIDFEKDYPEYASG GYIHYCEYPKLNHNLKALEAVWDYAYDKVSYLGT NIPIDHCRKCGFVGDFKTTAKGYQ CPQCGNDDPKSVDVVKRTCGLGNPVQRPTIEGR HKEMCARVKHLKDASV"
gene	167238..167774	/locus-tag="SSP0145"
CDS	167238..167774	/locus-tag="SSP0145"
		/note="similar to gi 27469089 ref NP-765726.1  [Staphylococcus epidermidis ATCC 12228], percent identity 72 in 176 aa, BLASTP E(): 1e-73"
		/codon-start=1
		/transl-table=11
		/product="putative anaerobic ribonucleotide reductase activating protein"
		/protein-id="BAE17290.1"
		/db-xref="GI:72493969"
		/translation="MNILKIRHGQGHIAKIEAQS FVDGEGVRCSLYVSGCPFACENCY NKVAQNFKYGEFPHEDTLEEIMEYCAPNYISGLS ILGGEFFCNVDITLKCAQTFRKRF GNTKSLWVWTGFLFEYLERDSAERKTLLLELIDVL"

gene	167856..168851	VDGPFINHLYPNLPYKGS MNQRV
CDS	167856..168851	IDVQASLQKRRVCEYIKS" /locus-tag="SSP0146" /locus-tag="SSP0146" /note="similar to gi 49485155 ref YP-042376.1  [Staphylococcus aureus subsp. aureus MSSA476], percent identity 55 in 327 aa, BLASTP E(): e-110" /codon-start=1 /transl-table=11 /product="putative choloylglycine hydrolase" /protein-id="BAE17291.1" /db-xref="GI:72493970" /translation="MCTGFSFLSKSQAILGRMT DFVYHLEGQPAVQPRHFYWESRVE YKGMTQYGF IGAGSDMEGFLFGDGLNEHGVGVS I QYFRGYASYATEVREGYMNIAQNE VITWVLGYKNK NIDDLIENGKQVNVVAHVLNDIAE VPPLHYHITDDTGRSVELTFQDGK IVINENPIGVL TNNPDLNWHYENLRNYTAVTPHK PEAKNVMGQSLGSLGNEG GTYGLP GGYTSPERFIKTAYLK NYLIGSEDPEYDVMDAFK LLDSVSIPKGAVLDENGDMHYTLY QTVFNLTTRTMYLKWYDTNQITELQLTEDLILKE DMTIFESVQAFVTNKL NHTSS"
gene	complement(169138..1700 64)	/locus-tag="SSP0147"
CDS	complement(169138..1700 64)	/locus-tag="SSP0147"  /note="similar to gi 49482569 ref YP-039793.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 61 in 308 aa, BLASTP E(): e-112" /codon-start=1 /transl-table=11 /product="putative dioxygenase" /protein-id="BAE17292.1" /db-xref="GI:72493971" /translation="MNIIGHHHISMYTKGAQINK NFYTQTLGLRLVEKSVNQDNPTMY HLFYGDEIGTPGTLLSFFEIPNLGKNRPGTNSIH RVSLLPDESALTYFERRLNEQHI TTTQMTYLNHHALLFKDMDGLEILLANNHRNTP NAWRKNPYTDIPEAYQILGMGPVE LRLRDIQPTLHFLKNDLRYSLRENVDET VLTLD S DGLYTDFVLVEEQGSRARPGQGYV HHIAVNTPNDS DLYAVLDTINHNPGNHSGIIDRY FFKSLYYRHNSIMFEFATAAPGFT VDTAIKDLGKKLNLPDFMENQRTEIEEKLHDL"
gene	170479..170964	/locus-tag="SSP0148"
CDS	170479..170964	/locus-tag="SSP0148" /note="similar to gi 30020510 ref NP-832141.1  [Bacillus cereus ATCC 14579], percent identity 43 in 160 aa, BLASTP E(): 1e-36" /codon-start=1 /transl-table=11 /product="truncated"

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		/protein-id="BAE17293.1"
		/db-xref="GI:72493972"
		/translation="MEKLSKLTGVSTSSLNEIEK GNTIPSINTVWKISNGLKLSFSSL MSEAESDYVQVNKEDVVPVTEDDGKYRVYPYFPF EKSKSFEFFFYVELDPGATLDSEPH LSGSEESIIIIVDGQLEMHLENEVIDLGKGDALRF KSDITHSYTNHGEDMTLISMVIDY K"
gene	171194..171466	/locus-tag="SSP0149"
CDS	171194..171466	/locus-tag="SSP0149"
		/note="similar to gi 30022817 ref NP-834448.1  [Bacillus cereus ATCC 14579], percent identity 43 in 87 aa, BLASTP E(): 3e-12"
		/codon-start=1
		/transl-table=11
		/product="truncated conserved hypothetical protein"
		/protein-id="BAE17294.1"
		/db-xref="GI:72493973"
		/translation="MNKINTRIETLDFLRGFALI GIMLVNIVVIANIGIPESSQDITY KKFLDFFIESKFFSIFHIYLVLVFIFLCKEQKRN LEINILYICAVF"
gene	171406..172209	/locus-tag="SSP0150"
CDS	171406..172209	/locus-tag="SSP0150"
		/note="similar to gi 396084 emb CAA80248.1  [Bacillus acidopullulyticus], percent identity 42 in 269 aa, BLASTP E(): 2e-52"
		/codon-start=1
		/transl-table=11
		/product="truncated conserved hypothetical protein"
		/protein-id="BAE17295.1"
		/db-xref="GI:72493974"
		/translation="MQRAEEKPGNKYFIYLRRLI ILAIFGLIHMQLQPGEALVVYSIF GLLLIPFFNLNKFINLVIGILLIMVLYLDAKIL TPLPYFILGLASAQFGMIFKFNRY KIWSVVALISGIIISTIGWYLLEKAYVVPNFKLLR QKSEVSINHYAENVDDHYHHLITIF SPFMSIFYASCLILLLNISWARKVLSPLKYYGSM ALTNYIGQTLLIYLAISIFSGKHW THVDTLWICVCVYVFQLLISTYWLKYFKLGPLEY IWKMATYMKKIKMIK"
gene	172633..173283	/locus-tag="SSP0151"
CDS	172633..173283	/locus-tag="SSP0151"
		/note="similar to gi 3676428 gb AAC61946.1  [Staphylococcus aureus], percent identity 50 in 201 aa, BLASTP E(): 9e-55"
		/codon-start=1
		/transl-table=11
		/product="putative permease"
		/protein-id="BAE17296.1"
		/db-xref="GI:72493975"
		/translation="MDIISVLILFAIFLGGLVRT"

		YFGFGEALVSMPLLTLLIGLDIHTS VSVIGLAGILVASFNIFLDFKNIEYRLLAALLIG SFLGVPLGIWILNFVNTSVVQWLL GLFLFSYGTYAFLRKVYFKNKAKMILKSKAWAGL TGIISGVLGSLYNHGVVVIYST LTGLSVKTLSSSTIQVHFLITAILVVIGQGTGDIW TSATLPFIFLSMSVFTYFSVNW"
gene	complement(173425..1738 47)	/locus-tag="SSP0152"
CDS	complement(173425..1738 47)	/locus-tag="SSP0152"
		/note="similar to gi 27466966 ref NP-763603.1  [Staphylococcus epidermidis ATCC 12228], percent identity 79 in 133 aa, BLASTP E(): 2e-56" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17297.1" /db-xref="GI:72493976" /translation="MKKLMYSSAFYTLLGLLSGL FYREMSKAENFSGYSQLNITHTHL LVLGTIMFLIFMIIIEFQLKLTSNRQLFNFFYIF HLGVLITVTMQFINGIAAMKDFNV SPAIAGIAGLGHIMITLAFILFFVLLNKRINAYT GKNV"
gene	complement(174106..1749 63)	/locus-tag="SSP0153"
CDS	complement(174106..1749 63)	/locus-tag="SSP0153"
		/note="similar to gi 23100728 ref NP-694195.1  [Oceanobacillus iheyensis HTE831], percent identity 50 in 284 aa, BLASTP E(): 4e-72" /codon-start=1 /transl-table=11 /product="putative 2-dehydropantoate 2-reductase" /protein-id="BAE17298.1" /db-xref="GI:72493977" /translation="MNNVAIIIGPGAVGSTIAFDL RDASLNVKLLGRRNETLHYYSNNA LDTKYQLDVCALNEYHETVDFLFITVKIPQLDVT LTSYQHLLHKNTIIILAQNHGQQL HKFDHPYVYQAVVYISGQKTGNTITHYRDHKLIL DQNAHTQALHQCISNSSLNIELTT DIDNAIWYKLLVNLAINSVTALTRSTASVLEVPG IKKLCEQLLLEGINIAKAEHVHFE PNIVNTILNIYDGYP AEMGTSMYYDIVDGRSLEI DGIQGYLFYKARKHHLNTPILDIT YHLLLAQQK"
gene	175046..175858	/locus-tag="SSP0154"
CDS	175046..175858	/locus-tag="SSP0154"
		/note="similar to gi 57286520 gb AAW38614.1  [Staphylococcus aureus subsp. aureus COL], percent identity 72 in 268 aa, BLASTP E(): e-108" /codon-start=1

gene	175855..176703	/transl-table=11
CDS	175855..176703	/product="3-methyl-2-oxobutanoate hydroxymethyltransferase" /protein-id="BAE17299.1" /db-xref="GI:72493978" /translation="MKTLNQLQDLKVNKEKISMV TAYDYPSAKQVEAADIDIILVGDS LGMTVLGYDSTVQVTVADMIHHTKAVRRGAPNTY LIVDVFPFGAVGVNDQYDLEIAVKL YKETDANAIIKAEGAHLTQYIKNCSNMGIPVVS HLGLTPQSVGIMGYKMQAGNKEAARQ LIEDAYAVQQAGAVMLVLEAVPSDLAAEISDKLD IPVIGIGAGKETDGQVLVYHDLN YAVEHRAKFVKQFGDFSVGIDALKQYNNEVKA EQFPGEAHTYKKQIMNEVTE" /locus-tag="SSP0155" /locus-tag="SSP0155" /note="similar to gi 23100730 ref NP-694197.1  [Oceanobacillus iheyensis HTE831], percent identity 65 in 281 aa, BLASTP E(): e-103" /codon-start=1 /transl-table=11 /product="pantoate beta-alanine ligase" /protein-id="BAE17300.1" /db-xref="GI:72493979" /translation="MTQLITTIEEMRSIIANLHN QRRSVGFIPTMGALHDGHLKMMSL SLNENDVTIISIFVNPLQFGPNEDLDSYPRDIVG DTAKAESVGVDYIFHPTVKEMYPE LPTIELKAGRLASVLEGAERPFGHFDGVVTVVNKL FNIVRPHKAYFGKKDAQQLAIVEK MVEDFNHPIEIKGVDIVREDDGLAKSSRNIIYLT KNERIEAVHLYKSLCLAQSLYKNGE RNSEKIIKATRDYLTETSGTIETVAIYSYPELV EQTQIKDSIFISLAVKFSKARLID NIIIEG" /locus-tag="SSP0156" /locus-tag="SSP0156" /note="similar to gi 27467184 ref NP-763821.1  [Staphylococcus epidermidis ATCC 12228], percent identity 71 in 494 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="putative malate:quinone oxidoreductase" /protein-id="BAE17301.1" /db-xref="GI:72493980" /translation="MSEKNSKDVILIGAGVLSTT FGTLLKELAPDWNIKLFERLDKPA IESSNERHNAGTGHAALCELNYTVEQKDG SIDVEKAKEINEQFEISKQFWSHLVSKSQ IQNPQAFIRPLPHISFVQGDKNVNF LKRRFEALSPLSMFKGIEYTEDHEK LKVWMPLMMEGRDPNETVAASKIDEGTDV NFGELTRKMAKNLSEHDNAELFYRHEVQDF SRRKDGKWEVKIKDLKTKKVEHHITDYLFI GAGGAAIPLLQKTGIPESKHLGGFPITGEFL VCNNPEVVAKHEVKAYGKEPEGTPPMTVP HLDRRYIQD
gene	176953..178440	
CDS	176953..178440	

		ENSLLFGPFAAIGPKFLKNGSNLD LFKSINPSNVITMLSAAAKNFPLIKYSIQEVLAK KEDRMKELRRFVPDAKDEDWDIMQ AGKRVQVIKDTKEHGRGFIQFGTEVVNSKDHSVI ALLGESPGASTSVSVALEVIEKNF PEQLKQWEPKLKEIIPSYGQSLIEDYALLKQIRQ ASNAELELNHK"
gene	complement(178592..178834)	/locus-tag="SSP0157"
CDS	complement(178592..178834)	/locus-tag="SSP0157"
		/note="partial similar to gi 57285494 gb AAW37588.1  [Staphylococcus aureus subsp. aureus COL], percent identity 57 in 77 aa, BLASTP E(): 2e-19" /codon-start=1 /transl-table=11 /product="truncated conserved hypothetical protein" /protein-id="BAE17302.1" /db-xref="GI:72493981" /translation="MEALAQILSEVANSNISYDP VTLEKFGKMYDEPKGFGPLLASY KAGEMGLLDQSSNDFEKLTKGKPDFTFETYLHKHY KN"
gene	178948..180822	/locus-tag="SSP0158"
CDS	178948..180822	/locus-tag="SSP0158"
		/note="similar to gi 31616158 gb AAK38834.2  [Staphylococcus aureus], percent identity 44 in 673 aa, BLASTP E(): e-147" /codon-start=1 /transl-table=11 /product="truncated biofilm-associated surface protein" /protein-id="BAE17303.1" /db-xref="GI:72493982" /translation="MVNKDNNHVEKNSEISKIQI SENNIIRNNVEDKKFDEAVLKDEK QDKQQDEKLKPNENNNRKFTTEIKTEDVGHFNGTI NDKKMENDAIQEDAIQTRTKENLN NQSQTNNHIKTKVTVKRATTFENIKTVNKSETP NKNIIGTSRAYKKLTDKDIILRK LLAKHDLYHPVVTKSREMIEDSSLEALDYSNY TFQTLIFQPEPLTTKEVLDSKTIP FQIHSYLTGANSQDVYKINLQLDPIIANHVKKIT VNPSGRSSSVELVRLANKECKATN IWQVNFIRASDGLFGGAEILSQYTAENGKIELDD TVRNILEKMEDHSDKLNLIYVKD SQENKKIKTSETSGYFLTPSETLINSIVSSNSDT ANSAFKASSGAIQFDSDIGEIGGI TVDQQILKNGTFNYGGPLIDSGLNKQWRYHYQID PKLVPIYIGSIELHSYDFYGVSGFD KTYYPKNKVADLAIDKDGSGSITSSNLNDLIVFN NALPETVGIRLVIKYNQSPNNILT RNAEYDENGNLISNTTKVKEDFAFYGYLTDKNGG MIKNTFGSSIIYIQDLDDKGLTDN FEFHKSHTDPFNQDTDGDGKNDGDEVLYGTSP VGKPIADDITTEDTTVIGKVNLD"



gene	180838..181224	/locus-tag="SSP0159"
CDS	180838..181224	/locus-tag="SSP0159"
		/note="similar to gi 31616158 gb AAK38834.2  [Staphylococcus aureus], percent identity 45 in 111 aa, BLASTP E(): 1e-25"
		/codon-start=1
		/transl-table=11
		/product="truncated biofilm-associated surface protein"
		/protein-id="BAE17304.1"
		/db-xref="GI:72493983"
		/translation="MKILDENGTLSIDTLNEDG TFSMQVPKPKPGTYTIAIESPNYT NDEVNTFKVIDIKEILKPSINPVNDQSKEIEING VEGSTIIIKDENNVIVGQTILNNG QTTSIINLKTIKSRNYFNNSNSRKKWH"
gene	181259..182392	/locus-tag="SSP0160"
CDS	181259..182392	/locus-tag="SSP0160"
		/note="similar to gi 31616158 gb AAK38834.2  [Staphylococcus aureus], percent identity 47 in 324 aa, BLASTP E(): 2e-81"
		/codon-start=1
		/transl-table=11
		/product="truncated biofilm-associated surface protein"
		/protein-id="BAE17305.1"
		/db-xref="GI:72493984"
		/translation="MTSRLAPTMKDFTSNDTQIT GESEPNSTVEITFPDGQKVTTTAD DQGHYIVDIPAGSLNNGGEVSAKATDKAGNESPK TIRNIVDETAPMAPTMKDFTSNDT QITGESEPNSTVEVTFLDGQKVTVIADQGDYIV DIPSGSLNNGGEVSAKATDKTGNE SPKTTKDVADETVPEAPKVDNVTNSDIQIIGKTE PHASVTIQFPNKQIITGKADEQGD FSIGILSEIKLLGNEILIINITDKAGNISNKTSV IVIDKTEPNAPIVDELTDTDITIIT GQGEPNTKVIINLPNGKRITGRVNSHGKYEIKLP KDITLNINDKISILLEDDSIQLS ASMLSASIYRASEKWCHGFSVPAETYIQSVTPY IISGLVSRK"
gene	182413..182760	/locus-tag="SSP0161"
CDS	182413..182760	/locus-tag="SSP0161"
		/note="similar to gi 30021303 ref NP-832934.1  [Bacillus cereus ATCC 14579], percent identity 52 in 109 aa, BLASTP E(): 2e-25"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="BAE17306.1"
		/db-xref="GI:72493985"
		/translation="MGIIIIILEIILGIFFIMTG LKILSGAMKQEFKLGYPPIFNKI TGLFELIGGIAMLVGIFYIPLAIFASILLALTML"

gene	complement(182981..183433)	AGAGSLVFLGKDPIKKALPAIVLF VLNLIILYLLIV"
CDS	complement(182981..183433)	/locus-tag="SSP0162"  /note="similar to gi 56965571 ref YP-177305.1  [Bacillus clausii KSM-K16], percent identity 47 in 137 aa, BLASTP E(): 4e-34" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17307.1" /db-xref="GI:72493986" /translation="MSSKVMNWILTL CVVGIISL LSNWIGYSIMPLNALPGILSLMAI ALLGLILHDIVPFNIPSIAYIGITGLLLTIPGVP GAAHIVEWTEKVDLLSLATPVVAY AGVSIGNSWADFAKLGWKT VVVGIVILISTYIGS ALVAEIVLRIQGIV"
gene	complement(183439..184242)	/locus-tag="SSP0163"
CDS	complement(183439..184242)	/locus-tag="SSP0163"  /note="similar to gi 56965570 ref YP-177304.1  [Bacillus clausii KSM-K16], percent identity 56 in 260 aa, BLASTP E(): 4e-78" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17308.1" /db-xref="GI:72493987" /translation="MEQQNNLWKDWRLHSIVLVI VIISEVIGAHKIPLGMTSILLLPV VYAVLLGLAVYFTPLIKHKQAKNSEPMVFISVAL LIAKFGVEAGPALPKIIAAGPALI LQEIGNLGTIVFSLPLAILLGLRRESIGMTHSIG RESNLALITEKFGIASPEWRGVMS MYIFGTIFGAIFFSIFSGIIISILPLSPIAYAMA TGVGSGVMTAAALGPLLEMYPDQT STITAFSGVSNLLTSVTGLYVGMLIALPLTRKYY SLIMNIKNKFTKEQE"
gene	184429..185598	/locus-tag="SSP0164"
CDS	184429..185598	/locus-tag="SSP0164"  /note="similar to gi 56962361 ref YP-174086.1  [Bacillus clausii KSM-K16], percent identity 38 in 382 aa, BLASTP E(): 4e-67" /codon-start=1 /transl-table=11 /product="putative permease of the major facilitator superfamily" /protein-id="BAE17309.1" /db-xref="GI:72493988" /translation="MQHAYRQLILGMVCLFIVMA IGRFAYTPIMPFMQQTGHMDNQSA GLLATINYLGYLIGAIIPMWLVIVNKVTDLKIYV

		FINIISTLMMGLLDDEFTVWTLRL ISGITSGTVFVLASNVALEALRVAKKDGISGLLY SGVGLGIFTSSIFIFIYTSADTWK MTWIVLSLFSLIMGSFVLFGMREN PITENEDSNS SNNTNNVAVKLKKKFIWGFSIAYF CEGAGYIITGTFFVAIVKSIPELADYAALSWMFV GLGAIPSTILWSMMANKLGHAKAI YLAFILQIIAVVLPVFSGSMMSLVISSLFFGATF LGLTTLFMSKAQTLMFESASKINL VASLTVIYSLGQMIAPAFSGVLIGESGNYNAALI FAAVILCIGLLSSFYSYRVTD"
gene	185795..186769	/locus-tag="SSP0165"
CDS	185795..186769	/locus-tag="SSP0165" /note="similar to gi 49484964 ref YP-042185.1  [Staphylococcus aureus subsp. aureus MSSA476], percent identity 84 in 322 aa, BLASTP E(): e-161" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17310.1" /db-xref="GI:72493989" /translation="MKENFWRELPRPFFVLAPME DVTDVVFRHVSEAGRDPVFFTEF TNTESYCHPEGVHVSVRGRLTFTED EQPIVAHIWG DKPDHDFREMSIGMAEMGFKGIDLN MGCPVPNVATKKGSGLIQRPEIAAEIIQAAG GIPVSVKTRLGYSEIDEWRDWLRH VFEQDIANLSIHLRTRREMSKVDAHWE LIGEIKK LRDEIAPDTLLTINGDIPDRKTGL ELAKEYGIDGVMIGRGIFHNPYAFEKEPREHTSE ELLGLRLHLDLFDQYTENEPRQF KPLRRFFKIYVRGIRGASELRHQLMSTNTTDDAR KLLDEFEAQTEQVK"
gene	complement(187067..188257)	/locus-tag="SSP0166"
CDS	complement(187067..188257)	/locus-tag="SSP0166" /note="similar to gi 16081118 ref NP-391946.1  [Bacillus subtilis subsp. subtilis str. 168], percent identity 46 in 379 aa, BLASTP E(): 1e-92" /codon-start=1 /transl-table=11 /product="putative permease of the major facilitator superfamily" /protein-id="BAE17311.1" /db-xref="GI:72493990" /translation="MDDLKNNYVKKGSQAYIKII VALFISGFTIFSILYSVQPLIPHF TNAFNVSETVASLALSAATITLAIAMLFFGALSE VLGRKPIMIFSVISVSLALVQPF ILDNFTFLIVRLIQGICLAGLPSIAMAYIGEEIS SHNLPEAMGIYISGNAFGGAFGRI FTGFISSIYGYQTGLISIGIISVIAAILFTFLLP ASNHFQKQRF SVKALLVSYSKHLK NIRLLKPFMIGFLLLCNIAAFNYIGFVLADEPY HLHDSVISFVYLLFLIGMISSILN AKLRAQLGTLNALKFSILLLIFGIWITLLPPLPF"

gene	188370..189257	KILGLAFSVYAFFSGHAIASAVVT
CDS	188370..189257	SRAEDHKAQASSLYLLFYMGSSVGGTLGIFYG
		AIQWPGVVLMITAFMIIAFIIALT IKQK"
		/locus-tag="SSP0167"
		/locus-tag="SSP0167"
		/note="similar to
		gi 16081119 ref NP-391947.1
		[Bacillus subtilis subsp. subtilis
		str. 168], percent identity 32 in
		277 aa, BLASTP E(): 5e-40"
		/codon-start=1
		/transl-table=11
		/product="transcriptional
		regulator"
		/protein-id="BAE17312.1"
		/db-xref="GI:72493991"
		/translation="MEWHHFYFKQLAQTENMSE
		CAKMLNVSQSTLSRAIKNLEAELG
		IPLFNVRVGRTIKLNKYGIAFLKTTNNIINEMDIY
		KSNVLDATNVYNGKLVIGFLHSVG
		VTYISEFLKSFNLAYPNIQKLKLIQHDAKRLITML
		DDGEVDMIITTISETSQNTHEPL
		IVEKLYVTLHEQHRLSHCSEIAIEALVNEKFILL
		KPNLLLRQQVDEILKAYQFTPEIS
		FEGDEVITITATFISSGLGVSILPHLRDVRPLNLK
		QIPIKNHDAKRTIGLCYKNKSNKV
		PIINKTKKSLIEYFSKIQK"
gene	189710..190663	/locus-tag="SSP0168"
CDS	189710..190663	/locus-tag="SSP0168"
		/note="similar to
		gi 26554099 ref NP-758033.1
		[Mycoplasma penetrans HF-2],
		percent identity 23 in 296 aa,
		BLASTP E(): 1e-12"
		/codon-start=1
		/transl-table=11
		/product="putative RNA binding
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		/protein-id="BAE17313.1"
		/db-xref="GI:72493992"
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		MKVNNENYQEWFGNDDTNAGFSHQLNKGNTGSGY
		ITYDVPDSDNYTLEMDATPKFNNV
		KAKWEIKKTDIKEASVANSNESNDEAETDTNVES
		EDSEEPKITDEDESEDTESEETGYS
		AEMYNALVDEYNALTDGEKMNHVDDDVLEIEYDQ
		LEARVDALYDKKMDEEDKALEEEM
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		TSEDDAA"
gene	190690..191040	/locus-tag="SSP0169"
CDS	190690..191040	/locus-tag="SSP0169"
		/note="similar to
		gi 28379567 ref NP-786459.1
		[Lactobacillus plantarum WCFS1],
		percent identity 46 in 112 aa,
		BLASTP E(): 1e-23"
		/codon-start=1
		/transl-table=11
		/product="conserved hypothetical

		protein"
		/protein-id="BAE17314.1"
		/db-xref="GI:72493993"
		/translation="MNQNQTVRQTNRVAEMILGI
		LGSIFGILGGLFAIMLDGIGAEFG
		ATESGSITGLGIAVILTCIITLVLSCIINKKRVL
		IGVLLLVGGILNIVFISFFGILSG
		ILILVAGILALIRK"
gene	191299..192045	/locus-tag="SSP0170"
CDS	191299..192045	/locus-tag="SSP0170"
		/note="similar to
		gi 57285324 gb AAW37418.1
		[Staphylococcus aureus subsp.
		aureus COL], percent identity 68
		in 247 aa, BLASTP E(): 1e-98"
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		SWFGKAFAERLPTFKDVIKMANE
		TQINLNIELKGVSGSNGTALSESMVTQVAEQLKE
		LDSNIEVLISSFNVYLVKLAEALL
		PEYPRALIFKSAAFQGDWRTLLDFCGSNIVNIED
		AKLSQARVKMIKNAGYTILNVWTVN
		KSLRANQLANWGVGDGIFTDHADDMIHLERP"
gene	192302..192763	/locus-tag="SSP0171"
CDS	192302..192763	/locus-tag="SSP0171"
		/note="similar to
		gi 57286554 gb AAW38648.1
		[Staphylococcus aureus subsp.
		aureus COL], percent identity 67
		in 147 aa, BLASTP E(): 1e-53"
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		/transl-table=11
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		regulator"
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		/db-xref="GI:72493995"
		/translation="MESNSNNNDYENLLFYFAYK
		TFINTADEIIEKYGLNRQHHRFLF
		FIEKVPGITIKDLLKSLEISKQGSHTLKKLKDE
		AYIIEKQTATDKRVKALYSTDKGT
		KLVRELNKKQNDMFQDIQKKVGNDWYAIMEELAS
		YRTGFQEVKYLKDDFNK"
gene	192923..194566	/locus-tag="SSP0172"
CDS	192923..194566	/locus-tag="SSP0172"
		/note="similar to
		gi 27469128 ref NP-765765.1
		[Staphylococcus epidermidis ATCC
		12228], percent identity 71 in 547
		aa, BLASTP E(): 0.0"
		/codon-start=1
		/transl-table=11
		/product="putative
		indole-3-pyruvate decarboxylase"
		/protein-id="BAE17317.1"
		/db-xref="GI:72493996"

/translation="MKKRVGQYLMDCISDVGVDK  
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RAVESAGKYVHSLGEGNFDDYRNMYSITTAQA  
YITPENAQSEIPRVINAALYEKRP  
VHIHLPIDVANSEIDVATPFEIEQRPQTDVTKYM  
TMVKDKLQSADKPVIIITGHEINSF  
KLHEKLEQFVKQSQIPVVQLSLGKGAFNETSPYY  
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NIGAKLTDSATAGYSYQFDIDDVVMINHHFKMN  
ETKDTEVSLVDLLDGLNAINYVNN  
AEFPKFKQPKAHDYDLTDEPLTQETYFKMMQDFI  
REEDVILAEQGSFFGAYDLALKH  
NNKFIGQPLWGSIGYTLPATLGTQMATDSRRNLL  
LIGDGSLLQTLVQEISTMIREKIKP  
IIFVINNDGYTVERKIHGENAMYNDIKMWDYKLL  
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LLQIEAQPDTHMFIIEVKMGVHDAPHKLNAIGQAF  
AKQNG"

gene complement(194711..1949 /locus-tag="SSP0173"  
95)

CDS complement(194711..1949 /locus-tag="SSP0173"  
95)

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/translation="MFALSNACSNSTISITWILCSN  
FWAAKSLFFCLMIWAIFKKSFSTL  
RTSKSFLTSTKTEFKSFTFSLCIMKMSAKHINHL  
SLFRYIEICQRYIVIL"

gene complement(195140..1963 /locus-tag="SSP0174"  
15)

CDS complement(195140..1963 /locus-tag="SSP0174"  
15)

/note="similar to  
gi|27467289|ref|NP-763926.1|  
[Staphylococcus epidermidis ATCC  
12228], percent identity 60 in 384  
aa, BLASTP E(): e-132"  
/codon-start=1  
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protein"  
/protein-id="BAE17319.1"  
/db-xref="GI:72493998"  
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SLVDLGADVDYVHQHLLSLPLDQF  
SLNFAKKNKQGIQAMGLTIDFEEAHHHRKASDIF  
NMINESTLPNRVKERSMLIFDVIA  
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LEDLGIDEIKSPVPTGNGKIKIA  
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CDS complement(196333..1970 /locus-tag="SSP0175"  
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37)

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37)

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15)

/note="similar to  
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protein"

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		YLTQQLNVAFLTYRKCIINLEKQ
		IFSRSSIVQRLAKIMDKATFAVAFTNYNHIVILA
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		DVRIASSLVFTSLNDFKNAYEECELVFMLNEENV
		SFASFEDVEEKTLLYQINEEIRER
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		LQMFQGVVYGIPMSSFDTYFDQYK
		TQHHYESDAEIPAEGEKEICEHFKAVYLDEAYKP
		FPQEPIDQLTEAIEAVFKSWDNDR
		ARVYRQLNEIPH DIGTAVNIQEMVFGNSGEKSGT
		GVAFTRNPITGEAKLFG EYLLNAQ
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		LETHYKDMQDIEFTIENENLYILQ
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		VKSIDQLLHPNFDEQSLKQTSVIT
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		MRPETS PEDIEGMVASEAIVTTHG
		GMTSHAAVVARGMGKCCVTGCS DLEINITDKVVH
		YKGGSLYEGDIISVDGAKGDIYFG
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		AQDIQAGYQFGAKGIGLVRTEHMF
		FAPERLIEMRRFILFDTQDKRIAALNTIKQYQKN
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		NPMLGHRGCRLAITYPELYIMQAE
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		TMIETPRACLIASELAKECDFFSFGTNDLTQLTF
		GFSRDDAGTFIGTYSELGILEHDP
		FQTL DVEGIGELIKIASQQAKSANPDITIGVCGE
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gene	205311..206126	/locus-tag="SSP0181"
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		12228], percent identity 74 in 262

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gene	complement(206311..2071 74)	/locus-tag="SSP0182"
CDS	complement(206311..2071 74)	/locus-tag="SSP0182"
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gene	complement(207283..2078 28)	/locus-tag="SSP0183"
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gene	207922..209106	KFEMFKMEIQPGGKMHSDPHHPGSEEYIIIVNDGV
CDS	207922..209106	LEIEVDGKQYTINHHQAFRNSDL PHSYFNPGTSIVALTSTMYQ" /locus-tag="SSP0184" /locus-tag="SSP0184" /note="similar to gi 16800015 ref NP-470283.1  [Listeria innocua Clip11262], percent identity 41 in 381 aa, BLASTP E(): 2e-79" /codon-start=1 /transl-table=11 /product="putative transporter" /protein-id="BAE17329.1" /db-xref="GI:72494008" /translation="MENYRKIKPFNWLLFIGILL VGANLRAPITSIGVALPDIKADLA MSNSAVSVITVVPLLAFAVISLFAARTSNQFGLE KTIFLALCLIFIGIIVRSMTEISW LYIGTVLIGIGIGFNV LAPAVIKAKFPLHIGIM TGYYTVVMNVFGGLSSYGTAPLLK SFHYNVAISLIDIVTLVTIIWSFQLKGKQEMAT ALPRKSVNVWKSPISWQITILMGG QSLIFYSLINWMPAYLSQSGMSISEAGVYLSVLQ ISIIPFTFITPIFATKMKSQFTLT FVTGLLFIAGVIIMLCVPQLAIIISTILIGVAGGI AFGLVNTFFSLRTEHSQTAAKLSG MAQSIGYLFAAMGPLLFGLVHDMTGTWIASLSIL LFTAVIITLFGSQAGRNRITIEQSL QK" /locus-tag="SSP0185" /locus-tag="SSP0185" /note="similar to gi 49483510 ref YP-040734.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 56 in 494 aa, BLASTP E(): e-168" /codon-start=1 /transl-table=11 /product="putative cardiolipin synthase" /protein-id="BAE17330.1" /db-xref="GI:72494009" /translation="MQLIFDPGVSPiYRGVLAFF FVINVILAFVIVFLDRDRRDATA T WAWLFLLFVMPVLGFFIYIFFGRGIRKKRERGFA HNQIEDGMKRVQAQLQDSTNKISD SDNPiVRKHRDIATLLTKEPSFLSNDNNIDIYT DGHDLFSQMKEDLRNAKTYIHMEY YVLNLDGLGTEIINILEQKAEGLKLLYDAVG SKSVHKSFKKKFRENGGQVEAFFQ AKIPLINFRVNNRNHRKIVVIDGMTGYVGGFNVG DEYLGLNDKFGYWRDTHLRVRGDG VDALQLSFIHDWNSQAKREQLEYNMKYFPDNAYQ GGNVSMQLALSAPSDNWHQIEFGY MKMIMNAKSSiYMHSPYFIPDKGYINALRIAAS GVDVRLIIPNKPDIHIFVYWATITS VAQLIRDGVKVYTYENGFIHKKMMIIDDEVASVG SSNMDIRSFELNFEVNAFMYDEQI TKQLKAAFLDLKVSKELTEERYNQRSNWIKFKQ SIAKLASPIL" /locus-tag="SSP0186" /locus-tag="SSP0186"
gene	209327..210811	
CDS	209327..210811	
gene	210972..212357	
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gene	212461..213774	
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CDS	213864..215243	

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gene	215426..216823	/locus-tag="SSP0189"
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gene	complement(216901..2179 08)	/locus-tag="SSP0190"
CDS	complement(216901..2179 08)	/locus-tag="SSP0190" /note="similar to gi 15615816 ref NP-244120.1  [Bacillus halodurans C-125],

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percent identity 58 in 327 aa,
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CDS       complement(218088..2189 /locus-tag="SSP0191"
78)

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[Staphylococcus aureus subsp.
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75 in 296 aa, BLASTP E(): e-122"
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gene      complement(219104..2198 /locus-tag="SSP0192"
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CDS       complement(219104..2198 /locus-tag="SSP0192"
26)

/note="similar to
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[Mannheimia succiniciproducens
MBEL55E], percent identity 36 in
244 aa, BLASTP E(): 3e-37"
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gene	220311..221933	
CDS	220311..221933	
		/locus-tag="SSP0194" 63) /locus-tag="SSP0194" 63) /note="similar to gi 4574119 gb AAD23899.1  [Staphylococcus xylosus], percent identity 88 in 186 aa, BLASTP E(): 2e-90" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="BAE17339.1" /db-xref="GI:72494018" /translation="MAHSNNPEHQLDEAKDIVIN AIGETMDLYGINRSVGNLFGTMLF EDSMTLDEMREQLQMSKPSMSAGVKRLQEFDIVK QQFTRGSRKQHFIAEKDFNFNFSN FFTRKWRREIVINAEAVHDAVAILNKIINDESTD AAIKTEANETKQQLIDTLPHYEWL DHLSDALESGEIFKYFPIPENNYKED" /locus-tag="SSP0195"
gene	complement(222103..2226	
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CDS	complement(222103..2226	
	63)	
gene	222866..224359	

CDS	222866..224359	/locus-tag="SSP0195" /note="similar to gi 4574120 gb AAD23900.1  [Staphylococcus xylosus], percent identity 92 in 497 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="glycine betaine aldehyde dehydrogenase" /protein-id="BAE17340.1" /db-xref="GI:72494019" /translation="MELVNQLSRRQYIDGEWVDS SNQTTRKIINPFNQEVIFEVAEGT AEDSERAILAARRAFEKGEWSLETSENRGKKVRA IADLIVTHREELARLETLDTGKTL EESYADMDDIANVFNYFAGLADKDGELIDSPIP NTESKVIKEPIGVVTQITPWNYP LQASWKLAPALATGCSLVMKPSEITPLTTIRVFE LMEEVGFPKGVINLVLGKGSEVGE PLSAHKEVDLVSFTGGIKTGKHKIMQAADHVTDV ALELGGKNPNVIFDDADFDLAVDQ ALNGGFFHAGQVCSAGARIIVHNDIKEKFEAALI ERVKNIKLGNGFDSETEMGPVISA EHREKIENYMEIAKAENATIAIGGKRPEREDLQD GFFFEPTVITNCDTSMRIVQEEVF GPVVTIEGFSTEAEAIELANDSIYGLAGGVFTQD IGKAERVVNKLKMGTVWINDFHPY FAQAPWGGYKQSGIGRELGKEGLAEYQVEKHILR NTNPEPVNWFGKA"
gene	224416..226098	/locus-tag="SSP0196"
CDS	224416..226098	/locus-tag="SSP0196" /note="similar to gi 4574121 gb AAD23901.1  [Staphylococcus xylosus], percent identity 95 in 560 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="choline dehydrogenase" /protein-id="BAE17341.1" /db-xref="GI:72494020" /translation="MKQSYDYIIIGGSAGSVLG SRISEDVSNNVLVLEAGRSDYPWD LLIQMPAALMYPAGNKLYDWIYETTPPEPHMDGRK VGHARGKVLGGSSSINGMIYQRGN PMDYEKWAKPEGMDSWDYAHCLPYFKRLEKTFGA TKDDQFRGHHGPIKLRRGPADNPL FQAFFDAGVEAGYNKTPDVNGFRQEGFGPFDSQV HNGRRVSASRAYLHPAMKRKNLEV QTRAFVTKLNFEGNKVTGVTFKKNGREHTVNAKE VILSGGAINSPQLQLSGIGDSEH LRS LGIEPRIHLPGVGENFEDHLEVYVQHACKEP VSMQPSLNKLMKPFIFGLQWIFGRK GAAASNHFEGGGFVRSNEDVDYPNLMFHFLPIAV RYDGTKAPAAHGYQVHVGPMSNS RGHLKIKSKDPFVKPDFVFNYLSTEEDKREWVEA IKVARNILGQKALDPYNGGEISPG PEVQTDEEII EWVKRDGETALHPSCSRMGPASD EMSVVDPETFKVHG MENLRVVDAS VMPRTTNGNIHSPVLMMAEKAADIIRGKKPLDPE YIDFYRHGVHDKDAGTIK"



gene	226149..226304	/locus-tag="SSP0197"
CDS	226149..226304	/locus-tag="SSP0197"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="BAE17342.1"
		/db-xref="GI:72494021"
		/translation="MYLLLSLTADKGLDFVGSFF VHVRTLPFLILKAFTSSFSTDAR ITHCYVT"
gene	226447..227334	/locus-tag="SSP0198"
CDS	226447..227334	/locus-tag="SSP0198"
		/note="similar to gi 48870927 ref ZP-00323644.1  [Pediococcus pentosaceus ATCC 25745], percent identity 57 in 288 aa, BLASTP E(): 8e-92"
		/codon-start=1
		/transl-table=11
		/product="putative transcriptional regulator"
		/protein-id="BAE17343.1"
		/db-xref="GI:72494022"
		/translation="MELRTLRYFWTVAAEEHAISK AAAVLNITQPTLSRQMDLEIELG VELFYRENKGIMLTEEGIFLKNRAEEILSLTNQT QQEFENKKQQALSGHITIGCVEAD NSDTLAMILEEMVREHPLITFHIVSGIGSEISER LDKGLLDIAILIEPIAMEKEYEQVP LPRPERWGLLVSEDSFPRGQSSIHPGDLKKTLL MSRRPENQKMI SEWSQIAVNDLQV IGTYNLIFNIFSLVRNNVGS AVVIEGVTSNRNLD NLA FIPFKPELYTHCVLVWKK SRI QTPILKNFIKRFKEMNHPQ"
gene	227460..227780	/locus-tag="SSP0199"
CDS	227460..227780	/locus-tag="SSP0199"
		/note="similar to gi 48826012 ref ZP-00287241.1  [Enterococcus faecium], percent identity 79 in 104 aa, BLASTP E(): 4e-43"
		/codon-start=1
		/transl-table=11
		/product="conserved hypothetical protein"
		/protein-id="BAE17344.1"
		/db-xref="GI:72494023"
		/translation="MAKKQTAGRDNLGSFAPKFA ELNDDVLFGEVWSRESELSPYKRS LITITALITGRNFEQLTAHLKIGKENGVTKEEVA EIITHLSFYVGWPKAWSAFNI AKD IYND"
gene	227804..228217	/locus-tag="SSP0200"
CDS	227804..228217	/locus-tag="SSP0200"
		/note="similar to gi 48826013 ref ZP-00287242.1  [Enterococcus faecium], percent identity 70 in 134 aa, BLASTP E(): 4e-55"
		/codon-start=1
		/transl-table=11
		/product="conserved hypothetical protein"
		/protein-id="BAE17345.1"

gene	228381..228971	/db-xref="GI:72494024"
CDS	228381..228971	/translation="MAKHEEVKEGIIFSIGETND AFADSFIGQSFLNTLVNEDNIDVV VGNVTFEPGCRNNWHVHTEGYQILLVTGGEGWYQ EEGKPSQKLAPGSVIVTHKGVKHW HGATKDSWFEHIAITSGASEFLESVSDEHYESIE K" /locus-tag="SSP0201" /locus-tag="SSP0201" /note="similar to gi 45533192 ref ZP-00184184.1  [Exiguobacterium sp. 255-15], percent identity 54 in 191 aa, BLASTP E(): 4e-52" /codon-start=1 /transl-table=11 /product="putative oxidoreductase" /protein-id="BAE17346.1" /db-xref="GI:72494025" /translation="MKTEVIAKSTDVTNPQDVEA LVQNAIEIFGRVDVLINNAGLIPQ SFLGDNNIDEWNQTIDVNLKGVLYGIGAVVPKMR AQKSGHIINIASIAGHQVNPGGAV YCATKFAVRALTEALRQEEVTVGSHIRTTIVSPG AIETELLNHITDQGLKQGMEDVYK DALNPNEVAKALVNAIDTDASTSINEVVIRPTRQ LP" /locus-tag="SSP0202" /locus-tag="SSP0202" /note="similar to gi 28378584 ref NP-785476.1  [Lactobacillus plantarum WCFS1], percent identity 51 in 127 aa, BLASTP E(): 8e-32" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17347.1" /db-xref="GI:72494026" /translation="MSEQHWHSDLLKQFKEADDM HVSPFYDDGQTLATPTWIWSVVVD GKLFVRAYNGQNSRWYQSAKAQQAGQIQLAQQTF DVQFIPVHGDKQLDESINGAYKEK YGNSAYLPPMLEPGPVSATVKIEPK" /locus-tag="SSP0203" /locus-tag="SSP0203" /note="similar to gi 15673857 ref NP-268032.1  [Lactococcus lactis subsp. lactis Il1403], percent identity 37 in 456 aa, BLASTP E(): 4e-82" /codon-start=1 /transl-table=11 /product="putative permease of the major facilitator superfamily" /protein-id="BAE17348.1" /db-xref="GI:72494027" /translation="MNKKLVLVIVLGAYFMIMMD TSITMTALNEMQQSLHMSSGTLTW VQSAYVLLFGGLLLLGA KLGDVLGLKHVFLCGLC LFLIFSITTGLATNTMMLIISRAG

		QGIAAALVSPSILAFINLIYDDGPEKRKAVSFYS TIAGIGASGGLIVGGILTSLVSWR LCFLINIPMCIIIFILLAIKLLPQTTTSSYPPRID LFGALLSVVSILLIVLGMERLNMA FSLINFLVILIGLILLITFIAIEHKVKYPIIELS LFKNKIRSSGYLLRFLFLSTSFYS WYYMSIYFQDSFNLSPNLNTGLLLICTTGVMFIVA LNIHKLLKSQTNISVLIKILISI VGMILLIFCLNHQVGITMFIPLILIGVGQGFIF TPLTNLGVYQVTNEQSGIASGLVN LAHQIGSSAGIVFELIIATTLHLILNFENNNSSL TLISMVIGTVIQIIMLLYVLLVFK KKENKYEI"
gene	complement (231059..2332 18)	/locus-tag="SSP0204"
CDS	complement (231059..2332 18)	/locus-tag="SSP0204"
		/note="similar to gi 5924067 gb AAD56434.1  [Staphylococcus epidermidis], percent identity 64 in 717 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="teichoic acid biosynthesis protein" /protein-id="BAE17349.1" /db-xref="GI:72494028" /translation="MKSISVIVTYYNSEDYIERC LISLKKQRFQDFELILVNDGSTDQ SKPLATQILKDWDIPIKAIDLPEMTGHAHARNMG LKEVESPYFIFIDSDDYLASYALS FYMKKLNQFDALIAPIHGFTLDIPQYVDQNLVRT QYLNTKTHSNQFLRKQTACNIVFK TAIARGHNLQFNEDLNVFVDWSFILEFIKYANGF VRVSRFPFYIKGEIYDPFVKPALS KQDFGITFNDYVVSFSDSVQRAPLKENKVF IKNK MKNIYKHSFEPSSRKNPERYKYN ELLPKVTRELIPTLFKNEKPLFILESMLLMVNKR KSAFKINKLRKKARLVKSILLRRK NKNRALYQLTDSQDKVSPNTIVFEAFAGKNYS PKYIYEYMMKRYPNYEFIWVFKNP SKVQIPGLAKKVKKGSKAYYEAYSKAKYWVS NAR LPLYLNKKPNQVYIQNWHGTPLKR LANDMKVIRMPGTTTDDNYKRNFREETS RWDYLVSPNRYSSKIFETAFWMKPEQLLEIG YPRNDVLVNHANDKSYIQEIKENLNL PADKKVIMYAPTWRDDEFVKKGKYL FNLQIDL DNLQAQLGDDYVLLRMHYLIS NALDLRGYEDFA IDVSNYSDISELYLIS DCLITDYS SVMFDYGVLKRPQFF FAYDLKYGQDLRGFYLDY HNDLPGPI HQDPYQLTEDLKNLDQ VSIDYNDKIN QFYDDFCSLENGQASKAISDLITK NNN"
gene	233538..233981	/locus-tag="SSP0205"
CDS	233538..233981	/locus-tag="SSP0205" /note="similar to gi 56420652 ref YP-147970.1  [Geobacillus kaustophilus HTA426], percent identity 37 in 145 aa, BLASTP E(): 4e-18" /codon-start=1 /transl-table=11

gene	234158..234481	/product="putative acetyltransferase"
CDS	234158..234481	/protein-id="BAE17350.1" /db-xref="GI:72494029" /translation="MTIRCAKDNELKLINKVIPK LFKEAMMVNFDLSDASLRDMSSQL LLQGAKYYVLI EENICKGFVLIDKKT DYLEQQDY GFIYELYVFEGYRRQGVAKKLIYF VNDDFFKRQHIGEVRLNVNVQNKAKLLYEKVG FQE RNITMSMKVVE"
		/locus-tag="SSP0206" /locus-tag="SSP0206" /note="similar to gi 52142287 ref YP-084542.1  [Bacillus cereus ZK], percent identity 66 in 108 aa, BLASTP E(): 2e-39"
		/codon-start=1 /transl-table=11 /product="putative truncated permease of the major facilitator superfamily"
gene	234661..235452	/protein-id="BAE17351.1" /db-xref="GI:72494030" /translation="MKNYRYFIITMIIIMTMINY VDRGAISYAQEDIINEFGFDNIAW GSILGYFGYGYMLGSLFGGVTADKKGPKFVWLIA GTLWSLFEIGMAFAGEIGMVLFGG SALAG"
CDS	234661..235452	/locus-tag="SSP0207" /locus-tag="SSP0207" /note="similar to gi 47528555 ref YP-019904.1  [Bacillus anthracis str. 'Ames Ancestor'], percent identity 56 in 255 aa, BLASTP E(): 4e-79"
		/codon-start=1 /transl-table=11 /product="putative truncated permease of the major facilitator superfamily"
gene	235715..236341	/protein-id="BAE17352.1" /db-xref="GI:72494031" /translation="MLFVILGLLGLVWIIIWYKV FTDYPEDNKHVSQEEIESIQSTEE TVHGEKTVETEHN AHEKWYHFFKSPTLIFNMVG Y FGFQYINFLILT WTPKYLQDEYHF ELHSLWYLGMLPWIGACFTAYFGGRLSDWLRVKT GSLRIARSGLAIFGMTLAAICFLI IPTTNQIGWIMFLMMLGNACIFLPNAVNW SVIID TAPKKTGT YGGITHFFVNSATIIA PTLTGILVTSYGYSSMFISAVVA VIGI IAMCFV KPGIKMKMPTS"
CDS	235715..236341	/locus-tag="SSP0208" /locus-tag="SSP0208" /note="similar to gi 48825620 ref ZP-00286863.1  [Enterococcus faecium], percent identity 61 in 204 aa, BLASTP E(): 1e-68"
		/codon-start=1 /transl-table=11 /product="putative nitroreductase"

		/protein-id="BAE17353.1" /db-xref="GI:72494032" /translation="MINNNFEEILMNRKSVKVFD EQVKIPKAEMDEMIKKATTAPSSV NMQPWRFLVVESEDEGKDTLRPLIRFNTRQNDSSA AMVVIFGDMKSQTNAEEIYGNAVK HDLMPEEVKQEMLKKVIPLYDNAPKEQMNDIVKI DSSLAAMQFMLVAKAHGYDTNPIG GFESDQIADAFGIDSERVVPVLIVAIGKAKNPAH GSYRLPTETVTKYV"
gene	236489..237631	/locus-tag="SSP0209"
CDS	236489..237631	/locus-tag="SSP0209" /note="similar to gi 27469130 ref NP-765767.1  [Staphylococcus epidermidis ATCC 12228], percent identity 51 in 383 aa, BLASTP E(): e-111" /codon-start=1 /transl-table=11 /product="putative enzyme of poly-gamma-glutamate biosynthesis" /protein-id="BAE17354.1" /db-xref="GI:72494033" /translation="MWKYGIILCFLFSCFLVLCV GCLNEKDKLTQTLSFYAVGDNLIH PVVYQDALQDNGQFNFESEMYDNLKDEVQSTDVSY INQESPLGGDERGLSGFKQFNTPE AIAQNIVHTGFNVVNGANNHALDQGTAGLENEIS VWKQFKSVFYFGTFDSPKQHDTIP VIEKNGIKMAMLSYTYGTNDIPREKPYQINYFDK VQIKKDIASAKEKSDAIVSAHWG NEGKTKPNETQQQYAKVFADAGADVVLGTHPHVI QPVKWWVGKDNHKTLLVAYSLGNFL NGQATGTEKNILGGNIRFNLEKNPKGVQINNVKW KSLVTHYENGEPYLKATPQNFKMY KLDHYKDEQAQYHALNDKKGMEVSRQRLVGITKD VIDKQYLDEKSY"
gene	complement(237727..238668)	/locus-tag="SSP0210"
CDS	complement(237727..238668)	/locus-tag="SSP0210" /note="similar to gi 49484498 ref YP-041722.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 68 in 311 aa, BLASTP E(): e-121" /codon-start=1 /transl-table=11 /product="putative inosine-uridine preferring nucleoside hydrolase" /protein-id="BAE17355.1" /db-xref="GI:72494034" /translation="MKQIYFNHDGGVDDLISLFL LLQMEDVSLIGVSAIGADSYVEPA ASASQKIINRFSKQPIHVAASKQRGKNPFPKDWR MHAFFMDALPILNEANQSHSNLLE HDAYEDIIEKLQKSHAPVTLLFTGPLTDLAKAVT VEPTIINKIERLVVMGGTFLEKGN VEEPEHDGTAEWNAFWDPEVSKTVFDTNIKIDIV ALESTNRVPLTWDIRQAWANERHY PGVDFLGVSYAAVPPLTHFQTNSTYFLWDVLTITA YVGEPELVQQHSVNASVYTEGPSQ

gene	239002..240399	GQTYIDDVHGRTISVVDDVEHDAFFKYITNLAKK
CDS	239002..240399	VEQ" /locus-tag="SSP0211" /locus-tag="SSP0211" /note="similar to gi 53771630 ref ZP-00183937.2  [Exiguobacterium sp. 255-15], percent identity 55 in 461 aa, BLASTP E(): e-153" /codon-start=1 /transl-table=11 /product="putative proline betaine transporter" /protein-id="BAE17356.1" /db-xref="GI:72494035" /translation="MKFKKEKVN RVSDQAKKGV VATGIGNAIEWFDFGLYAQLAVIL SANFFGNLPQEMQIVSTFAVFAFAFIVRPIGGIF FSLGDKYGRKIVLSTTILLMAAS TLMLGLLPTQDQIGIWAPILLLVVRMIQSFSTGG EYAGAMTYIAETAPDKTRGKLGSG LEIGTLAGNIMAAILAGLMYSLLSNQQMADWGW IPFILAAPLGIIGIILRSSLDESP AYESTLEEQEELEYSYLDIFKYYWKDVVVCFAGV AFLNVANYMVL SYMPSFLNSTINL GGTMGSILSTITMLVMIPAVFFFGWYSKVG NKR TIIFGLAGFSLSVLAFWLMSIPM IPFVILGLFIIALFMSTFEGVMP SLLPSMFHTKV RLRTL SLVYNIGAAVFGGLTPFIL STLVETTQQIAPSYLMFINVVGLIIFITMFKS TSNKS LRGSYPNVETQEDYDHVVK NPKDALWWEDEV RKD"
gene	240640..242145	/locus-tag="SSP0212"
CDS	240640..242145	/locus-tag="SSP0212" /note="similar to gi 15923270 ref NP-370804.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 43 in 505 aa, BLASTP E(): e-113" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17357.1" /db-xref="GI:72494036" /translation="MSKTVKIVIAVVIGVLLICG IGGAAAYYFTKNTPKNTYLLSEQE TAKQMKAYGEDRFENEFEFQDKMKDESYLINLNA SADVPEALLKSSDIPKSVADASKL GFKLGHDPDKEHSVIALTPTVADNEIGEFQWAAD KQNQYYAAPILDDVYKAKNNELVD VYKKITGETSSVEGTNNGITNDSLNLNLSLLSGTQ ISQDKIDEISKKYSEVITDKLDDD NFEKDDVTIKVNGEDKDVKKVTMNVSKGETKAIL TDILEKAKKDKDIKAI AEDQFNAK DYKKQLDDILKEVKD TDKAEFSPVKS VIWEDDNQ ILKRNLTMKDE DGSTVKLNGTSQV DDDNLMIDYKLTTDD DQEV ALKGKSTKKDDQYKD NYKVTFDNGYRKSDATLNTESQD GDKRNDKGQIEINANYDKTTIDFNNKLD TDTKNN TQKQELSLSTDIDNETV VINIKGD TKLKEDIKFKKAN AQDLNTMSDSDFRKLQREISN NTEDIVKDI AKDIKDKK"

gene	242196..243362	/locus-tag="SSP0213"
CDS	242196..243362	/locus-tag="SSP0213"
		/note="similar to gi 49482516 ref YP-039740.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 55 in 388 aa, BLASTP E(): e-131" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17358.1" /db-xref="GI:72494037" /translation="MKTIQLFRIYHSFLLKKWHL FFYLILMMCAFLTALLVVQYVNQD DAKFRIGIVDHDNSAETQLILNSMGNGTHLGKDI RIQRYNQNAQKLLKAQKLEGYYV FEKGMTKTFYKHGNLPIAVYTYDQTSTKSLVINQ LTDSVYSRLMLSMGGGLTYTTLS EANKDDKLQLLTDLLFTGLNRTGGFDYQPIQIFD TSSYYVVTGYLASIFIFALSLSFI LKMNQAKALKSRLHMYHFSFEKLTILIRSLFTLFY TGVWTLGCLCMIQILPNTFEPYN WPTVVIQLVYYYILMITGWLTIIDLICFRWFNIVL KIMLALMVILFSGQIIPTIYFKHL LNGMFNVQPFSEFTNQMLEIILNNYILDTPITFY MSFVITAIILLVIIVWRYRR"
gene	243359..244282	/locus-tag="SSP0214"
CDS	243359..244282	/locus-tag="SSP0214"
		/note="similar to gi 21281983 ref NP-645069.1  [Staphylococcus aureus subsp. aureus MW2], percent identity 43 in 304 aa, BLASTP E(): 2e-75" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17359.1" /db-xref="GI:72494038" /translation="MIQSFIFIIILKQWKQLVIF FTILTCTLLLIWAAYSSLNQSFKI PVAVQDQDQSQASHTLIQSIEKNDFVKVEKLDQE AIYLDESVSKEAVAAMHIPKDYS DKLKNNQLKLALTLYARDDFIGDITFEMISRSLY EQQIPYIVKKHLDDDGQETSLEKV SDTLNQHTPKSAIVHHVVNTNSETSSISLVFGI ILFVSSVQIVLHQRLKQNGPLTRL FIFQYSKLILFTTYILIHTLILMLVLGITTIFIQ QQLSFTFFAKSLVIIIVYELGVSW LLFKINTLSHRLFMAVIFALLMAVLYIFIQL"
gene	244293..244961	/locus-tag="SSP0215"
CDS	244293..244961	/locus-tag="SSP0215"
		/note="similar to gi 49482514 ref YP-039738.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 66 in 219 aa, BLASTP E(): 2e-80" /codon-start=1 /transl-table=11 /product="putative ABC transporter ATP-binding protein" /protein-id="BAE17360.1" /db-xref="GI:72494039"

gene	245161..245475	/translation="MIELKNLSKHYRKKCIFESL DMTFENLQLTVLLGENGAGKSTLL RMIAGLEQLTKGEIRYFGEQLSKKQRQDKIGYVP QDIALFEHMTVNENIRCFKALCKT PLSNVLIDEYARQLNLNERTMTISNLSGGTKRKV NVLIGLLSNPQILILDEPTVGIDL KSRFDIHNLLNTMKRERLIILTTHHLDEVEALAD QIKVIGNDPFYREILEDKHWAFEV YNNK"
CDS	245161..245475	/locus-tag="SSP0216" /locus-tag="SSP0216" /note="similar to gi 22127301 ref NP-670724.1  [Yersinia pestis KIM], percent identity 55 in 99 aa, BLASTP E(): 3e-24" /codon-start=1 /transl-table=11 /product="putative truncated gluconate transporter" /protein-id="BAE17361.1" /db-xref="GI:72494040" /translation="MSFLGEHLPLISLVIGVGVL LFLNIKLKINSILSLIFAAVLVGF MNGMKPLAILDTIKEGLGSTLGSLALIIGFGAVL GKLMVDSGAAQRIASTLIERFGAK YV"
gene	245536..245835	/locus-tag="SSP0217"
CDS	245536..245835	/locus-tag="SSP0217" /note="similar to gi 22127301 ref NP-670724.1  [Yersinia pestis KIM], percent identity 63 in 91 aa, BLASTP E(): 1e-26" /codon-start=1 /transl-table=11 /product="putative truncated gluconate transporter" /protein-id="BAE17362.1" /db-xref="GI:72494041" /translation="MILAPLVISIAIEAKTPFMK LAITMVVATTLSHNIFPPQEGPTA LVDAYNADMGMVYILGMIVFIPSVIIAGIILPRF MKRIDYPIPPLLQKKKKFYRQ"
gene	245837..246505	/locus-tag="SSP0218"
CDS	245837..246505	/locus-tag="SSP0218" /note="similar to gi 1009388 emb CAA62859.1  [Escherichia coli], percent identity 51 in 217 aa, BLASTP E(): 5e-59" /codon-start=1 /transl-table=11 /product="putative truncated gluconate transporter" /protein-id="BAE17363.1" /db-xref="GI:72494042" /translation="MPSFGLSLFVPLIPAILISI STILSLFITEDTILHEIVSFIGSA EISLIIPITAITAIVMFGLRKGDMDTMMKSFETGL KGVATIIFIVGAGGAFKEIILEAH VGDIADIMKGTNISPLIMAWLITALIRIATGQG VVSITAAGIVGPLIPTFDVSPVL MVLATAVGSNITITHVNDASFVLFKEYFNISIKDT"



gene	246996..248639	FKTWGCVVINDICNRINGCLNTGS IYLK"
CDS	246996..248639	/locus-tag="SSP0219" /locus-tag="SSP0219" /note="similar to gi 27468939 ref NP-765576.1  [Staphylococcus epidermidis ATCC 12228], percent identity 87 in 537 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="putative amino acid transporter" /protein-id="BAE17364.1" /db-xref="GI:72494043" /translation="MGQKDESSKINLPQLVLLGL GSLIGSGWLFGAWEASSIAGPAAI ISWIIGFVVIGSIAYNYIEIGTMFPQSGGMSNYA QYTHGSLLGFIAAWANWVSLVTII PIEAVSAVQYMSSWPWEWAKFTSGLMDGSTISNA GLFAVFVIIIVIFSLLNYWSVKLLT SFTSLISVFKLGVPLLLTIIMLIISGFDTGNYGHS VGTFMPYGSAPIFAATTASGIIFS FNAFQTIINMGSEIQKPEKNIARGIAISLTLSAI LYIVLQSTFITSMPTEMLHENGWS GINFNSPFADMAILLGLNWLAILLYMEAVVSPFG TGVSFVAVTGRVLRAMEQNGHIPK FLGKMNEKYMIPRVAIIFNAIISMVMVSLFRDWG TLASVISTATLVAYLTGPTTVISL RKMAPKMHRPFRANLLKFMAPFSFVMASLAIYWA MWPTTAEVILIIILGLPIYFFYEY KMNWKNTKKQIGGSLWIILYLIVLAFLSFIGSKE FKGMNWIHYPYDFIVIIIIALIFY KIGTSSYFESVYFKRAKKINKDMRADLREKRKSE HISEE" /locus-tag="SSP0220" /locus-tag="SSP0220" /note="similar to gi 49482427 ref YP-039651.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 65 in 393 aa, BLASTP E(): e-150" /codon-start=1 /transl-table=11 /product="putative ornithine aminotransferase precursor" /protein-id="BAE17365.1" /db-xref="GI:72494044" /translation="MLDLYEHTDKYSSKNYSPLK LALAKGRGAKVWDIEDNCYIDCIS GFSVNVQGHCHPKIIKALQEQSQRITMVSRLYS DNLGKWEKICKLANKENVLPMNT GTEAVETAIKMARKWGADIKNIDESSEIIAMNG NFHGRTLGSLSLSSQDSYKKGFGP LLNNIHYADFGDIEQLKKLINNQTTAIIILEPIQG EGGVNIPPTHFIQEVRLCNEYNV LLIADEIQVGLGRTGKMFAMEWENTEPDIYLLGK SLGGGLYPISAVLANQDVMSVLTP GTHGSTFGGNPLACAVSMAALDVLNEEHLVQNAL DLGDRLLKHLQQIESELIVEVRGR GLFIGIELNVAAQDYCEQMINKGVLCKETQGNII RIAPPLVIDKDEIDEVIRVITEVL EK" /locus-tag="SSP0221"
gene	249096..250280	
CDS	249096..250280	
gene	250325..251356	

CDS	250325..251356	/locus-tag="SSP0221" /note="similar to gi 57285371 gb AAW37465.1  [Staphylococcus aureus subsp. aureus COL], percent identity 69 in 343 aa, BLASTP E(): e-135" /codon-start=1 /transl-table=11 /product="N-acetylglutamate gamma-semialdehyde dehydrogenase" /protein-id="BAE17366.1" /db-xref="GI:72494045" /translation="MIEVGIVGGSGYGAIELIRL LIQHPNVNIKIYIFSHSKQDQPIKE TFPHLEQLTYHYETLNSEGIECDVIFATPSNV KHIVPQLLSKRIKIIDLSGDFRLT NRATYETYYGETAASQEYLN EANYSIAEWSNVNA QTTQLIANPGCFPTATLLALHPLI DKDIVKQDNIIIDAKTGVSGAGRSLAQHVHFAEM NENLSAYAIGKHKHKPEIEQYLSL LAQQEVKVTFTPHLVPMTRGILSTIYIKLNHAFT NEDLHNLFKDYYEDKPFVIRSLG QFPKTKEVYGSNYCDIGIYVDEENQTAILVSVID NLVKGASGQAIQNLNLMYGWKENT GLLQSPVYP"
gene	251380..252618	/locus-tag="SSP0222"
CDS	251380..252618	/locus-tag="SSP0222" /note="similar to gi 49482425 ref YP-039649.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 60 in 413 aa, BLASTP E(): e-141" /codon-start=1 /transl-table=11 /product="arginine biosynthesis bifunctional protein" /protein-id="BAE17367.1" /db-xref="GI:72494046" /translation="MRDIETIDTLNQLNIDLQGD VSSPLGFIAGGLHCGLRKKVDFG WIYSTTPATATGVYTLNQFKAAPLKLTEDSINKD KALQAIIVNSAIA NACTGEKGMQD ALDTQAWIAEQLNIEQHLVG VASTGVIGSFLPMD KIQYATQHVLKEQYNKSEAFNQAI LTTDTMTKHL SVKVEIDGTTVTIGGTAKGSGMIH PNMATMLGFITTDANIDANTLDYC LKQSIDQSFNMITVDGDSSTNDMVL CMANGQAQH TQIDALHPEWHKFVYALNFVCHYL AKSIAKDGE GATKLVTVKVGAHDVVEARKIAKS IVSSNLVKTAVHGEDANFGRIVTA IGYASRYIEPSATHVSLCQVSVLEKGMVDFDEQ RLKEELASDNILIEATVGN GEGEA AAYGCDLSY EYVRINASYRT"
gene	252631..253392	/locus-tag="SSP0223"
CDS	252631..253392	/locus-tag="SSP0223" /note="similar to gi 57285369 gb AAW37463.1  [Staphylococcus aureus subsp. aureus COL], percent identity 48 in 252 aa, BLASTP E(): 5e-64" /codon-start=1 /transl-table=11

		<pre> /product="putative acetylglutamate kinase" /protein-id="BAE17368.1" /db-xref="GI:72494047" /translation="MNYIVIKIGGSTLTELHETT IDDIAQLKQQDLHPPIIHGGGPF I NQALEQQGVDSLFEDGLRVTTDEVMSITSQILIG KVN PQLVSKMNDENIQSIGLNGID AKLFDVEPLNEKYGYVGEPININTAVIDHLTEEY IPVIASIGRHKTSRHLYNINADTL AYKIAQTLNAPIYLLSDIPGVMIDNKVKATLNSE HIKNYIEQE QIYGGMIPKVQDAIS AIEYGCQKV VIAAGNEAHVVERIRTGKGIGTTIV L" </pre>
gene	complement (253710..2549 42)	/locus-tag="SSP0224"
CDS	complement (253710..2549 42)	/locus-tag="SSP0224"
		<pre> /note="similar to gi 27469138 ref NP-765775.1  [Staphylococcus epidermidis ATCC 12228], percent identity 60 in 408 aa, BLASTP E(): e-144" /codon-start=1 /transl-table=11 /product="putative succinyl-diaminopimelate desuccinylase" /protein-id="BAE17369.1" /db-xref="GI:72494048" /translation="MSTFSVEEKVQILSDIVAMN TVNDNEIEVCQYFQNLFEQHG IKS TIDKVDERRANLIADIGEGSPVIGVSGHMDVVSE GNREQWSYDPFKLTEDNGYLYGRG AADMKSGLAALAIAL IEMHDAQLLTKGRIKFLAT TGEEMEQLGSQNL YEKG YMD DVDA LI IAEPCQDMMVYAHKGSMDYRIKSQG TSAHSSM PIFGVNAIKPLIEFIQDIDNAYQK ISKEIKGESLDFTHLLDRMKPSLPATFAVEEIES ALQGLVITNTLIKGGVQVNSVPED ADADFNIRTIPEYNNDQVKNLFNNTIEKHNANGS NLESELYLDLDPVLT TGQNSLIDT AKTIGKTAFNKDFVAAP IGGVTDASNLLRGKDES FPFLVFGPG EKPHQVDERVEKAMY LKFI DFYKELLITYSKNY" </pre>
gene	255153..255545	/locus-tag="SSP0225"
CDS	255153..255545	/locus-tag="SSP0225"
		<pre> /note="similar to gi 49485228 ref YP-042449.1  [Staphylococcus aureus subsp. aureus MSSA476], percent identity 59 in 129 aa, BLASTP E(): 1e-41" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17370.1" /db-xref="GI:72494049" /translation="MTLSLNKIHQA HQYTGVDF PKLFKAFKDMGIIVNTV NIEQGET SYIHQDGA EITDES VKVAVPIAQQTHLALVKDIL QRHQAGETDFPKFCDEMARAGIYK </pre>

gene	255775..256314	WYIDIIAGTCAYIDKENQVLITENIPQS"
CDS	255775..256314	/locus-tag="SSP0226" /locus-tag="SSP0226" /note="similar to gi 46908521 ref YP-014910.1  [Listeria monocytogenes str. 4b F2365], percent identity 52 in 172 aa, BLASTP E(): 4e-45" /codon-start=1 /transl-table=11 /product="putative FMN reductase NADPH-dependent" /protein-id="BAE17371.1" /db-xref="GI:72494050" /translation="MASVAIIAGGNKIESRLTGV VKYAEKYLNDEGIETDVIHVHQLD AEALITANFSNESINKTHKKIEEADGIIIVSPVF KAAYSGIVKTYLDLLPRGAFTGKT VLPLALGGTFAHVLAIQYSLDPVIKELGADTIHK GRFILDKHITSNEDGTYGYDQEAQ DGLNKTLKKFVSDKAQVIE" /locus-tag="SSP0227" /locus-tag="SSP0227" /note="similar to gi 1280354 gb AAA98144.1  [Staphylococcus aureus], percent identity 50 in 188 aa, BLASTP E(): 5e-51" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="BAE17372.1" /db-xref="GI:72494051" /translation="MPKVVDHEKKKQQIIQYAWQ SIVSNGAKGATVRNIAKLARMTPTG QIRYYYPNHHDLLKAVSVEVDSKVRGRIKAVYND GSLSPLDKVIQAMLKAMPLDEERY ADMEVWLAFAQYELHEVGKDSMGNEIFTLIKASMS FLEEHDLLDTSLNQYVAIMKMHAL LDGLALHKLLNPEQMINEIDIEHLIESEVKSRLR " /locus-tag="SSP0228" /locus-tag="SSP0228" /note="partial similar to gi 49478076 ref YP-037308.1  [Bacillus thuringiensis serovar konkukian str. 97-27], percent identity 54 in 156 aa, BLASTP E(): 1e-45" /codon-start=1 /transl-table=11 /product="truncated conserved hypothetical protein" /protein-id="BAE17373.1" /db-xref="GI:72494052" /translation="MISRYVLRMKQVGLILLAMT PVIDLILIIITMSVDLLNGAKATVP HGIAAVYIGVSI AFRKQMIQWADERFKYYVLKEG NLPEKKTGIAYAKAYFVSWLRHVL AYLIGTGLLWLIINIVGQDSVAALYHVIKIWTV ILGIDLLITLSYFIWPKPKKV"
gene	256481..257065	
CDS	256481..257065	
gene	257136..257609	
CDS	257136..257609	

gene	complement(257707..2583	/locus-tag="SSP0229"
	66)	
CDS	complement(257707..2583	/locus-tag="SSP0229"
	66)	
		/note="similar to gi 15614705 ref NP-243008.1  [Bacillus halodurans C-125], percent identity 30 in 213 aa, BLASTP E(): 3e-21" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17374.1" /db-xref="GI:72494053" /translation="MKFESITLCTSELEETLQFY EETLECPVEVINQDTFIVQIGETQ LQFCRSEDVIQPYHFAIDIPYNHFYDMKEHYQN ILFLLMEDGHHTTYFESFVAHAIIY FNDPSGNIVELIARVSNITDEPEFSRRISEIGFVC NETNAIYQALSDYKIETFEHAHFE PYALNFLGDTSDSYILLTPEDRRWSFSEKHSIA YPIDIKTETFHLSYDTRHQWHLKQ S"
gene	complement(258607..2601	/locus-tag="SSP0230"
	96)	
CDS	complement(258607..2601	/locus-tag="SSP0230"
	96)	
		/note="similar to gi 23097823 ref NP-691289.1  [Oceanobacillus iheyensis HTE831], percent identity 59 in 528 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="L-lactate permease" /protein-id="BAE17375.1" /db-xref="GI:72494054" /translation="MMLFVAFSAVIVPFIFLVLL RMSALKGMIISAFIVTFLGVFVWG MQGHVISASLLQGTHKTLTILYILFGALVLLNTL RQTGAVTRINEGFKKLSGDMRVQV IIVAFLFGSLIEGASGFGTPAVVTAPLMVALGFR PMIAVVTALIADSVAVSFGAVGTP VLVGLSTLNDADSSLFQATAERITTLDLLSGIFI PIILIIATLIIFFGKTNKLKSIVEM IPWLACIGFIYVASSFAYAFILFGPEFVAILGSLT GLIVAVVTASKGWLLPKNEWKDG DDSYTPKSEHDMPLLTAWSPYLMVVILLLLTRT VPLIKDFTTQVLDLSWNQILGFET ISSDWEFLYSPGTIILLLSALFAILIQRKSFKDLS QASVESLNTIKTTGITLVATLVMV HVFINSGINTSDLISMPEYIAENMSKYLGPILWF VAPFLGALGSFITGSATVSTLTFS PIQLNIAQSIGAEPYTVLAAQIIIGAAAGNMICVH NVVAVCAVVNMPGKEGSVIRKTLG PALLYCLLVGLSAYIITSIFF"
gene	260590..261843	/locus-tag="SSP0231"
CDS	260590..261843	/locus-tag="SSP0231"
		/note="similar to gi 56965377 ref YP-177109.1  [Bacillus clausii KSM-K16], percent identity 55 in 418 aa, BLASTP E(): e-138"

gene	262531..263505	/codon-start=1 /transl-table=11 /product="putative permease of the major facilitator superfamily" /protein-id="BAE17376.1" /db-xref="GI:72494055" /translation="MNKKLAKMGMPPTLLWGYIG VLIFMMGDGLELAWISPYLHDHGL SVHQTAILTTTCYGVTTAIGSWFSGVLVEIIGPRK VMLLGTLLEYIIIGHMIFVGLALPSM NYGLMIPSYAIRGFGYPLFAYSFLVWVAYRSPQK RLGAAVGWFWFVFTGGLSVLGSFY SSMAIQIFGHIFTLWTAILWVIVGTFLAVFVNDR KFEIENKGNKFKTHLKEMGAGITI LKREPRVAVACIVRIINQAAQYAFPLFLPIYLST KGIATTTWLNWGTIFIANIIFNL IFGALSDKIGWKNTISYIGGIGCAVFTLGLYFIP EIFTGNVFIIVGTGFLWGMCLAGF VPISALVPSLVHDGDKGPAMAILNLGAGLCVFAG PGLVALFYDSIGVQGMMLIFGLY VASAIMTRFLKTPEERGILNEKEAT" /locus-tag="SSP0232" 
CDS	262531..263505	/locus-tag="SSP0232" /note="similar to gi 48824874 ref ZP-00286199.1  [Enterococcus faecium], percent identity 61 in 321 aa, BLASTP E(): e-112" /codon-start=1 /transl-table=11 /product="ornithine carbamoyltransferase" /protein-id="BAE17377.1" /db-xref="GI:72494056" /translation="MKTCDFSADLHTLIDFTGE LKEKKKRGIPHPYLKGNLAFLFE KPSTRTRSAFSAAYDLGAYPEYFGQDIHLGVK ESSEDTAKVLGRMYDGIEFRGHHQ KDVEALAKNAGVPVWNGLTNEWHPTQMIADFFTL KEHWGTLQGKTLTYVGDARNNVAH DLLITGAILGVNIHVAAPKALQPDEDIQVMAQKY AAESSDILITDDIQQAIYQTDAL YTDVWFSGEDQSVLEPRINQLLPYQVNKEMLIN TMNPDVIVLHCLPAFHDVNTQVGQ QIYETYGLTEMEISDDVFKGEHAVIFDQSENRLH SIKAIMAVTLGDIF" /locus-tag="SSP0233" 
gene	263960..264418	/locus-tag="SSP0233" 
CDS	263960..264418	/locus-tag="SSP0233" /note="similar to gi 57286687 gb AAW38781.1  [Staphylococcus aureus subsp. aureus COL], percent identity 87 in 87 aa, BLASTP E(): 6e-37" /codon-start=1 /transl-table=11 /product="truncated phosphotransferase system glucose maltose N-acetylglucosamine-specific IIC component" /protein-id="BAE17378.1" /db-xref="GI:72494057" 

gene	264213..265496	/translation="MSKLFKAQQFGKSFMLPIA ILPAAGLLLIGGALSNPNTIKAY PVLDIALLQNIFILMSAAGNIVFQNLPVIFAVGV ALGLAKSDKRHGWSSSNWVFNYE CINEWFVDDHRYIGERQLGRRRSKYGIGNTNCRN RCIWRYYHRYYDSFVT"
CDS	264213..265496	/locus-tag="SSP0234" /locus-tag="SSP0234" /note="similar to gi 15923232 ref NP-370766.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 80 in 421 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="truncated phosphotransferase system glucose maltose N-acetylglucosamine-specific IIC component" /protein-id="BAE17379.1" /db-xref="GI:72494058" /translation="MIKGTAGLAAMLGFLIMNAS MNGLLTITDTLAKGNLAEEGQSMV LGIQTVETGVFGGIITGIMTALLHNKFHKISLPA YLGFFGGSRFVPIITSVSSIVLGV VIFFIWPTVQGWIFGIGGLVDKTGVIGTFFFGFI LRLLGPFGLHHIFYLPFWQTALGD SLEVKGHMVQGTQNIFFAQLGDPDVTKYFSGGSR YMSGRFITMMFGLCGAALAIYHTA KPERKKVVGGLMLSAALTSFLTGITEPLEFSFLF VAPMLYVIHAVLDGLAFMMADIFN ITVGQTFSGGFIDYLLFGVLQNEKTNFLWVIPI GIVWFVLYYVIFRYLITKFNFKTP GREDEGVTETVEATDRAKTIIQALGGKENIDVVD CCATRLRVTLNSDKAVDKTMLTFT EARGVIQKGNVQVIYGPVHTTIKNEVEELLEND K"
gene	265664..266293	/locus-tag="SSP0235"
CDS	265664..266293	/locus-tag="SSP0235" /note="partial similar to gi 49482798 ref YP-040022.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 60 in 198 aa, BLASTP E(): 2e-62" /codon-start=1 /transl-table=11 /product="putative truncated glucosamine-6-phosphate isomerase" /protein-id="BAE17380.1" /db-xref="GI:72494059" /translation="MIEVYKTLAALLNVNQIDLS NVVTFNLDEYVGLSAEHNQSYHVY MNAHLFNHNQAWNKNKIYLPVGDAPNIELESELY EQRLGEIGSADIQILGIGENGHIG FNEPYSSFESVTRVVDLTPSTINANSQHFENIED VPKQAI SMGLSSIMKAKRIILLAF GKNKQQA IKALLEGEVSEALPASILHKHPNVEVI IDDEIFTSLIEDGTL"
gene	266539..267387	/locus-tag="SSP0236"
CDS	266539..267387	/locus-tag="SSP0236" /note="similar to

gene	267443..268573	gi 16119885 ref NP-396590.1  [Agrobacterium tumefaciens str. C58], percent identity 37 in 273 aa, BLASTP E(): 2e-58" /codon-start=1 /transl-table=11 /product="similar to quorum-quenching N-acyl homoserine lactonase" /protein-id="BAE17381.1" /db-xref="GI:72494060" /translation="MVNVKKERMKVYVLDNGRMK MDKNLMIANSNQATLDDPKANNEM HEFPIYTVFIDHPDAKILFDTACNPNAMGDSGRW ISATQKAFPYFADEACHLPNRLEQ INVDPKEVDFVIAASHLHLDHAGCLEYFTNATIIV HDELSGAMKTYARNQQEGAYIWA DIDAWVKNLKWRTIKKEEDNLKLV DGVRILNYG SGHAWGIIGLEIESAELGTIILAS DAIYTKESIEDTLKPPGILYDSIGWTKSVEKIQR LAKEKNAQIWFGHDGEQFEGFRKS TEGYYE" /locus-tag="SSP0237"
CDS	267443..268573	/locus-tag="SSP0237" /note="similar to gi 23100256 ref NP-693723.1  [Oceanobacillus iheyensis HTE831], percent identity 66 in 375 aa, BLASTP E(): e-147" /codon-start=1 /transl-table=11 /product="putative Zn-dependent alcohol dehydrogenase" /protein-id="BAE17382.1" /db-xref="GI:72494061" /translation="MKTRAAVLREMGKDAPYTES HPLTIETLELQGPQSNEVLKIGA VGLCHSDLSVINGSRPRPMPMVLGHEAAGEIIEV GENVAEFEVGDHIVCTFIPSCGHC IPCREGRPALCENGAAANEKGEMLEGGFRYESDR DEVMHHLGVSGFADYAVVSTNSI VKVDKKIPFEKVAIFGCAVITGIGAVINTARINA GSTVAVVGLGGIGLNAILGARLAG ASEIIALDINEEKFALAKSLGATAVFNSGEAHTI EDIKQYTQGGVDYAFETAGVVPAM DVAYQITRRGGMTTTTGLPDPKHQFSFPQVTLAA EERTIKGSYVGSCVPDRDIPRFIN LYHQGRLPVNELLTDTLPLEHINEGFDRDLARGEA ARLVVKMD" /locus-tag="SSP0238"
gene	268584..269900	gi 42519794 ref NP-965724.1  [Lactobacillus johnsonii NCC 533], percent identity 56 in 435 aa, BLASTP E(): e-137" /codon-start=1 /transl-table=11 /product="phosphotransferase system cellobiose-specific component IIC" /protein-id="BAE17383.1" /db-xref="GI:72494062"
CDS	268584..269900	



		/translation="MSRFNDTLEKYLLPVASKLG SNKILISLRDGIIVAMPLIIIGSL FLVISGIAIPGWIEWLEAQGIQPYLMKAVNGTGF LMGLVASFGVAHSIARQYDTDGVS AGIISMAAFLVVTNPVMTGGKTSEEAIPQMYMGS QGLFVALIIGIFSGLIFQWFINRN IRIKMPDQVPPAVAKSFSALIPGAVIILLWLIYY IALDNLFPFGNIHDLIVNTLGVPLS LMGSTLIGTIILVGLNSAFWVFGIHGANVVNAV MPIWLKNIDENRIVYQANPHGDL HIITQPFIDNFVFMGGGGSTIGLVIVIAILAFKK RSSKITKTMAPLTLMPGIFNINEP TLFGLPVVLNVRLIVPFILAPMINATITYFAMAS GLVHLTNGTAMPWTIPPIISGFLA TGHVSGSLVQMVCIIVDILLYPPFYRTMEKYNLQ LEQKEADETKEI"
gene	269919..270815	/locus-tag="SSP0239"
CDS	269919..270815	/locus-tag="SSP0239" /note="similar to gi 42519793 ref NP-965723.1  [Lactobacillus johnsonii NCC 533], percent identity 60 in 300 aa, BLASTP E(): 1e-97" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17384.1" /db-xref="GI:72494063" /translation="MVKRLLSANASEIVEMTATE LKQSIKASDGRVVLSENVVTRTPV IPDITNAELARAFGADLILLNGLDAFDPKVVNV EDKQVINELRRLVCRPIGVNLEPV DKTATMSEEKLNIVEGRQASSKTVKALEKLGINF ICMTGNPGTGVTNDKIVNAISETR KHFTGLIIAGKMHSAGVDEPVITETYVDQFIDAG ADIILVPSIGTVPGFDEEQKLNIV KAVHRREGLVMSAIGTSQESSDPSTIRDFAIRNK ICGVDIQHIGDAGYCGLAPVNNIF ELSKAIRGERHTVSMIARSIQR"
gene	270852..271172	/locus-tag="SSP0240"
CDS	270852..271172	/locus-tag="SSP0240" /note="similar to gi 48826183 ref ZP-00287408.1  [Enterococcus faecium], percent identity 64 in 104 aa, BLASTP E(): 1e-30" /codon-start=1 /transl-table=11 /product="phosphotransferase system cellobiose-specific component IIB" /protein-id="BAE17385.1" /db-xref="GI:72494064" /translation="MAEKTIMLVCAAGMSTSM LQKMQKEAEKQKLDRDIFAVSTSEA DQKIESDNIDVLLLGPPQVRFKKDEYTKKCEKDI PVAVIEMRDYGTMMNGENVLNTAEQ LMTK"
gene	271183..271509	/locus-tag="SSP0241"
CDS	271183..271509	/locus-tag="SSP0241" /note="similar to gi 48869880 ref ZP-00322617.1

		[Pediococcus pentosaceus ATCC 25745], percent identity 57 in 107 aa, BLASTP E(): 9e-28"
		/codon-start=1
		/transl-table=11
		/product="phosphotransferase system cellobiose-specific component IIA"
		/protein-id="BAE17386.1"
		/db-xref="GI:72494065"
		/translation="MSEAENSLEFAMSLIAYSGD AKSHAMEAIYAAKKNAFEEAEKKL KLAEVSLLEAHHIQTNMLTKEAQGDEIKMSLLTI HSQDHLMTAITFKDMAAEMIDLYK KMDSKA"
gene	271743..272537	/locus-tag="SSP0242"
CDS	271743..272537	/locus-tag="SSP0242"
		/note="similar to gi 57285143 gb AAW37237.1  [Staphylococcus aureus subsp. aureus COL], percent identity 68 in 264 aa, BLASTP E(): e-103"
		/codon-start=1
		/transl-table=11
		/product="ABC-type amino acid transport system periplasmic component"
		/protein-id="BAE17387.1"
		/db-xref="GI:72494066"
		/translation="MKKILLGILTLLLTVVGLAAC GTSDKKDNDNKNKTASENKTFVVG TEGTYAPFSYHDKQDKLTGYDIDVMKAVAKEMGY KVKFKETQWDSMFAGLDSGRFNVI ANQVGINDERKEYKFSEPTYTSEAVLVVNKNNK DIKSFDDVKGKKLAQTFTSNYGKL AKSKGAELTKVDGFNQAMDLLQSNRVEGTFNNDI SYLDYKKQKPNADVKIIEGNAEKS QSALTFSKKEDDATIEKVNKAMKKLKDNGELAKI SKKWFGEDVSKS"
gene	272521..273240	/locus-tag="SSP0243"
CDS	272521..273240	/locus-tag="SSP0243"
		/note="similar to gi 49484629 ref YP-041853.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 89 in 239 aa, BLASTP E(): e-117"
		/codon-start=1
		/transl-table=11
		/product="ABC-type amino acid transport system permease component"
		/protein-id="BAE17388.1"
		/db-xref="GI:72494067"
		/translation="MFLNLNTEQQHALDAAGQAF APMLEGLVKFSIPITLVTFLLGLV IALLTALMRISTSRILRGIARFYISIIIRGTPMIV QLFIIIFYGIPELGRLLTNNSQW TLAPVIAAIIGLSLNVGAYASEIIRGGIMSIPKG QTEAAYSIGMNYRQTIQRIILPQA IRVSVPALGNTFLSLIKDTSLLGFILVAEMFRKA QEVASTTYEYLTIIYLLVALMYWVV CFIISIAQNIFYESYLERGYRS"
gene	273237..273968	/locus-tag="SSP0244"

CDS	273237..273968	/locus-tag="SSP0244" /note="similar to gi 15925402 ref NP-372936.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 83 in 242 aa, BLASTP E(): e-110" /codon-start=1 /transl-table=11 /product="ABC-type polar amino acid transport system ATPase component" /protein-id="BAE17389.1" /db-xref="GI:72494068" /translation="MIELKNIKKSFDDKEVIKGI DLNVNQGEVVTFIGRSGSGKTLL RMINALELPTEGAVYVNGETYSNADKKSQIKVRK QSGMVFSYNLFPKTALENVMEG LITVKKTKKDEAKQQALALLEKVDLTAVKDQRPN ALSGGQQQRVAIARALAMNPKVML FDEPTSALDPELVNDVLRVIKDLANEGMTMIIVT HEMRFAKEVSNKIVFIHDGVIGES GPPEQIFNHPQSAELQRFLNMIREV"
gene	274312..274827	/locus-tag="SSP0245"
CDS	274312..274827	/locus-tag="SSP0245" /note="partial similar to gi 57286778 gb AAW38872.1  [Staphylococcus aureus subsp. aureus COL], percent identity 42 in 135 aa, BLASTP E(): 1e-23" /codon-start=1 /transl-table=11 /product="putative truncated transcriptional antiterminator" /protein-id="BAE17390.1" /db-xref="GI:72494069" /translation="MLSKRQYHILMFILECETFV QIHHLATHFNVTERTIQYDLEYIE DMASNLGLIIQRTKQEGVKITTTPEQLKRFAHKS THTTIHYAKEERLLYITLKLLEAN TPTSSQVLATTVSVSRRTIVEDLKSQVNWLEQHD YLAIAECAFDLAHLNKFVRYG VTAYQYMSKLLK"
gene	complement(274922..275839)	/locus-tag="SSP0246"
CDS	complement(274922..275839)	/locus-tag="SSP0246" /note="similar to gi 47527176 ref YP-018525.1  [Bacillus anthracis str. 'Ames Ancestor'], percent identity 59 in 303 aa, BLASTP E(): e-102" /codon-start=1 /transl-table=11 /product="putative 2-dehydropantoate 2-reductase" /protein-id="BAE17391.1" /db-xref="GI:72494070" /translation="MRILVLGAGGIGGYFGGRLA ESGQNVTFVLRPKRSFLERNGLA IHSEQGDYHFNPLITKDDRVAPFDVILLSSKSY HLEQAMTDLPFVDGHTAIIPLLN GVAHIPQLQSIFGKDKVMGGYCVIETTLDMSGEI

gene	276053..276808	IQTSPFDKLFEGELDGSKSERAQK
CDS	276053..276808	IAQAFSETKAEFKLSTSIEQGMWHKYLMITVLSS
		ITTLMHAPIGPIRSDGGINFVRS
		LYNEVASIMRAHRAPLADDIVSQYMTSFNQLSYH
		FKTSMQRDMEKGLNIETGHLQGYL
		LNLADTYQIDAPLLKCVYQNHKVYKEMLK"
		/locus-tag="SSP0247"
		/locus-tag="SSP0247"
		/note="similar to
		gi 27468804 ref NP-765441.1
		[Staphylococcus epidermidis ATCC
		12228], percent identity 37 in 252
		aa, BLASTP E(): 4e-41"
		/codon-start=1
		/transl-table=11
		/product="putative metal-dependent
		membrane protease"
		/protein-id="BAE17392.1"
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		/translation="MSFKNDHKYQWKDMQ GKDFL
		LPFIYLLIGNFCLSIVILTIMIGIN
		ETQGKNNANFNANFSGTPGILMEMIAFIIIFALW
		ILFHRHSFRQSWKQGLQNIQHWK
		LIVITFIVIIIVFKEIYPYLVNAFAPEHWKFEETQ
		NDKMVEEMFATPVSTILAFFSIVI
		IAPMTEEFLLFRHLIIGELGKKLNFYVMSVISIIV
		FASLHVTEAKSPLEIVMYLAIAVG
		IVYVYMKSQRSLAVAIALHALNNLLAYIFMIIM"
gene	277150..277968	/locus-tag="SSP0248"
CDS	277150..277968	/locus-tag="SSP0248"
		/note="similar to
		gi 27467520 ref NP-764157.1
		[Staphylococcus epidermidis ATCC
		12228], percent identity 63 in 270
		aa, BLASTP E(): 1e-96"
		/codon-start=1
		/transl-table=11
		/product="ABC-type uncharacterized
		transport system periplasmic
		component"
		/protein-id="BAE17393.1"
		/db-xref="GI:72494072"
		/translation="MRKWFILGSLFVLTIIILAAC
		GKSNGEKEDKEITIAASPAPHGVV
		LEHAKEEMKKKGYDLKIKTVDYKVPNKLLDKGD
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		EAGKVFTTPMGVYSKKYKDIKDIPKGSTIYVSNN
		PAEEGRFLSFFVDKGLIKIKKGVV
		IEDAKFDDIVENKKDLKFNNKQGAEFLLPKTYNSK
		EGAAVIMNSNYAIDNGLTPHKDAI
		AIEGKSSPFANIVAVQEGHKNDKKFKELMKVLQS
		KEMKKFITDKYQDVIPYEK"
gene	278012..278944	/locus-tag="SSP0249"
CDS	278012..278944	/locus-tag="SSP0249"
		/note="similar to
		gi 15896788 ref NP-350137.1
		[Clostridium acetobutylicum ATCC
		824], percent identity 36 in 308
		aa, BLASTP E(): 2e-54"
		/codon-start=1
		/transl-table=11
		/product="lactate dehydrogenase"

		/protein-id="BAE17394.1" /db-xref="GI:72494073" /translation="MSKLGIIIGLGKVGTTQVLTDV QQLNLFSEIILIDDRADVASGEAL DHIHSQGLINTAHIKIRSGVYQDLTDADFIVIAA SEATDKNNGDRTLLAQGNHDIKIG IMSQIAEVTQEAVVILISNPVDSMVYFANQIDYP AHKIIIGTGTALETSRFKTIIADHY QIDPNNVEAFVIGEKGQHAIPVWSKVHIHGMELS EFEALSDRPAIDKSHISSIINEVS MDVIFYQKGWTNAAISKVTSFLIQSIALDQRTITP LTSLSSEYGLEDGAFSLPTLIDKK GIVQRFADITLDKEEERELKEAYEYIRQTIHTAQQ "
gene	279089..280180	/locus-tag="SSP0250"
CDS	279089..280180	/locus-tag="SSP0250" /note="similar to gi 57286566 gb AAW38660.1  [Staphylococcus aureus subsp. aureus COL], percent identity 41 in 184 aa, BLASTP E(): 2e-36" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="BAE17395.1" /db-xref="GI:72494074" /translation="MSMGGVMMMLERHVKLIRLML INRNQFLNADEIARYLNVSNRTAR NDIQYINSEILDDLIVSVKGRGYKLNQSLYSMQQ IETIVTDFTNKESELLIKLGYQLL MYQQPLTSEAIGKTFHLTKAEVTDYINKIKAWCI SFDVNIQITKKKGITVNGSEMNR NAILHLNQLSENVKTVDAFILAEHQYMKHQTEDF IYLTISTGVGMAYIRKELVSGVN GNFGEIGHTIIKGDSQYQCPVCKQYVCVENEISG LAISRKASHILNKHVSTREAIEMY LHQAHSSEITEMIDEVLILTQQLCTNLFNININ IVLGGGVTSKLPYKSSIENYAQK HYLIQNSTLNVLTISNLEANVLTGLYHVNK"
gene	complement(280586..281875)	/locus-tag="SSP0251"
CDS	complement(280586..281875)	/locus-tag="SSP0251" /note="similar to gi 56418819 ref YP-146137.1  [Geobacillus kaustophilus HTA426], percent identity 68 in 419 aa, BLASTP E(): e-161" /codon-start=1 /transl-table=11 /product="O-acetylhomoserine sulphydrylase" /protein-id="BAE17396.1" /db-xref="GI:72494075" /translation="MTQNPWHLDTLSIHGGQVVD DFSKARAVPIYQTSSYVFDNTEHA RKLFALEEDGNIYTRIMNPTQNVFEERIAALEGG VGALATSSGQAAIHLALLNIVESG DEIVASSNLYGGTYNLLNITFKKLGKIKVHFVDP HPDNFKNAITDKTKAVYAETIGNP RIDVLDIEAVADIAHNHNIPLIVDNTFPTPYLLR

		PFEFGADIIVHSATKFIGGHGTSI GGVIVDSGKFNWDNGKFPGLVEPDESYHGISYAK DVGEAAYITKARVQLLRDLGSAVS PFNVHEFLIGLETLHLRLERHSENALRVAQYLEQ HPKVTWVNYPGLKNNAYHQLAQKY LPDGQGAILTFGIDGTVDDIAKFVDGLNLFSLHA NVGDSKSLIIHPASTTHLQLSPED QKASGVVPELVRLSVGTENINDIIADLDNGFKES LGN"
gene	282093..282998	/locus-tag="SSP0252"
CDS	282093..282998	/locus-tag="SSP0252" /note="similar to gi 27469242 ref NP-765879.1  [Staphylococcus epidermidis ATCC 12228], percent identity 67 in 299 aa, BLASTP E(): e-110" /codon-start=1 /transl-table=11 /product="cysteine synthase" /protein-id="BAE17397.1" /db-xref="GI:72494076" /translation="MIAFDLIGNTPLVLLESFSN KDVQIYAKLEQYNPGGSVKDRLGK HLIETAIRENIIQKGDVVVEASAGNTGIGVAIAA NHYGVS AVIFAPEGFSEEKISIIK ALGAEVIRTDQTLGMAGAQAARDYELQTGAYYL NQFESYRNPETYKSTIGKEITDKL KDIDYFVGGVSGGTFTGVAEHLAATYHTESVIV EPEGSILSGGNAHSHDIEGIGSEK WPSFLPKALVSDIIKVSDDAAFQNVKLLARQEG LVGSSSGAALQGALEIKKHINKGV IVTIFPDGSDRYMSKQILNYKETIK"
gene	282995..284140	/locus-tag="SSP0253"
CDS	282995..284140	/locus-tag="SSP0253" /note="similar to gi 27469241 ref NP-765878.1  [Staphylococcus epidermidis ATCC 12228], percent identity 80 in 380 aa, BLASTP E(): e-176" /codon-start=1 /transl-table=11 /product="cystathionine gamma-synthase" /protein-id="BAE17398.1" /db-xref="GI:72494077" /translation="MNKKTQLIHGGQTTDPYTGA VTTPIYQTSTYMQDGIGDMRQGYE YSRSANPTRSALEGLIADLEQGESGFAGSGMAA ISAVIMLLDKGDHLLINSDVYGGT YRALTKVFNRFGIDAEFIDTTNIEAVEQYIKPET KMLYIETPSNPLLRVTDIKKSAEI AKKHHLISVVDNTFMTPYFQNPLTLGIDIVLHSA TKYIGGHSDVVAGLVATSDAELAE RLGFIQNSTGGVLGPQDSYLLIRGIKTLGLRMEQ VQRNTLAIIDMLQQHSAVKQVFHP SISDHLNNDIHEAQSEGHTGVVAFEVADIESAKK VISESHYFTLAESLGAVESLISVP ALMTHASIPKDIREKEGIADGLVRLSVGIEDTKD LVEDLEQSLNALG"
gene	complement(284238..>284900)	/locus-tag="SSP0254"
CDS	complement(284238..>284900)	/locus-tag="SSP0254"

900)

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/note="Start codon is not
identified similar to
gi|23097745|ref|NP-691211.1|
[Oceanobacillus iheyensis HTE831],
percent identity 42 in 156 aa,
BLASTP E(): 3e-31"
/codon-start=1
/transl-table=11
/product="putative truncated sugar
phosphate permease"
/protein-id="BAE17399.1"
/db-xref="GI:72494078"
/translation="RYFCKHTYRHCLYTARYIYC
TIWTFISKPIVQLTGNYSDIALSIF
WILIGIFGVVGGISGSIIDKKGIHFAFNFGVIAL
ACASVLLAYTPSIWLLPFIASSLF
GLSYIFLTGVLLVWGIKLFVKNASLGIGIPFLLL
AVGQVIGSSIAGIVIDILNYESF
IIFGIIIGLIPLLIYPKVEVTENKIPKGRYSKLQK
TNSDILNDTYAQHQTSNSNNDKYN HI"
gene      complement(284804..2854 /locus-tag="SSP0255"
87)
CDS       complement(284804..2854 /locus-tag="SSP0255"
87)

/note="similar to
gi|23097745|ref|NP-691211.1|
[Oceanobacillus iheyensis HTE831],
percent identity 42 in 223 aa,
BLASTP E(): 2e-41"
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/transl-table=11
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phosphate permease"
/protein-id="BAE17400.1"
/db-xref="GI:72494079"
/translation="MKFSKLVFPGIAMIATTYGL
GRFSFGLFLPDITNDLSLSASQAG
LISSLFYLAYCFTIVYSTLQTDITIGPKRMIILAG
ISVVIGLITIGVSSNAIILSIGVI
FTGASTGLVSPPYGYTISLWINLQDQGKANTLIN
SGTSMGLMFTGITAMLVFLDWRDT
YLIYALIALVVLFWNYIVIPKLQKDIKIHTGSLN
IRDISASTRIVTASTLLGISTAPF
GLSQNPLSN"
gene      complement(285621..2861 /locus-tag="SSP0256"
75)
CDS       complement(285621..2861 /locus-tag="SSP0256"
75)

/note="similar to
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[Oceanobacillus iheyensis HTE831],
percent identity 37 in 181 aa,
BLASTP E(): 5e-29"
/codon-start=1
/transl-table=11
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/protein-id="BAE17401.1"
/db-xref="GI:72494080"
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gene	complement (286349..286819)	/locus-tag="SSP0257"
CDS	complement (286349..286819)	/locus-tag="SSP0257"
		/note="similar to gi 57285077 gb AAW37171.1  [Staphylococcus aureus subsp. aureus COL], percent identity 44 in 152 aa, BLASTP E(): 2e-30" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17402.1" /db-xref="GI:72494081" /translation="MTDEYIYKNTVQPSWIDNNN HMHDAQYYSIFS DAVVGFFESIDF STDYRHSQDVTMFSVEAHISFLKELLLDESFYIK VHIYDYDAKRVHLFLTMYNSNDER NATYEAIMMGVGNETRRSMDFPKPIQEKIKHYFD QQNTFDV PKQLGHVIGIPKK" /locus-tag="SSP0258" /locus-tag="SSP0258" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17403.1" /db-xref="GI:72494082" /translation="MVLVALILFIISIVFLIYSI TLLMGKDGTMSLFTKEEKALTKG QKLTIIYLITIVLFVASLVWLLNLI"
gene	286997..287203	/locus-tag="SSP0258"
CDS	286997..287203	/locus-tag="SSP0258"
		/note="similar to gi 57286412 gb AAW38506.1  [Staphylococcus aureus subsp. aureus COL], percent identity 66 in 277 aa, BLASTP E(): e-112" /codon-start=1 /transl-table=11 /product="urease accessory protein UreD" /protein-id="BAE17404.1" /db-xref="GI:72494083" /translation="MSNNKQAWTGQLDLSVFNNNG KKS VARDVFFEKALKVMRPVYLNQ SDIPTFYIVNVGGGYLDGDRYTMNFNIDSDAKVI LTSQGATKIYKTLNDHVEQYQTFN IKNNGYAEYVGDP IIAFENAKFYQHN VFNLESTA SLFYTDILT PGYSKSDKRFSYTYM HLLNEIYVDDALVTFDNM LLD PQKQNV DGLGYME DYTHLGSCYFIHPSVNQKFIEQVY EEIKHFQHKYDCRFGITHLPTHGFSLRILSNK TQ VIESIITAVQCYVVKQIFDRDVDF LRKY"
gene	complement (287290..288132)	/locus-tag="SSP0259"
CDS	complement (287290..288132)	/locus-tag="SSP0259"
		/note="similar to gi 57286412 gb AAW38506.1  [Staphylococcus aureus subsp. aureus COL], percent identity 66 in 277 aa, BLASTP E(): e-112" /codon-start=1 /transl-table=11 /product="urease accessory protein UreD" /protein-id="BAE17404.1" /db-xref="GI:72494083" /translation="MSNNKQAWTGQLDLSVFNNNG KKS VARDVFFEKALKVMRPVYLNQ SDIPTFYIVNVGGGYLDGDRYTMNFNIDSDAKVI LTSQGATKIYKTLNDHVEQYQTFN IKNNGYAEYVGDP IIAFENAKFYQHN VFNLESTA SLFYTDILT PGYSKSDKRFSYTYM HLLNEIYVDDALVTFDNM LLD PQKQNV DGLGYME DYTHLGSCYFIHPSVNQKFIEQVY EEIKHFQHKYDCRFGITHLPTHGFSLRILSNK TQ VIESIITAVQCYVVKQIFDRDVDF LRKY"
gene	complement (288133..2887	/locus-tag="SSP0260"



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47)
CDS      complement(288133..2887 /locus-tag="SSP0260"
47)
        /note="similar to
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        [Staphylococcus xylosus], percent
        identity 97 in 204 aa, BLASTP E():
        e-109"
        /codon-start=1
        /transl-table=11
        /product="urease accessory protein
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        /db-xref="GI:72494084"
        /translation="MTDTIKIGVGGPVGAGKTQL
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        SMNFAAIDELKERNDDELIFIES
        GGDNLAAATFSPELVDFSIYIIDVAQGEKIPRKGG
        QGMIKSDFVINKTDLAPYVGASL
        DRMAEDTKVFRGNRPFTFTNLKTDEGLDEVIQWI
        EQDVFLKGLA"

gene      complement(288761..2894 /locus-tag="SSP0261"
50)
CDS      complement(288761..2894 /locus-tag="SSP0261"
50)
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        [Staphylococcus aureus subsp.
        aureus Mu50], percent identity 75
        in 229 aa, BLASTP E(): e-100"
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        /transl-table=11
        /product="urease accessory protein
        UreF"
        /protein-id="BAE17406.1"
        /db-xref="GI:72494085"
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        AFSHSFGLETYIQRDTVHDEESFQ
        QWLVLFLNEQLTYADGLTMLRVYDALNENDTKAI
        LKLDRIILFVQNLPKETRQGSQMG
        NRMVKLASELYSDWINWYHAQMKDKKASLHPAI
        CFTMLGHHLGVDIETIIDYYLYQN
        VSSLTQNAVRAIPLGQTAGQRIVHKMIPIMKETR
        DHIMTIPASQLGITAPGLEINQME
        HENVNVRIFIS"

gene      complement(289443..2898 /locus-tag="SSP0262"
95)
CDS      complement(289443..2898 /locus-tag="SSP0262"
95)
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        [Staphylococcus epidermidis ATCC
        12228], percent identity 88 in 150
        aa, BLASTP E(): 5e-73"
        /codon-start=1
        /transl-table=11
        /product="urease accessory protein
        UreE"
        /protein-id="BAE17407.1"
        /db-xref="GI:72494086"
        /translation="MIIEEIVGNIANFSDSEKGG

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gene	complement (289906..2916 21)	/locus-tag="SSP0263"
CDS	complement (289906..2916 21)	/locus-tag="SSP0263"
		/note="similar to gi 410516 emb CAA52680.1  [Staphylococcus xylosus], percent identity 96 in 571 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="urease alpha subunit" /protein-id="BAE17408.1" /db-xref="GI:72494087" /translation="MSFKMTQSQYTSLYGPTVGD SVRLGDTNLFARVERDYATYGDEA AFGGGKSIRDGMAQNPVNTRDDKQVADLVITNAM IIDYDKIVKADIGVKNKYIMKIGK AGNPDIMDNVDIIIGATTDIIISAEGKIVTAGGID THVHFINPEQSQVALESGITTHIG GGTGASEGTKATTVTTPGPWHLHRMLLAAESLPLN IGFTGKGQAVNHTALVEQIHAGAI GLKVHEDWGATPSALDHALQVADDYDVQIALHAD TLNEAGFMEETMAAVKDRVLHMYH TEGAGGGHAPDLIKSAAYANILPSSTNPTLPYTV NTIDEHLDMMITHHLNASIPEDI AFADSRIRKETIAAEDVLQDMGVFSMVSSDSQAM GRVGEVITRTWQVAHRMKEQRGLL DGDSEYNDNNRIKRYIAKYTINPAITHGISDYVG SIDEGLADIILWEPAFFGVKPDV IVKGGLINAAINGDANGSIPTSEPLKYRKMYGQL GGNLQSTSMTFVSTTAYENDIGKL LGLKRKLRPVHNIRKLSKKDMKNNNATPDLDVDP QTYEVFVDGEKITSEPA TELPLTQ RYFLF"
gene	complement (291627..2920 31)	/locus-tag="SSP0264"
CDS	complement (291627..2920 31)	/locus-tag="SSP0264"
		/note="similar to gi 410515 emb CAA52679.1  [Staphylococcus xylosus], percent identity 86 in 134 aa, BLASTP E(): 1e-63" /codon-start=1 /transl-table=11 /product="urease beta subunit" /protein-id="BAE17409.1" /db-xref="GI:72494088" /translation="MKPGEIIVKRTEIEVNQGHN ATILNVKNTGDRPIQVGSHYHFFE ANPALQFDHEKAYGKRLDIPAGAAVRFEPGDEKE VQLVEYSGKRKIYGFHGDVNGSID ESRVYKLEDDSTATEVIAEQDKTSENANKGRG"
gene	complement (292047..2923 49)	/locus-tag="SSP0265"
CDS	complement (292047..2923 49)	/locus-tag="SSP0265"

		/note="similar to gi 581787 emb CAA52678.1  [Staphylococcus xylosus], percent identity 99 in 100 aa, BLASTP E(): 3e-49" /codon-start=1 /transl-table=11 /product="urease gamma subunit" /protein-id="BAE17410.1" /db-xref="GI:72494089" /translation="MHFTQREQDKLMLVIAADLA RRRQQRGLKLNYPEAVAIISFELL EGARDGKTVAELMSYGKQILNEDDVMEGVADMLT EMEIEATFPDGTKLITVHHPIV"
gene	292565..293467	/locus-tag="SSP0266"
CDS	292565..293467	/locus-tag="SSP0266"
		/note="similar to gi 27468778 ref NP-765415.1  [Staphylococcus epidermidis ATCC 12228], percent identity 52 in 294 aa, BLASTP E(): 3e-88" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17411.1" /db-xref="GI:72494090" /translation="MDAIRIVLKNISQVLLLNN WTGLFILLGLFIGSWKVGVMALIA SVIALLLAKRTNYSEEEINTGLSGFNPVLTAL TLFLVPKWYSLIIILVAIIITMPI GSAFREFFKPFVPMPLTMPYVFWLILLMSFQF KRVNADVNIPLNAIQEIQFSGHHI QFINAFLSGFSEIFLLKSVLAGTLILIGIFIASR KAGVYAIVANLIGFLAVIVLGNH DQINEGLFGYNVILTVLALGIAFRTRIQRPI LGILLTVVIHAGMTLLTPYGLPV FTLPFIIATWIMLFAGNQMQAQEI"
gene	293559..295037	/locus-tag="SSP0267"
CDS	293559..295037	/locus-tag="SSP0267"
		/note="similar to gi 57286681 gb AAW38775.1  [Staphylococcus aureus subsp. aureus COL], percent identity 62 in 485 aa, BLASTP E(): e-175" /codon-start=1 /transl-table=11 /product="putative ABC-type dipeptide oligopeptide nickel transport system periplasmic component" /protein-id="BAE17412.1" /db-xref="GI:72494091" /translation="MKKMVALLATTAIVLAGCSG SGNESKSKTLNVELPLKTTSIAPY ETDVPVKIGSAESLFKAGANGKVQKLLVD TYNQK SPTQLDLKLKDDIKFQNGKKVTGQ AVKASLEESIKKSDLVKGSLPIKEIKVDGQ NVSI TTKEAYPELVSELASPFSAIYDTK ADSDVTKAPVGTGPYQIKDYKQSQNIKLDQ FKDY WQGKPKLDHVNVTYQEDGNARSSD LSSGKADVITDVPVEKEKTLNQGDKTTTSSV SGF

		RTSLIMYNHTSKKMTKPVREALDK VVDRESIAKNVSKNHATPATGPFNTKLDFIDKQQ VQKQDIDEAKKIMAAQGYTKAHL KLTVSTYNGRPELPKMAQVLQSDAKKANIDITIR NVDDIEGYLKDKSQWDASMYSFGT IPRGDTGYFFNQAYKPEGAINAGGYDNAKVTKLI DQFNKTVDKTERNRLTNEIIDITD KDKANSYLTMYMDNIVGMNKKVKNLKATPEGIYLI DYKVDKAK"
gene	295034..296014	/locus-tag="SSP0268"
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gene	296011..296832	/locus-tag="SSP0269"
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gene	296825..297604	/locus-tag="SSP0270"
CDS	296825..297604	/locus-tag="SSP0270" /note="similar to

gene	297597..298286	gi 27467979 ref NP-764616.1  [Staphylococcus epidermidis ATCC 12228], percent identity 49 in 254 aa, BLASTP E(): 2e-66" /codon-start=1 /transl-table=11 /product="putative ABC-type oligopeptide transport system ATPase component" /protein-id="BAE17415.1" /db-xref="GI:72494094" /translation="MTNILEITNLSIADRFGNKL IQHVDLGLKKSKVNVLIGESGSGK SLTARAMVQQIPNTLDMQYDCMTYEHSEMSDMHN LLGKEIGFISQNYTHSFNDHTKLG KQLISIIYRQHYKTDKKGAKKIVEQALSWEVNPS QMMSKYRFSLSGGQLARVQIASVL MLNPKVIIADEPIASLDAVTGVSIMNLIKHLAEV HKVTLLLITHNLSHVLDVDFSDWIHV IKNGEMVESNHIDAFKNNNDVKPYSLKLFNSRSL KKGDYHA"
CDS	297597..298286	/locus-tag="SSP0271" /locus-tag="SSP0271" /note="similar to gi 27467978 ref NP-764615.1  [Staphylococcus epidermidis ATCC 12228], percent identity 46 in 230 aa, BLASTP E(): 2e-55" /codon-start=1 /transl-table=11 /product="putative ABC-type oligopeptide transport system ATPase component" /protein-id="BAE17416.1" /db-xref="GI:72494095" /translation="MLNLTDVSFSYKHEAILKKI QLSIQADEIVGIVGESGSGKTTLA KIMLGLLQPTHGEVITHKERVLPFIQHAVDSFNP KFKIRKSMEEPIKYQRRGESQKAA QRLSDLMAYMQLDTKLMDRLPEELSGGQLQRFNT IRTLMLEPDILICDEITASLDVIA EQRMIDILRHYYKTTHKGMILISHDLAFLNQIVN RFIVMKNGEIVDDFETKDLFNVTR HEYTKTLLSIY"
gene	298529..299440	/locus-tag="SSP0272" /locus-tag="SSP0272" /note="similar to gi 57286403 gb AAW38497.1  [Staphylococcus aureus subsp. aureus COL], percent identity 55 in 302 aa, BLASTP E(): 5e-91" /codon-start=1 /transl-table=11 /product="putative ferrichrome-binding lipoprotein precursor" /protein-id="BAE17417.1" /db-xref="GI:72494096" /translation="MKKLIFPLLALMLILAACGN NSSDDASKKDKKEKTYTQDSGKKV KIPKDPKRIVVLGATYAGGLKELDANIVGVANIV DDSKVLKDKFKDVKVDAENVESV"
CDS	298529..299440	

gene	299742..300155	AKLKPDLIITYNTDKNLKKLNKVAPTIAFDYMKH DYKEQHKELGKIVGKEDKAEDWIK DWEKTKDDGNEIKDAIGEDTTVSIIKDFDKKIY ALGKTYGHGSEILYDSFGLKMPEK VEKATKKNDLADISEEQIPEMSGDYVVTTPVAKGA DLSFENKDIWKNTAVKNGKTFKV DEGIYWLNDPYSLDYERKDLKEKLLNH"
CDS	299742..300155	/locus-tag="SSP0273" /locus-tag="SSP0273" /note="similar to gi 54022168 ref YP-116410.1  [Nocardia farcinica IFM 10152], percent identity 31 in 114 aa, BLASTP E(): 2e-11" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="BAE17418.1" /db-xref="GI:72494097" /translation="MKKQQKIDNWVQLTKYVNYI DTMIEKKLKQEYNLSVKEFYVLYE IYKAKGKKYKINDLIKIVDLSQSAMSRLIVRIEK PTKALVVRQECLEDHRAMYIYLTE EGQDITEKALNTYESLISKVSFSNIRKLSQIDSI D"
gene	complement(300295..3017 22)	/locus-tag="SSP0274"
CDS	complement(300295..3017 22)	/locus-tag="SSP0274"  /note="similar to gi 57286524 gb AAW38618.1  [Staphylococcus aureus subsp. aureus COL], percent identity 80 in 472 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="putative amino acid transporter" /protein-id="BAE17419.1" /db-xref="GI:72494098" /translation="MKGFFNKILKREDPSVYQVK DAHLNRTL RVKDFLALGVGTIVST SIFTLPGVVAQHTGPAVALSFLLA AVVAGLVSF AYAEMSSAMPFAGSAYSWINVVFG EVFGWVAGWALLAEYFIAVAFVASGFSANLRGLV SPLGIELPKSLSNTLGT DGGIIDI VAAVVILLTACLLSYGVSAARIENILVVIKVLA VLLFIVVGLTAIDL SNYPFIPEH KVTETGSFGGWQGIYAGVSMIFLAYIGFDSIAAN SAEAINPQKTMPRGILGSLAIAVI LFVAVSLVLVGMFTYSAYADNAEPVGWALRQSGF GVVAAIVQAISVIGMFTALIGMML AGSRLLYSFGRDGLLPSWLGKLNKKNLPNRSII LTVIAVIIIGSMFPFAFLAQLISAG TLVAFMFV SIGIFGLRPREGKDIPMPAFKMPFYF VMPITTFVSVVVVFWGLGAEAKLY TLIWFIIGLLIYLLYGVKHKKRQS"
gene	302176..302556	/locus-tag="SSP0275"
CDS	302176..302556	/locus-tag="SSP0275" /note="similar to gi 57286497 gb AAW38591.1

		[Staphylococcus aureus subsp. aureus COL], percent identity 46 in 123 aa, BLASTP E(): 3e-23" /codon-start=1 /transl-table=11 /product="putative glyoxalase" /protein-id="BAE17420.1" /db-xref="GI:72494099" /translation="MNIQSSWLNLPVKDLKASAT FFENIGFTIKKNEAVLDMRGIET ADHKIIMLIEQQGFQKVAQQSDIVRHEALVSVSV KEAAEVDDLNNHVETAGGKVLQRG TKHEGFYGGFLSDIDGHLFNIIAM" /locus-tag="SSP0276" /locus-tag="SSP0276" /note="similar to gi 16799517 ref NP-469785.1  [Listeria innocua Clip11262], percent identity 48 in 269 aa, BLASTP E(): 8e-69" /codon-start=1 /transl-table=11 /product="putative hydrolase" /protein-id="BAE17421.1" /db-xref="GI:72494100" /translation="MIKAIADVKGDTFLKSDHTY DKAYFNRLYQKIVQQNIKFIVASG NQYQQLRSFFPDKVDNITFVAENGAVTYQNDALL TAHYFDQQQLIFEVLEMIHQTYHIS DVVLSGIHSAYVSDSSDEFLNFIRNYYYDIKKV ASFNEITEDHFKIALRIKDEDLV KQVTNEIEQRYKGRIRAVTSGNDSVDLILPSVKN GVAIKELLKEWDIQQDELLAFGDA NNDLEMLGLTIHSYAMANCSDLAIAKHRAPSN DESGVLQVIERYLQQ" /locus-tag="SSP0277" 15) complement(303493..3039 /locus-tag="SSP0277" 15) /note="similar to gi 27467028 ref NP-763665.1  [Staphylococcus epidermidis ATCC 12228], percent identity 41 in 144 aa, BLASTP E(): 6e-27" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17422.1" /db-xref="GI:72494101" /translation="MYKKILLAYDFDNSFNVPK ELENLTNGVENAEVTVFNVIPESE LETSVRYDNKHFEDLANEKNEVLSPFIQQLALD LTVTVKFSAGYIKQAILTEVKENA YDIIVMSNTREKSDIKNILGNVTHKIASNVDPV LIVN" /locus-tag="SSP0278" 92) complement(304025..3050 /locus-tag="SSP0278" 92) /note="similar to gi 15925579 ref NP-373113.1
gene	302607..303410	
CDS	302607..303410	
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CDS	15) complement(303493..3039	
	15)	
gene	complement(304025..3050	
CDS	92) complement(304025..3050	
	92)	

		[Staphylococcus aureus subsp. aureus Mu50], percent identity 71 in 353 aa, BLASTP E(): e-151" /codon-start=1 /transl-table=11 /product="putative dihydroorotate dehydrogenase" /protein-id="BAE17423.1" /db-xref="GI:72494102" /translation="MYKLIKPMFLQFDPEKAHGM TIDALKFVQNHPKLLPVIKKIFHY ENDSLQNQLKGIHFANPIGLAAGFDKSCEVPKAL ENAGFGSIELGGITPKPQPGNPKP RMYRLVEDQALINRMGFNNLGMNKALSYLRKHRY QIPVGLNVGVNKSTPYEARIEDYI KVIDTFKNDVTFFTVNISSPNTENLQSFHDKDEF SQLCEAIQTYKYKESLNVPFIKIL TSDLSLDGLGAMLTPIQTDFDGIILANTTQQREA LHSNHREETGGLSGKPLFERNLKL ISYAYKQTDGQFLIIGTGGIFNAEDVIKMMRQGA SLVQIYSALVFEGPGLTQKLNKQL AHYLKSNNGYNNVNEIIGLDVK" /locus-tag="SSP0279" /locus-tag="SSP0279" /note="similar to gi 49487367 ref YP-044588.1  [Staphylococcus aureus subsp. aureus MSSA476], percent identity 71 in 283 aa, BLASTP E(): e-117" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17424.1" /db-xref="GI:72494103" /translation="MNQAWQSQLPLSHIKNIVPV SGGDVNDAFRIETDQEDYFLLVQR KRKSTFFDAEIAGLNLFKVGITAPRVIDSGEIE DDAYLLLTYLDEGVSGSQEALGQL VARMHSEQQADNQFGFDLPYEGGDISFDNSWTNS WITLFVEKRLDKLKDRLVQQGLWG DADVTQYQAVRRVIVNELESHNSKPSLLHGDLWG GNYMFLTDGSPALFDPAPLYGDRE FDIGITSVFGGFTQAFYDAYHKHYPLSEGADVRL EFYRLYLLMVHLVKFGEMYAGSVD RSMQKILNQ" /locus-tag="SSP0280" /locus-tag="SSP0280" /note="similar to gi 57286496 gb AAW38590.1  [Staphylococcus aureus subsp. aureus COL], percent identity 69 in 72 aa, BLASTP E(): 1e-23" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17425.1" /db-xref="GI:72494104" /translation="MTLLDRINELANKEKIETLS
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CDS	305344..306201	
gene	complement(306535..306768)	
CDS	complement(306535..306768)	



		IEEKEEQQTLRQEYLMIRGQVIH TFSTLKVVDPLGEDVTPDKVYQLREEMGTLDID"
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CDS	complement(306746..307723)	/locus-tag="SSP0281"
		/note="similar to gi 26989208 ref NP-744633.1  [Pseudomonas putida KT2440], percent identity 42 in 312 aa, BLASTP E(): 1e-64" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17426.1" /db-xref="GI:72494105" /translation="MTTIQKHNGFKRTFQQGHLT LGLMLPFDNSENIALSFENQVDLA QYAENLGFSTSLFVRDNPLYSPHLGNVTNNYDPFV FLSYLSAKTSKIALGTSSIVATLR HPIHTAKAATSLDLISDERFLLGLATGDRPFEPF AFKIKETQLSKQFQDAIYAMNDLW QSHSPKISNSIFELYEDSGLQILPKHNHIMPAT GYSRQELSWIKKNMDGLMFYPQPF QKQKALLKEWHNNDVFKPFMHPLVIDLSLNPNEL VKPIKGGYRLGRNTLLNILKSYEK IGTNHMMHLTSDNRPYKSLLETEVDYIIPHFPP HLSQEEKNNIDITRQN" /locus-tag="SSP0282"
gene	307968..308750	/locus-tag="SSP0282"
CDS	307968..308750	/locus-tag="SSP0282"
		/note="similar to gi 9968803 emb CAC06168.1  [Staphylococcus warneri], percent identity 44 in 264 aa, BLASTP E(): 4e-56" /codon-start=1 /transl-table=11 /product="glutamyl endopeptidase precursor" /protein-id="BAE17427.1" /db-xref="GI:72494106" /translation="MLKRKLRGGLIFIIALLCTV ISINGNTYAATQTHQSTDQSAQSE DAKVGTNQIKTRVVLPNDDRTQIENTTNGHYQSV GYISIGDNIATGVVIDKNTVLTK HVANLSEGNMNFSPAAQNENTMPYGTTFSEKEIEV YPGNEDLALIHLNKNKDEQSVGDV VQPATLKDASAVTKDMPITVTGYPGDKSLATMWE SKGQILNTNTTEFEYNASTFGGNS GSPVFNENNEVIGIHQGGIEGESNSAVAMTDDVL SFINKNKS" /locus-tag="SSP0283"
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		/transl-table=11 /product="putative transcriptional regulator" /protein-id="BAE17428.1" /db-xref="GI:72494107" /translation="MTTTHVDPRVTRTKLLMDA FREIAKEKKLQTITIKDITERATV NRATFYAHFYDKYDIMDYTLSETVLKKNLNDALDV SSELNETTLSSSFITITSYIQETH NECKLNSEAYGQVVEKRVKEELEDIFLTLLVQQH PNETRESLAASARFLSWGlyGTAK HWFHSSQLSANDYIEGALPFLMKQILK"
gene	complement(309542..310294)	/locus-tag="SSP0284"
CDS	complement(309542..310294)	/locus-tag="SSP0284"
		/note="similar to gi 45358682 ref NP-988239.1  [Methanococcus maripaludis S2], percent identity 46 in 239 aa, BLASTP E(): 1e-62" /codon-start=1 /transl-table=11 /product="truncated conserved hypothetical protein" /protein-id="BAE17429.1" /db-xref="GI:72494108" /translation="MIWSTLGFVFFYMPITFVAN YSPGWLISATWQLTIICGLLLAPL FYEYVQINHQQIKVRERISWRSVGTSSIMVLGVV LVQIPQVSHIEIQVFIMSVLPLII GAFICYPLGNRKMMLVDNQLNTERIYGMTLVTL PIWVVIFICGVLKSGPPSSNQLLQ TFIVAVFSGIITTLFFYATNMVKHNQAKLGAVE STQATEIIFTLIGEMLLLDLPLPS TVSMIGIIITLGIIFIYSFMNSIIKENNNMTL"
gene	complement(310347..310505)	/locus-tag="SSP0285"
CDS	complement(310347..310505)	/locus-tag="SSP0285"
		/note="similar to gi 16078291 ref NP-389108.1  [Bacillus subtilis subsp. subtilis str. 168], percent identity 63 in 44 aa, BLASTP E(): 3e-08" /codon-start=1 /transl-table=11 /product="truncated conserved hypothetical protein" /protein-id="BAE17430.1" /db-xref="GI:72494109" /translation="MRAILIGILGALFFSVTFIL NHAMAKDEGNWLFSASLRFFIYVP HTFYNYIH"
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CDS	310801..312078	/locus-tag="SSP0286"
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CDS	312137..313084	/locus-tag="SSP0287" /note="similar to gi 57286688 gb AAW38782.1  [Staphylococcus aureus subsp. aureus COL], percent identity 74 in 311 aa, BLASTP E(): e-135" /codon-start=1 /transl-table=11 /product="putative inosine-uridine preferring nucleoside hydrolase" /protein-id="BAE17432.1" /db-xref="GI:72494111" /translation="MSKKIIMDCDPGHDDAIALI LAGAQNSPLDILAVTTVAGNQSV KNTKNALNVLEVMGRDDISVSVGATRPLIKPAS ASQIHGDSGLDGPKLPEVPALKPT QKQAVDVIIETLKQSKEPVTLVATGPLTNIATAL IKEPNITQHIESITIMGGGTFGNW TPTAEFNIWVDAEAAKRVFECGVCINVFGLDVTH QVLATDHVIDRFKQIKNPIANFVV ELLEFFKSTYKTHFDMGGPIHDACTILYLMQPD LFTMQHTHIDIEHQSPITYGTMSV DLNDIMNKEKNAYFATAVDVASAWTLMENMLASY EKHTH"
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CDS	313270..313854	/locus-tag="SSP0288" /note="similar to gi 15923202 ref NP-370736.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 58 in 188 aa, BLASTP E(): 1e-59" /codon-start=1 /transl-table=11 /product="putative peptidase" /protein-id="BAE17433.1" /db-xref="GI:72494112" /translation="MKNVMKWIVLLIIIIIVPLTW LILNINDIKENMNETFTTQNQDAD QGESEDSFSKFFDGSRETENFGGEYEFSEFDGKHY GIDYHLPEDTPIKAAADGKVTRTF DDD LGGKVIQIAESNGEYHQWYMH LNEFKVEVGD DVKAGDTIALSGNTGEQTTGAHLH"

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FQRMEEGGVGN DY AIDPKDYVEDLPNGEESLFEVE
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95)
CDS       complement(314030..3146 /locus-tag="SSP0289"
95)
          /note="similar to
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          [Bacillus halodurans C-125],
          percent identity 34 in 204 aa,
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          VLF AVRNGQLNFEQLYKMDDNSVINALTQIKGIG
          RWTAEVFLFLTQRKNILPIYDVG
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CDS       complement(314706..3150 /locus-tag="SSP0290"
59)
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          aureus MRSA252], percent identity
          70 in 118 aa, BLASTP E(): 1e-42"
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gene      315191..315619 /locus-tag="SSP0291"
CDS       315191..315619 /locus-tag="SSP0291"
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          percent identity 29 in 148 aa,
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gene	317703..318434	/locus-tag="SSP0293"
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CDS	318702..319859	/locus-tag="SSP0294" /note="similar to gi 57286483 gb AAW38577.1  [Staphylococcus aureus subsp. aureus COL], percent identity 73 in 384 aa, BLASTP E(): e-169" /codon-start=1 /transl-table=11 /product="putative aminotransferase" /protein-id="BAE17439.1"

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gene	319885..320883	/locus-tag="SSP0295"
CDS	319885..320883	/locus-tag="SSP0295" /note="similar to gi 21284209 ref NP-647297.1  [Staphylococcus aureus subsp. aureus MW2], percent identity 63 in 332 aa, BLASTP E(): e-123" /codon-start=1 /transl-table=11 /product="putative D-specific D-2-hydroxyacid dehydrogenase" /protein-id="BAE17440.1" /db-xref="GI:72494119" /translation="MTRIKLFGVRNEDKAFIEAW SNKHKVEVDLDEDLLTCETVSRVK GFDGVSISQQIPLDETIYKQLHDFGIKQIAQRSA GFDIYDFELAEKYNLIISNVPSYS PHSIAEYTVSQALNLVRNYNDIQKTAEYDFRWQ PDILSRSIRDLKVAVIGTGRIGSI VAKIFAQGFDAEVTAYDIAPNDDYRSFLTASTI NEAIQNADIVTVHIPASKENDYLF DETLFNEFKPGSVF INCARGTIVKTSALIDALDR GLIKGAALD TYEGEKGLFPSDQRH TAFNDDMLKQLIERPDVIVSPHIAFYTDAAVENL IVDALDATMEVIKTGDTRLRVN"
gene	complement(320934..321140)	/locus-tag="SSP0296"
CDS	complement(320934..321140)	/locus-tag="SSP0296" /note="similar to gi 57286481 gb AAW38575.1  [Staphylococcus aureus subsp. aureus COL], percent identity 65 in 67 aa, BLASTP E(): 6e-19" /codon-start=1 /transl-table=11 /product="putative copper chaperone" /protein-id="BAE17441.1" /db-xref="GI:72494120" /translation="MATETIQVEGMSCDHCKHAV ETALTELDGVSTADVSLEAGNVKV DFDDDKVTMPQMKDAIEDQGYDVK"
gene	complement(321186..323570)	/locus-tag="SSP0297"
CDS	complement(321186..323570)	/locus-tag="SSP0297"

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73 in 795 aa, BLASTP E(): 0.0"
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96)

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		SSIMHRMKKNALSLTIIATISAVTVTVLCFGAIS
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gene	complement(329318..329587)	
CDS	complement(329318..329587)	/locus-tag="SSP0302" /note="partial similar to gi 49398117 ref YP-031716.1  [Staphylococcus aureus subsp. aureus MSSA476], percent identity 51 in 82 aa, BLASTP E(): 8e-19" /codon-start=1 /transl-table=11 /product="truncated hypothetical protein" /protein-id="BAE17447.1" /db-xref="GI:72494126" /translation="MLLTVAFFSFDFKDFRNPLL KKETSYAIVKLNLTQYYQDL SIYSK QGEKRSYKVSFNGYNPSEQYVKLKHKGTYVEHIE YIIKQSFPSLK" /locus-tag="SSP0303"
gene	complement(330076..330282)	
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gene	complement(330419..331840)	
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gene	331996..333192	
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gene	336273..336854	DISTEVAAYRIYQYGELIETRANV DDLYTDDMVSFLIGCSFTFEHALLEAGIPIRHLE ENHNVPMYVTNIPANPSGQFKGNI TVSMRPMTMTQAIKATEITTRFKNVHGTPIHIGN PTEIGITDLALPDFGEPVTINENE VPVFWGCGVTPQSVALDAKPDLMITHAPGHMFIT DIPDSQLSD"
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gene	complement(336965..338035)	/locus-tag="SSP0310"
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gene	338276..339820	/locus-tag="SSP0311"
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gene  
CDS

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LVALFKYYFTNVQIVLNVDIGKLEAPHKAKRILE  
QSDSIVDRIAFSANQNDMIDFQSI  
ESQQYELAKRHIYEQFNKVVETLELQQSSISFIL  
LNWNTLTGDTHLTNGEYFRAGIIF  
EQLIEMNDRIQMIGYWLNYELHEQFKLDSSAQL  
TGIELYHQFDGKRPAFFTSAFYRK  
LFDQVLYQSENCMVVGSPDHFQIVMWDAEHYNPY

gene	345996..347393	YILNHHAQYLNHKEYQINIINAH PTYKIKHMTLDKNNGALYTVWQHYNTRYGMDEET IAYVNRISYPKMDISEVKVNDTIT YHLKLLTNAIQIIEFKKYLC"
CDS	345996..347393	/locus-tag="SSP0315" /locus-tag="SSP0315" /note="similar to gi 49484983 ref YP-042204.1  [Staphylococcus aureus subsp. aureus MSSA476], percent identity 70 in 457 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="putative permease of the major facilitator superfamily" /protein-id="BAE17460.1" /db-xref="GI:72494139" /translation="MTQQGNTQNYKGDNKLILGI VLGVVTFWLFQAQSLNVVPTLQQS FDSNIGTISIAVSITALFSGMFVVGAGSLADKVG RVSITYIGLWLSIIGSLLIIISNL PLLLIVGRVIQGLSAAAIMPSTLAIMKTYFEGKE RQRALSYWSIGSWGGSGLASLFGG MVATFVGWRWIYILSIIIALAMYLIKGPETKS ESTLKQRFDYSGILFVIMMLSIN VVITQSGTFGITSPILGLIIIFIVATIIIFLKVE NRVGNPLIDFKLFNNKAYTGATLS NFLNGVAGALLVANTFVQQGLGFNAFQTGLLSI TYLITVLLMIRVGEKVLQKVGAKK PMLLGTLFNMVGIMLISLTFLPSVIYVVVCIIGY LLYGLGLGFYATPSTDMAISNSPE DKVGVASGIYKMASSLGGAFGIALSGALFGVIAS ATNVQIGAFAGLWLVNIMALLSLI IIMFMVPATKTKAKC" /locus-tag="SSP0316" /locus-tag="SSP0316" /note="similar to gi 15923092 ref NP-370626.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 76 in 391 aa, BLASTP E(): e-176" /codon-start=1 /transl-table=11 /product="putative metal-dependent amidase" /protein-id="BAE17461.1" /db-xref="GI:72494140" /translation="MVKQLIDILKNKESRMIEIR RYLHEHPELSFHEEETPKYIEAFY KDKDCEVETNVGPNGLKVTIDSGKPGKTIAIRAD FDALPIQEDTGLSFSSKNDGVMHA CGHDAHTAYMLILAETLIELKSQFKGVVIIHQ AEEVPPGGAQAMIQDGVNLGVVDHV LGVHVM SHMPAGNIYYREGYVQTGRDFFKLKVNG QGGHGSSPHTANDSIVAGAHFVNA VQTIVSRRLNPFETGVVTIGSFDGKGQFNVIKDS IEIEGDVRALTD DTKHTIKKEIQR LTEGLEATFGVTCELDYHDDYPALYNDPEFTQFV VDSIQSADTDAIQKVERCEAQQPS EDFAYYAKALPSTFIYAGAAPEDGNIYPHHPKF NISEKALRVSAEAVGVTVMNYLK" /locus-tag="SSP0317"
gene	347483..348658	
CDS	347483..348658	
gene	348919..349383	

CDS	348919..349383	/locus-tag="SSP0317" /note="similar to gi 27469030 ref NP-765667.1  [Staphylococcus epidermidis ATCC 12228], percent identity 51 in 153 aa, BLASTP E(): 7e-41" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17462.1" /db-xref="GI:72494141" /translation="MNGDKKISELLDNYKKPLKK LFKYDKSKARAFDKDSRSKVEGQK GIFVIFNNKQPIFVGQVGGYMTGYKITQKDLNDK LGQFNVKSDSGTARFRRVFAEQNS LDEAETKEIKAENYGLKFQFIKVKGNPSMINILE ILALEYAKENDINLYNFL"
gene	349426..350118	/locus-tag="SSP0318"
CDS	349426..350118	/locus-tag="SSP0318" /note="similar to gi 52078856 ref YP-077647.1  [Bacillus licheniformis ATCC 14580], percent identity 31 in 237 aa, BLASTP E(): 1e-25" /codon-start=1 /transl-table=11 /product="putative esterase" /protein-id="BAE17463.1" /db-xref="GI:72494142" /translation="MSIRELSLSFHHQEIKIKLP KNYFKTNGKSYPLVIVQDGDYLFK DVKKDVIFVGIVPNNRKKDYTPWKS VVGDI EYGG QADAYITWVADAVIPYLRKCFRIS QDRKDIGIAGASFGLVSLYALFKHADTFGHYIL ISPSVWYPDFVKFMKSQPIINSTH HIYWYVGQLEGKQSNHLNQYMVPQTEAAVDILNE LLVSETSVFYFDTNRKGLHRQYYF KKYFNRAINKLF"
gene	350589..351005	/locus-tag="SSP0319"
CDS	350589..351005	/locus-tag="SSP0319" /note="similar to gi 27467114 ref NP-763751.1  [Staphylococcus epidermidis ATCC 12228], percent identity 56 in 138 aa, BLASTP E(): 2e-40" /codon-start=1 /transl-table=11 /product="putative truncated permease of the major facilitator superfamily" /protein-id="BAE17464.1" /db-xref="GI:72494143" /translation="MTRIALILSIIGSLMLIISG NVTLLLLGRIVQGFSAIIMPATI SIVNDFEFGDDRQKALSFWSIGAFGGTGLSSFFA GAMATFISWQSIFVLSILLSLVAL LLVKNLPESKQVKAQSNHFDYIGLTIFVIMIASI SL"
gene	351053..351766	/locus-tag="SSP0320"
CDS	351053..351766	/locus-tag="SSP0320" /note="similar to gi 27467114 ref NP-763751.1



		[Staphylococcus epidermidis ATCC 12228], percent identity 46 in 224 aa, BLASTP E(): 1e-50"
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		/transl-table=11
		/product="putative truncated permease of the major facilitator superfamily"
		/protein-id="BAE17465.1"
		/db-xref="GI:72494144"
		/translation="MSAVFIICIFIFYKVEKAKQ SPFIDLELFKNKPFIGAVIANFLL NTGVGVIALFNIYAQGGLKFSAFQAGLLTLPYLI TLLLVVRLGEKSIKRFGAKRAMVV GPIFTATGILLFSLTFFNTSIYVVVALIAAVFFG GGTGLFARPALSTAVSTTPAEKVG VASGIFKMSSTLGGAFGIAIMTSIFTGVSQSQGT VDTAASIGFVVGTCLVIGGVCASA LVIPTRKVRQGEKGQVTEG"
gene	complement(351863..352135)	/locus-tag="SSP0321"
CDS	complement(351863..352135)	/locus-tag="SSP0321"
		/note="similar to gi 52081185 ref YP-079976.1  [Bacillus licheniformis ATCC 14580], percent identity 50 in 56 aa, BLASTP E(): 4e-09" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17466.1" /db-xref="GI:72494145" /translation="MSKFKQSSKHLNLSFHQIQ ASDRITAIYKALYQFNDVVLGLVFL IGSILFFNSSTVTNGTILFVIGSIQMTIRPLIAF VHDLHLAFKRKQ"
gene	352256..352789	/locus-tag="SSP0322"
CDS	352256..352789	/locus-tag="SSP0322"
		/note="similar to gi 49484748 ref YP-041972.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 54 in 177 aa, BLASTP E(): 1e-49" /codon-start=1 /transl-table=11 /product="putative 6-O-methylguanine DNA methyltransferase" /protein-id="BAE17467.1" /db-xref="GI:72494146" /translation="MHYKSNYQSPIGQIALTSDG ENITGLWLPNHKDFETQYKDELMT ADLPIFDKAKRWLDAYFSGNNPKIDFPLKATGTS FREQVWQILLEIPQGETWTYGEIA QKIAEKRGAEKMSQAVGGAVGSNPISIIIPCHR VVGKDGSLTGYGGGIDTKIELLKL EGLDMNVFYRPHKSTKP"
gene	352935..354512	/locus-tag="SSP0323"
CDS	352935..354512	/locus-tag="SSP0323"
		/note="similar to gi 27467949 ref NP-764586.1

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[Staphylococcus epidermidis ATCC
12228], percent identity 66 in 520
aa, BLASTP E(): 0.0"
/codon-start=1
/transl-table=11
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transporter"
/protein-id="BAE17468.1"
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/translation="MLKEKKGFSSVFIYSTAVIG
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SETFGWYYMLLYTVILGFCIFVLFSPIGKLKLGK
PKDKPEFKTVSWLAMLFSAGMGIG
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FIDYGFHPWAVYGIVALGLAYSQF
RKGENGLISRTLRLPILGDKVDGPIGNIVDILAVF
ATVIGVAVSLGVGAIQINGGLHYL
FGVPSNSVVQGIIIAIVTVLFLYSAWSGLSKGIQ
YLSNLMVLAAILLIVIFVVGPTL
LILNMMTSGTGDYLSLVFNSLDVAPLNEQKSEW
LQSWTIYYWGWMSWSPFVGTFIA
RISKGRSIREFIIAVLGVPVVISIIWFSAFGVTG
ITVGQSHSSILKMPPETQLFGIFN
ELPFGFILSIVALALIASFFITSADSATYVLGMQ
TAYGTLNPSGFIKIVWGLALAAIA
YVLLLAGGDTGLSALQSAIIISALPFSVVVFLMM
VSLYKDANSERKALGLTLKINEKR
SETYTKLIEEENRKRYE"
gene      complement(354768..3559 /locus-tag="SSP0324"
37)
CDS      complement(354768..3559 /locus-tag="SSP0324"
37)

/note="similar to
gi|9937368|gb|AAG02427.1|
[Staphylococcus haemolyticus],
percent identity 77 in 386 aa,
BLASTP E(): e-175"
/codon-start=1
/transl-table=11
/product="3-hydroxy-3-methylglutar
yl CoA synthase"
/protein-id="BAE17469.1"
/db-xref="GI:72494148"
/translation="MTVGIDQINFYVPRFYVDMA
KLAESRQVDPNKYLLGIGQTEMSV
SPMSQDIVSMGANAAKAIVTDEDKKQISMVIVAT
ESAIDSAKASAVQIHNLLGIQPF
RCIEMKEACYAATPAIQLAKDYLAQRPDEKVLVI
ASDTARYGLHSGGEPTQGAGAVAM
MISQNPRIELNDDAFAFTEDVYDFWRPSGQSY
LVDGALSKDAYIRSFQESWQEYAR
RYNKSLADFKSLCFHVPFTKMGKKALDSILTDDI
DAETKERLTSGYDAATYYNRYVGN
IYTGSLYLSLISLLETHDLSANDTIGLFSYSGS
VGEFFSGKIVEGYQDVLDIQGHKD
LLNNREEISVETYESFFNRFNLEFDHETELENE
KNTIFYLESINDHIRNYNTLN"
gene      356042..357193 /locus-tag="SSP0325"
CDS      356042..357193 /locus-tag="SSP0325"

/note="similar to
gi|9937369|gb|AAG02428.1|
[Staphylococcus haemolyticus],

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gene	357196..358479	percent identity 74 in 381 aa, BLASTP E(): e-159" /codon-start=1 /transl-table=11 /product="acetyl-CoA acetyltransferase" /protein-id="BAE17470.1" /db-xref="GI:72494149" /translation="MNKIAIVSAKRTPIGRFKGK LSHYSAVELGKTKLEAAIKAINLD SQNIEQVIYGNVLQAGNGQNPARGIAINAGVPNT TPAMTINEVCGSGLKSIILGKQLI QLGEAKVVAVGGVESMTNAPQLILNDSETPVDSF MHDGLTDAFMNVPMGITAEKIAEK YDVTREAQDAFANESQLKAHQATQAKKFENEIVP LEDVNGDWMTTDEGIRGNSSVEKL STLKTIFKEDGTVTGGNASSINDGASTIILMDEV YAKENGFEILAFVGAHAEIGCDPE LMGYAPYHAVTKLLNQADKAIEDFDVEMTEAFA AQSIPVSKNLGIAEEQLNLYGGAI ALGHPIGASGTRLVTTLVNILTQEDKQTGIATAC IGGGLGIAIAIEREV" /locus-tag="SSP0326"
CDS	357196..358479	/locus-tag="SSP0326" /note="similar to gi 9937370 gb AAG02429.1  [Staphylococcus haemolyticus], percent identity 80 in 425 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="3-hydroxy-3-methylglutar yl-coenzyme A reductase" /protein-id="BAE17471.1" /db-xref="GI:72494150" /translation="MEALDKSFRHLSREDKLNLT VQKGWLNEENKNTLLNNPLIPEEI ANSLIENVIGQGTLPVGLLPEIIVDDKSYVVPMM VEEPSVVAASYGAKLVNQTGGFK VISSERLMIGQIVFDGVSDTEILSQQIYNLETQI KQIADEVYPSIIERGGGYRKIDID TFPNEGLLSLKVSVDTKDAMGANMLNTILEGITA YLNELKDVDILMSILSNHATASV VKVQGEITVDALSKGDRDGEAVAKRMERASVLAQ VDIHRAATHNKGVMNGIHAVVLAT GNDTRGAEATAHAYASKDGQYRGLATWKYDEERQ TLVGTIEVPMTLATVGGGTKVLPI AKASLDLMKVDSAQELGHVVAAVGLAQNFAACRA LVSEGIQQGHMSLQYKSLAIVVGA QGEEIAQIADMLKTQPRANTAVAQQLLDELRLQK Q" /locus-tag="SSP0327"
gene	358668..359642	[Staphylococcus aureus subsp. aureus MRSA252], percent identity 73 in 323 aa, BLASTP E(): e-141" /codon-start=1 /transl-table=11 /product="Drp35" /protein-id="BAE17472.1"
CDS	358668..359642	

		/db-xref="GI:72494151" /translation="MDSNELPVLAYKDGENSEVAP IPAHEQQQLPTVTAEPWLEISKQGL QLEGLCFDRQGNLLLCVFGGTIFHVNLPDKKVT ELFKSHKQNPAAVKIHKDGRLFVC YLGDFESTGGIFMVDADGNDAQDIVSDIGTEYCI DDPVFDSKGGFYFTDFRGYSTNLK GGVYYVSPDFKSITPVIQNLAVANGVALSTDEKT LWVTETNANRLHRIDLLEDGVTIA PFGASIPYYFTGHEGPDSCCIDSDNLYVAMYGQ GKVLFVNKKGSPIGQILMPGRDQG HMLRSTHPAFIPGTDQLIICANDIENDGGSWIYT VKAFAKGHQSYQFH"
gene	complement (359873..360304)	/locus-tag="SSP0328"
CDS	complement (359873..360304)	/locus-tag="SSP0328"
		/note="similar to gi 27469026 ref NP-765663.1  [Staphylococcus epidermidis ATCC 12228], percent identity 61 in 143 aa, BLASTP E(): 8e-48" /codon-start=1 /transl-table=11 /product="putative secretory antigen precursor" /protein-id="BAE17473.1" /db-xref="GI:72494152" /translation="MNIKKKLVNVFIATTLMTG TVTFQAINESQTTNAAVNYYYKNQ CTWYVFKKRASVGKAVPNGWGNKYWYSKAKKAG YRVGKKPAKRAVMQSTSGTYGHVA YVETVYNNGSIKVSEYNYNRPLAYGTRVLSKSSA AKYNYIY"
gene	360487..361833	/locus-tag="SSP0329"
CDS	360487..361833	/locus-tag="SSP0329" /note="similar to gi 30018581 ref NP-830212.1  [Bacillus cereus ATCC 14579], percent identity 66 in 422 aa, BLASTP E(): e-166" /codon-start=1 /transl-table=11 /product="Na+ H+ antiporter" /protein-id="BAE17474.1" /db-xref="GI:72494153" /translation="MSNYHLLIGTAVAILVTLIH GYEFSEVEEMMYKGIRHALPAIVI IILVGLVIGSWIGSGVVATMIYYGLQLIDPRYFL VVVVILCGIVALAIGSSWSTMATV GVASMGIISMGISAGMVAGAVICGAYFGDKMSP LSDTTNLAAGLTGVDLFEHIKHM YTTIPALIIISLVAFFIIIGHRFGTKNFDTKNINAI LDTMQNHFLITPWLLLIPLIVIAL VVLKVPAPAIACMGIVLGFFAQIFVQGGTITEAL TALQTGYTIDSGNKLVDLNFNRGG LESMFYTTISLTLVAMTFGGVLEYSGMLKALITQI LKIAKSTGTLIASVIVSCIGTNIT CSEQYISIIIVPSRMYINAFKEKELHPKNLSRALE DGGTLSSVFVPWNTCGVFIASLTG VSVIEYAPYAILNYTVPIISIIIFGYIGFKIVKLS NQDNEITNQPNKSTQTDANNA"

gene	362064..362939	/locus-tag="SSP0330"
CDS	362064..362939	/locus-tag="SSP0330"
		/note="similar to gi 27469024 ref NP-765661.1  [Staphylococcus epidermidis ATCC 12228], percent identity 65 in 291 aa, BLASTP E(): e-109" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="BAE17475.1" /db-xref="GI:72494154" /translation="MDIKHMKYFVEVVDQKGMTN ASKHLFIAQPTISKAIKDLEQELD MTLFDRSKRQLVLTDAGSIFYKKCKEILTLYNDV PKEINSLGLLETGHISIGLSAVMN MNQFINILGEFHQKYPNVTYSLVENGGKMIETQL INDEIDIGITTLPVDQSIFHSVTL YQEDLKLVLNKEHHLANETHVDMSMLKDEDFILF NEDFYLNDKIIEAAKNAGFIPNTI SKISQWNFIENLLNAHLGVSILPENIVHLLDSSF SNKTLEDPGMRWELGVIWKKDKYL SHATKQWIDFMKERL"
gene	363184..363579	/locus-tag="SSP0331"
CDS	363184..363579	/locus-tag="SSP0331"
		/note="similar to gi 49484742 ref YP-041966.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 60 in 123 aa, BLASTP E(): 3e-37" /codon-start=1 /transl-table=11 /product="holin-like protein" /protein-id="BAE17476.1" /db-xref="GI:72494155" /translation="MMLLQQFKKIITVLIQVLVI MGITYLGNVIQRYMHIPIAGSIVG LLLLFFLLQFKVIPAKWVNEGSNFFLTMTMVEFFV PSVVGIMDVVPMINLNFILFFSMI LLGTCCVALISGFIAEKMVKKNQDGNGVN"
gene	363580..364266	/locus-tag="SSP0332"
CDS	363580..364266	/locus-tag="SSP0332"
		/note="similar to gi 27469022 ref NP-765659.1  [Staphylococcus epidermidis ATCC 12228], percent identity 70 in 225 aa, BLASTP E(): 1e-86" /codon-start=1 /transl-table=11 /product="holin-like protein" /protein-id="BAE17477.1" /db-xref="GI:72494156" /translation="MLILEAIIMIILTIAMYIGA KKLQQKFQTPFLNPALIASIGIII VLLLFVRVDYKTYMLGGKWINYLLNCTVVCLAFPL YQNRHKILKYARVIFSSVLMAVML NFVVFVSILKLFGYSKETIVTMLPRSITAAVGIE VSHQLGGIDTITVMFIITTGLIGS ILGAYLLRLGRFRSSIAGKMTYGNASHAFGTAQA LDIDSETGAYSSIGMILTAVLSSI VLPILILFLY"

gene	364478..366220	/locus-tag="SSP0333"
CDS	364478..366220	/locus-tag="SSP0333" /note="similar to gi 57285235 gb AAW37329.1  [Staphylococcus aureus subsp. aureus COL], percent identity 75 in 579 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="pyruvate oxidase" /protein-id="BAE17478.1" /db-xref="GI:72494157" /translation="MGKIKANEALVKALQAWDID HIYGIPGDSIDAVVDSLRTDNI EFVHVRHEEVGSLAAASYTKLTGKIGVALSIGGP GVVHLLNGMYDAKMDNVPQLILAG QTDSTALGTAKFQETDISNMVDDVAVYKHQISEN DKDVFGIVNEAIRTAYEKKGVAVL ILPNNLLNNKVKDTTSKGVDTAPPARVAPKPRSV KKATKLINKSKRPVMLLGTGAKHA KDEVREFIEAFKIPTIVTLPAKGILADHPYNLG NLGKIGTKVSYQTIQDADLLIMVG TNPYVDYLPKKNIKAIQVDTNLENIGHRFVDNA GIIGDSKLALQQLTDSAKHVKNRD FLNKTLEKATWDSWMAKDMADSSSPIRPERLMD AINQVRTDDAIFSIDVGTSTVWST RYLNLTVNNKFIVSSWLGTMGALPGAIAAKRAY PNRQVVGIAGDGAFEMVMQDFATA VQYDLPMTIFVLNNQELSFIKYEQQAAAGELEYAI NFTDMDLAKFAESCGGVGYTLKDP NRIDEVVEEAMSQDKPTIVNVYVDPNAAPLPGKI VKDEAINYGKWAYRSITEDKKLDL DEIPPMSTAVKRFF"
gene	366554..367948	/locus-tag="SSP0334"
CDS	366554..367948	/locus-tag="SSP0334" /note="similar to gi 53771340 ref ZP-00183037.2  [Exiguobacterium sp. 255-15], percent identity 51 in 452 aa, BLASTP E(): e-141" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17479.1" /db-xref="GI:72494158" /translation="MGKHSFRHLRIKTPHTYALL LMIIIISSILTYLIPAGEYAREKK DGQTLVVPGSYEQVQHGVSFFDIFRAIPEGLMS GGEIVFYIFLVGGAFGIVHKTGAF ENGVNKAMQSLGKYKVLMIPLTMTIFSILGFSIG LAETIIIFVPIGIIIARTLGYDAL TGAAMVILGAASGFMGMLNPFTVGVAQTVAELP MFSGWGLRSIIYIFILIAAITTVM LYARKVKHDKTKSYVYELEQSEGHTVTSMHIARF TKRQASGLGLIVLAIILNVYGIFS YGWSFNEMSANFILAGLLAGFIGGLGLNGTFDAM IDGMKDILFGAMIVGFAKGIIIVIL ENGQVIDSIVYGMTLLNGVPSALVIIAMFILQF MLNFFIPSGSGQALTMTPLMVPIS DLLDINRQITVLAFAQYGDASNVLFPTSAILMGA LAVGKITYTQWLKFAWKIILTWVL

gene	complement(368198..369196)	ICCGMSIALIVGY" /locus-tag="SSP0335"
CDS	complement(368198..369196)	/note="similar to gi 2673748 emb CAA05973.1  [Lactobacillus casei], percent identity 49 in 332 aa, BLASTP E(): 2e-77" /codon-start=1 /transl-table=11 /product="transposase" /protein-id="BAE17480.1" /db-xref="GI:72494159" /translation="MDSYKHLTIEERERIFFLKA KGYSLRKIAKDICRSPSTVSRELA RNASSGSYNPTYAHNNYKCNKKKCGRKLKLSKI LFDKVKFLFLNQQWSPEQIANRLK SEGFHLAISYNTIYRAIYLGFLDPPKLSHGNGRC IRLLRHRGKTRHTKSHQENRGRIR ISYSIHDRPQIINDRERIGDWEADTVMGKTGKSC LVTLVDRKTGYLLCGKVPKKKSEF VKQKIVDLLGTLPNNKRLSITPDRGKEFSKHPEI TSELDNIPFYFPDPHSPWQRGRTNE NTNGLIREYIAKGIDIDNITEEQIEHYVYKLNTR PRKRFDWKTPAELFNDKVLHLI"
gene	369346..371334	/locus-tag="SSP0336"
CDS	369346..371334	/locus-tag="SSP0336" /note="similar to gi 27469020 ref NP-765657.1  [Staphylococcus epidermidis ATCC 12228], percent identity 81 in 658 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="glucose-specific PTS transporter protein IIABC component" /protein-id="BAE17481.1" /db-xref="GI:72494160" /translation="MLPVAILPAAGLLLAIGTAM QGESLQHLYLPFIQNGGIQSVAEMM TGAGGIIIFDNLPMIFAMGVAIGLASGDGVAAIAA FVGYLVMNKTMGAFHVSPPDNVND AASGYASVLGIPTLQTGVFGGIIIGALAAWCYNK FYNISLPSYLGFFAGKRFPIMMA TTSFILAFPMAWIWPSIQTGLNAFSEGLLDSNTG LAVFLFGFIKRLLI PFGLHHIFHA PFWFEFGAWKNAAGEMIHGDQRIFIEQIREGSKL TAGKFMQGEFPVMMFGLPAAALAI YHTAKPENKKVVAGLMGSAALTSFLTGITEPLEF SFLFVAPVLFVHAILDGLSFLIL YLLNVHLGYTFSGGFIDYVLLGVLPNKTQWWLVI PVGVVYAFIYYFVFRFLILKFKYK TPGREDKQAQFTNSSASELPFNVLKAMGGEENIK HLDACITRLRVEVKEKGKVDVAGL KALGASGVLEVGNMMAIFGPKSDQIKHMSLIM KGEITKPQETTVEESEEVEVHIE RASEVNIYAPGNGQVIPLSEVPDQVFAQKMMGDG VGFIPADGKIVAPFDGTVKTIPT KHAIGLESQGLELLIHIGIDTVKLNGEGFESFV

gene	371509..372054	ETDDRVHKGQVLMQIDLDYITAHA
CDS	371509..372054	PSTVTPLIITNLEDRQLSVEDVKDVTAEQLIIKV IDDK" /locus-tag="SSP0337" /locus-tag="SSP0337" /note="similar to gi 23024986 ref ZP-00064170.1  [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293], percent identity 39 in 170 aa, BLASTP E(): 8e-31" /codon-start=1 /transl-table=11 /product="putative acetyltransferase" /protein-id="BAE17482.1" /db-xref="GI:72494161" /translation="MNYRPAMNVMPNVSLIPPEL NMAETLYDLIKSNFSLSPFLDFI KEDVTVEDEKAYLKMMIQQHAKNKARLFMIYYEE TMIGTIDLHHIDQANYKAEVGYWI AEGYTGKQIVTKCVKQLCHYAFETLSLNKLTIMA DVNNIASCKVAEKAGFKFVATDYE DVFNGERFRDMNRYVLLKRDF" /locus-tag="SSP0338" /locus-tag="SSP0338" /note="similar to gi 48860785 ref ZP-00314694.1  [Microbulbifer degradans 2-40], percent identity 41 in 319 aa, BLASTP E(): 3e-54" /codon-start=1 /transl-table=11 /product="putative 1-aminocyclopropane-1-carboxylate deaminase" /protein-id="BAE17483.1" /db-xref="GI:72494162" /translation="MLHNKLDIANLNTPIQKLDQ LSDALGKNIYIKRDDYTGSEISGN KVRKLEYTMQYVLDHGYDTIITTGAITSNHRAT AALCAKCNVSYLVLRGEMAEYEGN LFLDAMLGAHIHIIIEPTSSREDAMDKLYKTFEGQ GKTPFLIPVGASDWIGTHGYVNAY NEIIKQQDELKVHFDSINVAVGSGGTYAGLWYGQ MINCETTQIIGYAVDQSAHTFKNK VIEIIKQLDETIQSYETITINDAYIGLGYGKATD EELQFYIDIAQKEGIILDPTYTGK AFRGLVHEIKSGAYDNQDNILFIHTGGLQGYTQE TRLRLQTMLHKIDLSLLK" /locus-tag="SSP0339" /locus-tag="SSP0339" /note="similar to gi 57285233 gb AAW37327.1  [Staphylococcus aureus subsp. aureus COL], percent identity 71 in 132 aa, BLASTP E(): 4e-50" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17484.1"
gene	372210..373196	
CDS	372210..373196	
gene	373322..373723	
CDS	373322..373723	



gene	373838..374164	/db-xref="GI:72494163"
CDS	373838..374164	/translation="MTERKLVAERNFEVNGYDID AMGIVSNIVYIRWFEDLRTDFINQ YMPYSDMMNQQISPILMNTAEYKTPITIHKPV GRCYLVKASKLRWEFEFEIESEDA VHCIGKQSGTFFDLQKKKVTRLPEVFQTILS" /locus-tag="SSP0340" /locus-tag="SSP0340" /note="similar to gi 57285232 gb AAW37326.1  [Staphylococcus aureus subsp. aureus COL], percent identity 67 in 107 aa, BLASTP E(): 1e-36" /codon-start=1 /transl-table=11 /product="thioredoxin" /protein-id="BAE17485.1" /db-xref="GI:72494164" /translation="MPKTLTSIEAFHEFIAEHRL VVIHIMRDHCSVCHAVLPQIAGIV NEFPDVPLGVINQSELEEIAGELSIFTVPVDLIY FNGKEMHRQGRFIDMQQFEHQTL MYKSMV" /locus-tag="SSP0341" /locus-tag="SSP0341" /note="similar to gi 15895774 ref NP-349123.1  [Clostridium acetobutylicum ATCC 824], percent identity 36 in 164 aa, BLASTP E(): 4e-26" /codon-start=1 /transl-table=11 /product="putative acetyltransferase" /protein-id="BAE17486.1" /db-xref="GI:72494165" /translation="MRIERICPNEAEALYNMCKK IDQETQYMLYLPDERSFDKDLSE DIKRNFIYIGVKTDDNQILGYLSVHISMLAKVRHI GYIVTGLINDLHQQGLATQMFNET IKWAQRKGLRRLELTVITSNKPAVNIFYEKLDFKI EGIKHESVFMEEHYFDELYMAMML NQD" /locus-tag="SSP0342" /locus-tag="SSP0342" /note="similar to gi 27469013 ref NP-765650.1  [Staphylococcus epidermidis ATCC 12228], percent identity 57 in 321 aa, BLASTP E(): e-107" /codon-start=1 /transl-table=11 /product="putative esterase" /protein-id="BAE17487.1" /db-xref="GI:72494166" /translation="MIRKIATIVGIGVATSYVYA KVKEKRSYKSFLLEEIIIRATKMKS SFLNVENAQQALEKVKDETKALYEGTDYYFNHN V QTTTVQESTVYIVNDNKDRQQPVV LYIHGGAWFQNPLKYHFDIDSLAGELGAKVIMP IYPKVPATYKETFTLLETLYTQL LKQVENPHQLTIMGDSAGGQIALSFAQYIKTLNL AQPSNIVLISPVLDTFSNPEAKI YEKIDPMLAIDGSKYFIKLWANGLDLTDWRVSP
gene	374595..375086	
CDS	374595..375086	
gene	375253..376227	
CDS	375253..376227	

		FGDIEGLGHITISIGTKETLYPDA VKLSNMLNARNIQHDFMPGYNLFHIHPIFPIPEK EQFIAKINKIIKQN"
gene	complement(376471..376791)	/locus-tag="SSP0343"
CDS	complement(376471..376791)	/locus-tag="SSP0343"
		/note="similar to gi 57285230 gb AAW37324.1  [Staphylococcus aureus subsp. aureus COL], percent identity 64 in 105 aa, BLASTP E(): 1e-33" /codon-start=1 /transl-table=11 /product="putative truncated permease of the drug metabolite transporter" /protein-id="BAE17488.1" /db-xref="GI:72494167" /translation="MLISGILMNFKAPIWQFTMS QIDISVILYLAFGIILGTAMAFFF FIKSLNYLSAKETTLFGTIEPVMAIVASALWLKW VFLPFQLLGIVLIILILALSLKK DKER"
gene	complement(376861..377379)	/locus-tag="SSP0344"
CDS	complement(376861..377379)	/locus-tag="SSP0344"
		/note="similar to gi 57285230 gb AAW37324.1  [Staphylococcus aureus subsp. aureus COL], percent identity 62 in 167 aa, BLASTP E(): 4e-56" /codon-start=1 /transl-table=11 /product="putative truncated permease of the drug metabolite transporter" /protein-id="BAE17489.1" /db-xref="GI:72494168" /translation="MKQQRFLGIILAILGASFW GLGGTVSDYLFKHQNIDINWYVTA RLISGLLLLTIFKILNPRQSIFIVFRNVTNTIQ LLIFSTLGMLLVQYAYMASINYGN AAIATLLQYIAPVYITLWFIIRKKETFKLFDVIA ILLTLTGTFLLLANGSLDSLMSVSS SSMIWGIISGLS"
gene	377483..378364	/locus-tag="SSP0345"
CDS	377483..378364	/locus-tag="SSP0345"
		/note="similar to gi 16077582 ref NP-388396.1  [Bacillus subtilis subsp. subtilis str. 168], percent identity 28 in 295 aa, BLASTP E(): 1e-32" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="BAE17490.1" /db-xref="GI:72494169" /translation="MYKGIIIEDNGEERIQYPDE YWRHIVLKTRLDQAFMEQIPIHWH SALQFVFVLRGKLTIRISDKNIVLNTGDGIFINS"

		NVVHEIQGLEHISEFYCWNIEIPN ISSYMEYKYL SYISQQAEMVPYIYL SHKNLSHHA LLACIESVGTIYQKQEAYFQLDIM TYFYKIVKWL MQYMKQQPTELTYHFDYRVKQMS YIHKHFQDKITLGHLSQNIY LSEA EAIRLFKKYVKQTPFEYLLRYRLEQSKSILDKDR LSTITEIAMACGFSTTSYFIKVKF ARYGMPKQYQKYHHTN"
gene	complement (378537..3796 94)	/locus-tag="SSP0346"
CDS	complement (378537..3796 94)	/locus-tag="SSP0346"  /note="similar to gi 27469138 ref NP-765775.1  [Staphylococcus epidermidis ATCC 12228], percent identity 44 in 411 aa, BLASTP E(): 8e-95" /codon-start=1 /transl-table=11 /product="putative succinyl-diaminopimelate desuccinylase" /protein-id="BAE17491.1" /db-xref="GI:72494170" /translation="MSKFTEAEKVQILEDLVAIK SVNDNEMEVCMYLKDLLSQHNIDA KIVKINDTRANLVAEIGESGPVLGISGHMDVVSE GDIKKWTYDPFKLTEVDGKLHGRG AADMKSGLAALVLSLIDIHQGLLEYGRIRLLAT AGEEIVGEGAKAFQEQQGYMTDVEA LVIAESSQDRIIYAHKGSMDIRVISRGKASHSSM PQLGFNAISPLVKFVYKADEGFKS FNKRNDLLGDVLMNATIFNGGNQVNSIPEHAESE FNIRTIPEHDNDQFITYFNEILKQ VETDKTDIEIDTYMSRPPVYTTGENKLASLAHDL GEKYLNSDLPLEASPGVTDASDLL VDKDEDFSIMYGPLIHQAHQVDEYVEKDVYLT FIDLYTEFFPTYLKSMK"
gene	complement (379890..3802 19)	/locus-tag="SSP0347"
CDS	complement (379890..3802 19)	/locus-tag="SSP0347"  /note="similar to gi 27469012 ref NP-765649.1  [Staphylococcus epidermidis ATCC 12228], percent identity 40 in 96 aa, BLASTP E(): 2e-11" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17492.1" /db-xref="GI:72494171" /translation="MSKSVKLVVSIYLAVVVIIC CSYLIMILVGSFQGNDMRGSVLDT DNTKNIENVDYINNTSKSLESNASPSDSVPKISQ SSIDTTSNKLSSIQDAHTWSLDN SISKNHV"
gene	380655..381812	/locus-tag="SSP0348"
CDS	380655..381812	/locus-tag="SSP0348"  /note="similar to gi 27469011 ref NP-765648.1  [Staphylococcus epidermidis ATCC 12228], percent identity 74 in 385

gene 381814..382266  
CDS 381814..382266

aa, BLASTP E(): e-173"  
/codon-start=1  
/transl-table=11  
/product="poly-gamma-glutamate  
synthesis protein PgsB"  
/protein-id="BAE17493.1"  
/db-xref="GI:72494172"  
/translation="MLLIIICVGLILWLGIVEKR  
QHSDRLEKIPIRININGIRGKSTI  
TRLIYSILREDQYRVIGKTTGTDARMMYWFTPRE  
YPVYRKPPQGANIGEQRDI IKKVVK  
QKANALVNECMAVNPDYQITFQKELVKANIGVIV  
NVMEDHMDVLGPTLDEVAEAFAT  
IPYKGHLIVMKDDYTDFFAKVAKRRTKLIVVNK  
EEVPESFLRKFGYIVFPDNVAIAM  
GVAEALGIDRDIALQGMLNAPPDVGAVEVKYYNA  
NNSTNVYVNAFAANEPQSTKAILN  
KVETYNYPYNKIVLILNCRSDRIDRTRQFCEDFI  
TDVEFDTLICTGKSTQMVTDMKG  
LPEKKYLNFEKGDKIEVERAVYNESQNALMFCVG  
NIHGPQKQIAEYIEGIK"  
/locus-tag="SSP0349"  
/locus-tag="SSP0349"  
/note="similar to  
gi|27469010|ref|NP-765647.1|  
[Staphylococcus epidermidis ATCC  
12228], percent identity 88 in 150  
aa, BLASTP E(): 3e-71"  
/codon-start=1  
/transl-table=11  
/product="poly-gamma-glutamate  
synthesis protein PgsC"  
/protein-id="BAE17494.1"  
/db-xref="GI:72494173"  
/translation="MIGSELYFSLFVGIVLSLIF  
AEKFGISPAGLVVPGYLALIFDQP  
IMLLSVLIISCITYFIVNHGISRIVILYGRRKFA  
AMILTGMVLKFVFDLIYPLSPFQM  
VEMSGIGVVIPGIIANTIQQQGVIIITLSTCMLLT  
CITYVILFFYSFIN"  
/locus-tag="SSP0350"  
/locus-tag="SSP0350"  
/note="similar to  
gi|27469009|ref|NP-765646.1|  
[Staphylococcus epidermidis ATCC  
12228], percent identity 59 in 357  
aa, BLASTP E(): e-124"  
/codon-start=1  
/transl-table=11  
/product="poly-gamma-glutamate  
synthesis protein PgsA"  
/protein-id="BAE17495.1"  
/db-xref="GI:72494174"  
/translation="MKNSKKFSMEERILKWTKRH  
KKRNSIYTGIIFVVALILLVFAMT  
SQKIEPVKAIGKAPNEISMTYLGNIENNHIRKN  
NLNDAFASIKEILKGS DYSTASLE  
MTKFSDDRKTNI SKNLENVFLKGLNLKSLNVIN  
QVTDNITARDFMKSVEAQTGYNLY  
TGNGSNPINSKTVQQTIKGKKIANVSFTDVESNY  
TDTLKNTTSVSLEPSIYMP LIKKL  
KENNDYVVVNVDWGITDERSVTTRQREYAHSLSE

gene 382282..383352  
CDS 382282..383352

gene	383342..383500	AGADVIIIGHNSVVQEIEKYKNTDI
CDS	383342..383500	FYSLGNTTSEDFLSKNKQGLAVQQTWNGKQSKFM
		ITPIKSQGGKVTKSSPNVVEERKL
		LNNIESKNLDLKKENGGYVYEH"
		/locus-tag="SSP0351"
		/locus-tag="SSP0351"
		/note="similar to
		gi 27469008 ref NP-765645.1
		[Staphylococcus epidermidis ATCC
		12228], percent identity 61 in 52
		aa, BLASTP E(): 5e-13"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="BAE17496.1"
		/db-xref="GI:72494175"
		/translation="MNIKQHWISITIISIVLVIF
gene	383503..385095	LLIVFARANEGLDQYEKNELKTS HQYLSKGA"
CDS	383503..385095	/locus-tag="SSP0352"
		/locus-tag="SSP0352"
		/note="similar to
		gi 27469007 ref NP-765644.1
		[Staphylococcus epidermidis ATCC
		12228], percent identity 65 in 538
		aa, BLASTP E(): 0.0"
		/codon-start=1
		/transl-table=11
		/product="putative
		gamma-glutamyltranspeptidase
		precursor"
		/protein-id="BAE17497.1"
		/db-xref="GI:72494176"
		/translation="MSIYNKKS LIVILLTIIIS
		FIFFMITKKDNYDKDDL YENKIAD
		HNQDKSDKNYG VASNNPIATRVGEKILKDGGNAV
		DASMGVSYALAIT EPHSSGLGGGG
		AMLSYDQGENVAPKQWQYKDI SSFNFKQKDEIGT
		PGFVIRGIHDAHKEAGKMDEKKILN
		YVIPLAEDGFEVDSE LERSLKLYGSDIDRNSPFF
		DGKQTKREGDVVKQ PALASTIKGI
		RDKGPDYFYDKIGKSVSKQVDDEINEKDFESYKT
		EKKEPVGTDYLN NKVYSASNPLGG
		TLMLQGLEIDEATDNQAAPDNRLDYITGILKSRA
		LMYRNRDIINGQDE DYDEYLSQDY
		LLGRLNEVNFNSNFNTNNVDNTSTTHFVVIDKDG
		KLTSTNTLASFFGSGKFMKEGFY
		MNNSLSNFSNPASP NYGGKHKEPRSFTAPSIVV
		GPDIYMGIGTPGGNKIPTTLNEVL
		VDYLRGDGTLQESIDKPRFYNDGGKIFYENATSK
		QDVDIFKSLGF EIEEKRNDPNFGS
		VQAALYNKNDKTVEIGQDVGNR"
gene	complement (385354..3866	/locus-tag="SSP0353"
	91)	
CDS	complement (385354..3866	/locus-tag="SSP0353"
	91)	
		/note="similar to
		gi 57286525 gb AAW38619.1
		[Staphylococcus aureus subsp.
		aureus COL], percent identity 80
		in 445 aa, BLASTP E(): 0.0"
		/codon-start=1
		/transl-table=11

gene	387201..387917	/product="putative aminotransferase"
CDS	387201..387917	/protein-id="BAE17498.1" /db-xref="GI:72494177" /translation="MNKSEQLINEDSQYFAKPGR IKYYPLAISHGYGATLVDVEGNTY IDLLSSASSQNVGHAPEQVTEAIKAQVDQFIHYT PAYMYHEPLVKLAKKLCEISPGQY EKRVLFGLSGSDANDGIIKLARAYTGRPYIISFV NAYHGSTYGSLSMSAISLNMKYY GPMLPGFYHIPFPDNYRGMFGSNQPNVSEYLAP LKEMFEKYVPAEEVACIMIETIQG DGGLLEPVDGYFEALQDLCKEHGILLAVDDIQQG LGRTGSWSSVSHYNIEPDLITFGK SLAGGLPMSAIVGRSEIMDYLEAPAHFFTGANP VSCEAALATIAMIEDQNLLQASTD KGNVYVRKRIDAWTEQFNTVGNVRGKGLSIGIDIV SDKINKTRASEAALKICNRCFDNG VVIIAVAGNVLRFPPLVITYEQLDTALNVLEAA ISDFESGKLDNYDTAGQGW" /locus-tag="SSP0354" /locus-tag="SSP0354" /note="similar to gi 57286701 gb AAW38795.1  [Staphylococcus aureus subsp. aureus COL], percent identity 73 in 238 aa, BLASTP E(): e-100" /codon-start=1 /transl-table=11 /product="putative 4-diphosphocytidyl-2-methyl-D- erithritol synthase" /protein-id="BAE17499.1" /db-xref="GI:72494178" /translation="MIYAGILAGGIGSRMGNVPL PKQFLDLGKPILVHTVEKFLLTS EFDKIFIATPQKWISHTKDTLRKHHITDDRIEVV QGGSDRNETIMNIIISAAEKENGIS DDDVIITHDAVRPFLTRRIKENIESVLKYGAVD TVITATDTIITSADGDSIQSIPVR SEMYQQQTPQSFNVNLLRNSYNDLSDEDKQIMTD ACKILVVAGKQVKLVMGELYNIKI TTPYDLKVANSIIKGGMLSD" /locus-tag="SSP0355" /locus-tag="SSP0355" /note="similar to gi 57286702 gb AAW38796.1  [Staphylococcus aureus subsp. aureus COL], percent identity 74 in 342 aa, BLASTP E(): e-150" /codon-start=1 /transl-table=11 /product="putative zinc-binding dehydrogenase" /protein-id="BAE17500.1" /db-xref="GI:72494179" /translation="MINQVYQLVAPRQFEVTYNN EDIKSNKVIVRPLYLSICAADQRY YTGSRNEKVLKKKLPM SLIHEGVGEVVYDSKGEY EIGTRVIMVPNTPVEKDDVIAENY LPSSKFRSSGFDGFMQDYVMDHDRVVEIDDSIE DLSTIAYSELVSVSWHALQRFERK"
gene	387910..388938	
CDS	387910..388938	

gene	389014..390702	SISNKNSFGIWGDGNLGYITAILLSKLYPQAKIY
CDS	389014..390702	VFGKTDYKLSHFSFVEHIYHIDEV
		PANVTFDHAFECVGGKGSQSAVNQIIDLVSPEGT
		ISLLGVSEYPIEVNTRLVLEKGLT
		MFGSSRSGAQDFREIAEFYKNNPDVVEKLALLKG
		NEFDVKTINDAVNAFETDLSTSWG KTVIKWTM"
		/locus-tag="SSP0356"
		/locus-tag="SSP0356"
		/note="similar to
		gi 57286703 gb AAW38797.1
		[Staphylococcus aureus subsp.
		aureus COL], percent identity 69
		in 562 aa, BLASTP E(): 0.0"
		/codon-start=1
		/transl-table=11
		/product="putative glycosyl
		glycerophosphate transferase
		involved in teichoic acid
		biosynthesis"
		/protein-id="BAE17501.1"
		/db-xref="GI:72494180"
		/translation="MSKSKIIIDNIYWERIQLFI
		EGHVEDIKLNKKNFVLRNLTETKE
		LKANDVKVEGKQFKARFNVAILDGNYLPSGEYL
		IVYKGDFDYIANINETLLDPNNYE
		LEETALEQYSDEMTQNGKNNLLLDHFTFTFKKGG
		NSSKTEYTVKPMISSEVNEFVLNI
		IFKAPMPKMNVPVKKRITDLKLKYNKYSFNVRNFI
		FQSIFKITKFFHLKKGNTVLFSTSD
		SRAEMSGNFYVYNEMLRQNLDKKYKIHAFKSN
		ISVRRNFIDKFKFPYLLGKADYIF
		VDDFHPLLYTVKFRKSQEIIQVWHAVGAFKTVGY
		SRTGKKGGPFFNSVNRNYTKAFV
		SSETDIPFYGEAFGIKEQNIPTGVPRTDILFDQ
		DYEKAIVADMEEALPIVKGKQVIL
		FAPTFRGSGHHTAHYPFFKIDFARFARYCRENNA
		IVLFKMHPFVKNNLNIPREYQEYF
		VDVSDFREVDNILDITDILISDYSSLVYEFVFK
		RPMLFYAFDLEDYITSRDFYEPYE
		TFVPGKIVESFNDLIVALDQKDFDVEKVEPFLDK
		HFKYQDGRSSERLVRNVFGS"
gene	390853..392577	/locus-tag="SSP0357"
CDS	390853..392577	/locus-tag="SSP0357"
		/note="similar to
		gi 57286704 gb AAW38798.1
		[Staphylococcus aureus subsp.
		aureus COL], percent identity 54
		in 572 aa, BLASTP E(): 0.0"
		/codon-start=1
		/transl-table=11
		/product="putative
		glycosyltransferase"
		/protein-id="BAE17502.1"
		/db-xref="GI:72494181"
		/translation="MKFSIIVPSYNSEKYIAELL
		NSLQNQSYDKKDFEVILVDDCSSD
		NTLNVVEAYKNKLNLI IKQLDTNSGGPGKPRNTA
		LQLAQGEYVFFVDSDDYINKDTLK
		DVSKFVDQNHADVVLVKMEGVNGRGVPKSMFKET
		SDAVTLANSRIIYTLSPTKFYRTS
		LLRDHAIEFPEDLRSADQLFTMKAYVNAKRIAV
		LADKPYYYATKREGEHMSSAYVSP

gene	392762..393346	EDFYKVMSLITEEILNSPLENKNEVLGYFIDRHF SFSRTNNFSLKIADDDKEAWMDAL GDFIQKVPTVVDELVNSDFKPLLHYARLKDMKHY QMVEESYKNGKFHSYSAQEGTLKI QFDEGEPYFVFKKLVKPDIRMSHFENDQGFELE LEFISSIINPNHVASMIQLKLLSR NKKEFIYIPLTMNDQTRFKFKADLNDLMPYLIKE KVWDAHLEMRVDNMTIEKRIGNKR VKYPYSKETSTITQYNNQYYRFTPYFTKDFDNLS FYITSNKLNEMLAVEIKDKQTIQL RSLEFNILSEGMTAVILPHMFTYGYLTSVTTKD TLTYHLSVGEKVKDKDLKKNFKIE TPHLVLYKY"
CDS	392762..393346	/locus-tag="SSP0358" /locus-tag="SSP0358" /note="similar to gi 23114979 ref ZP-00100256.1  [Desulfitobacterium hafniense DCB-2], percent identity 39 in 188 aa, BLASTP E(): 3e-41" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17503.1" /db-xref="GI:72494182" /translation="MTKSKIDVKDLINIGLFTAV YFIFIAPPGILGIPIFMLLLPAM IGLVGGIPVMLLITKTQKFGALTICGVVVSLLLA IMGHPWMALILSVPVIVIAADMVMA MGQYKSWKLNSIGYIIFSFWPIGNLLPFYFMRNS YLAFIQDKYGTDYEATVEGLFSIG MIPILITTTIIGAWIGAYIAKGILKKHFKRAGII " /locus-tag="SSP0359" /locus-tag="SSP0359" /note="similar to gi 23114980 ref ZP-00100257.1  [Desulfitobacterium hafniense DCB-2], percent identity 37 in 218 aa, BLASTP E(): 9e-39" /codon-start=1 /transl-table=11 /product="ABC-type cobalt transport system permease component" /protein-id="BAE17504.1" /db-xref="GI:72494183" /translation="MYNQVLSQNHIFNFDPRIKI GLMLIISLISLTGGVTGQGIFIRL IIMVIPVLLLIVIGKYKIGIACIVLTVAAWYGEA FVSIEQSQVATLLVFVPSGIITRF LPSLAMGYIIFKTTQVEVLILGLERMKLSRKITI PIAVMFRFIPTIRMESASIKDAMK IRGISLRFAFKKPMQYIEYRIVPLLNNSVIKIGNE LTIASITRGLNLTHKRSSIVTLKI RWLDWLFIVGTLTLLCITYYIV"
gene	393348..394067	
CDS	393348..394067	
gene	394077..395531	
CDS	394077..395531	/locus-tag="SSP0360" /locus-tag="SSP0360" /note="similar to gi 23114981 ref ZP-00100258.1  [Desulfitobacterium hafniense DCB-2], percent identity 45 in 486



aa, BLASTP E(): e-111"  
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/protein-id="BAE17505.1"  
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INLTINDSEVICLTGASGCGKTTI  
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VSQVSGSVFQNPQSQFFCLNTTSE  
LAFEPENFGVEPNEINTQIANSAYEFNIEHLLDR  
GIFNLSGGEKQLIACTTIQVSGHD  
IIILDEPSSNLDFKTISKLRKMLNIWKQEGKTII  
IAEHLRLHYLMDVVDRFIILAQGT  
RKQYDKDTFNKLSHETLAEGLRTHLDMKPKV  
HHNVACGTLTLKDFNFKYKPRPL  
SINIPKIELNKGKVTAVIGHNGSGKSTFARCLTG  
VERKFKGKVDNDEVTLKRGHRLNN  
VYLVFQDVNNQLFAESVGEELRLSHADLDDETIQ  
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QRLAIASAVETSRDILIFDEPSSGLDGQRMREIS  
GIIDDLATNGHTIIVITHDYELL  
SCADEILHLENGHVKDQYTMNDAILGKLQSF FEI  
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gene complement(395654..3977 /locus-tag="SSP0361"  
26)  
CDS complement(395654..3977 /locus-tag="SSP0361"  
26)

/note="similar to  
gi|27468879|ref|NP-765516.1|  
[Staphylococcus epidermidis ATCC  
12228], percent identity 25 in 691  
aa, BLASTP E(): 1e-60"  
/codon-start=1  
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/protein-id="BAE17506.1"  
/db-xref="GI:72494185"  
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KVIILLPLNKPKINLNGSTITIE  
DGIIINNADLFQMFQDLVELSLPLQLFFEKDT  
CLSTSYFDFNHIKLVEQFRNLILE  
NLHLPLQDENTASLYISNIIDFLIKEAKVTLNTV  
YIPPLNTKHPLQQITEYIHNNIY  
HKISTKNVSKAFYISQSYISILFSSILNMNFKHY  
TTSRLIALSLFDLIQNDQSIYDVA  
IKYQFTNVSTYSKHFKHYYIQMPPKYIYNFRQEY  
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AKRVDHIAKTLNLSTLSFSDTFNEPHTFIQLERL  
DDLVFHDAMISEQNDILVFPKVNI  
SILDTQIIHLNAFKLQQVLTSIHQLIDRNYHITL  
KITSKFLTNQSSTFLRKLLELKN  
NLNHITLQLDLTFNEAKSMTESINNIKQSYPOIK  
IGVIIDKIIENSANILQIRRFMSL  
LETDLYFINLDLISLAELITQKISPIQQDLDLKA  
RIVLFIHSLGSKHAKKLIFNHLTH  
SAIKSCYHYSKQETHVAITQFLIEFNQLIGGFGY  
PYYSDDYDRIMLFNQYQSAMPVVH  
IYGLLSPYYKQPITTLPYAIVTKTKTHYHILLFN  
NLSESTISVNINHFIKSFPIFSS

gene	398064..399080	LINSEYGLINNLIPQNINQTYIDKSLLKQINRTN
CDS	398064..399080	YPRCLKLTMHYFKDPLIFKLTKSAL LNIMISIN"
		/locus-tag="SSP0362"
		/locus-tag="SSP0362"
		/note="similar to
		gi 20806727 ref NP-621898.1
		[Thermoanaerobacter tengcongensis
		MB4], percent identity 31 in 337
		aa, BLASTP E(): 1e-43"
		/codon-start=1
		/transl-table=11
		/product="putative transcriptional
		regulator"
		/protein-id="BAE17507.1"
		/db-xref="GI:72494186"
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		TVSNVLNNKSSELSDKTKDKVLNA
		IETLNYPEPNQFARGLKTGRSNIIAFIVPDQNPF
		TEVLTEISHECQKHHLHVAVASSE
		ENEDKQQDLIETFVSQNVSAIILVPVKSQFQMKR
		EWLKIPIMTLDRELESTSLPSITV
		DNEEAAYIATKRVLESTCKEVGLLLANPNISTTI
		GRKNGYNKAISEFDLNVNPSLIHY
		SDQQLGTNAQIYSGYEATKLLSKGIKIVATNH
		LLLLGALQAIKESEKEIKKDVIIV
		GFDDSYWNEIYTPKLTVISQPVKEMQVAAKMIY
		KLIKGDVTSIKLSTKLIIRESCS FNKT"
gene	399165..399419	/locus-tag="SSP0363"
CDS	399165..399419	/locus-tag="SSP0363"
		/note="similar to
		gi 53611566 ref ZP-00342323.1
		[Azotobacter vinelandii], percent
		identity 57 in 57 aa, BLASTP E():
		9e-12"
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		/transl-table=11
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		permease of the major facilitator
		superfamily"
		/protein-id="BAE17508.1"
		/db-xref="GI:72494187"
		/translation="MDTSSNSVREKTWMGVPRII
		FAALIAIFIFMTGDGIEQAFLSKN
		IVDLGFSSGQASLVFTVYGVMVVVGSWLAQFYQM
		SMVREK"
gene	399374..400456	/locus-tag="SSP0364"
CDS	399374..400456	/locus-tag="SSP0364"
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		gi 53611566 ref ZP-00342323.1
		[Azotobacter vinelandii], percent
		identity 50 in 348 aa, BLASTP E():
		e-104"
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		/transl-table=11
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		permease of the major facilitator
		superfamily"
		/protein-id="BAE17509.1"
		/db-xref="GI:72494188"
		/translation="MVSAVLSDVYGPRKVMVLGT
		VIWLVFHILFLVFGLGLENYSMML
		LMYGIRGLGYPLFLYGFLVWVTYITNKARLATAI

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CDS

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400473..401957

GWFWAMFSVGMGVIGTYLPSFTIP  
HIGFMGTLWMSVIWIGVGGLIAFYVVGKRNIPN  
VDKPIKERYVKVLKEVGIVYKNPD  
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QQWLWTWGTMHITCIVGDVVGIV  
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IFAIAILCAVLFGITQSAFVPIFA  
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/locus-tag="SSP0365"  
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/note="similar to  
gi|27469003|ref|NP-765640.1|  
[Staphylococcus epidermidis ATCC  
12228], percent identity 60 in 493  
aa, BLASTP E(): e-178"  
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NRDQGVVGQMSEPLTLIQTEPGYN  
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DTRTTQQCQSIKNQFGETLLKNPILEGFTLPKLL  
WLQENEPHWQALDVFLPKDYVR  
YKMTGDISMEYSDAAGTLLNTDTKQWDTRVGEQ  
LAIGDIYPKLINSHDFVGNLTEDV  
KAALGLDNDVAVFAGGADNACGALGAGVINEAQA  
LCSIGTSGVVLTCQENEKSLGNN  
IHYFNHALPQMTYTMGVTL SAGDSLNLKRTMFD  
DESFDIVQQAESQIGANGLLFA  
PYLQGERTPHGDAYIRGSFIGLSSNTVKADFARA  
TIEGITYSLYESYRYMMQANSNSN  
RVISIGGSKSNFWLQLQADVFNAEVTPLKYEEG  
PGMGAAMLAAAYGLGWFKSMEDCVD  
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TLTQQLLTIK"

gene  
CDS

401976..403046  
401976..403046

/locus-tag="SSP0366"  
/locus-tag="SSP0366"  
/note="similar to  
gi|16077682|ref|NP-388496.1|  
[Bacillus subtilis subsp. subtilis  
str. 168], percent identity 59 in  
352 aa, BLASTP E(): e-121"  
/codon-start=1  
/transl-table=11  
/product="sorbitol dehydrogenase"  
/protein-id="BAE17511.1"  
/db-xref="GI:72494190"  
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EMKEVKVPKIGATDVLVKVMAVG  
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VGSNVTRFKVGDRAIEPGVPCGE  
CEYCKSGKYNLCPDVEFLATPPVDGAFS  
QYISHP  
EGFLFHIPEALSYEEATLNEPFSV  
GVQACKRANVQPGSTVIMGMGPVGLMAVVA  
AKA  
FGATKIIIVSDLEKIRLDEALKLGA  
THAINIKEGVATRINEITKGGVNYAFETAGNP  
IALQNALAALNNGGTLAIVGLPQQ

gene	403921..404595	ENIELNIPFIANHEINIVGIFRYANTYDMGLEML ASTSADLNTMFTDAYDLNEAKEAM EQARTNKSGSLKVMVYPNGKPE"
CDS	403921..404595	/locus-tag="SSP0367" /locus-tag="SSP0367" /note="similar to gi 53771322 ref ZP-00182843.2  [Exiguobacterium sp. 255-15], percent identity 42 in 217 aa, BLASTP E(): 4e-47" /codon-start=1 /transl-table=11 /product="putative 2-haloalkanoic acid dehalogenase" /protein-id="BAE17512.1" /db-xref="GI:72494191" /translation="MYKAIIFDVYGTIFDISSLE KHMDQFDEAQASSISQLWRKTQLQ HMFLLKQIMQRYITFDDLTKDALRYTLDEHKVQYN REDINQLFDAFLDLDFKEIPRVF SDLKAKNIDIGVLSNGNDSMLMPLVDNSKISEYI DTVMSVDEIKQYKPSASYALILN YYHLTREEILFVSSNSWDITGAANFGFDTVWINR DKVQFDYNGQSPTMTVSNLNLVK WLEMNK"
gene	complement(404785..405774)	/locus-tag="SSP0368"
CDS	complement(404785..405774)	/locus-tag="SSP0368"  /note="similar to gi 27469138 ref NP-765775.1  [Staphylococcus epidermidis ATCC 12228], percent identity 46 in 359 aa, BLASTP E(): 7e-86" /codon-start=1 /transl-table=11 /product="putative truncated succinyl-diaminopimelate desuccinylase" /protein-id="BAE17513.1" /db-xref="GI:72494192" /translation="MVAEIGSGKPVVGVSGHMDV VTTGDTEQWNYDPFKLTEDDQGR HGHGSADMKSGLAALAI SLIEIKKAGTLNQG TIR FMATAGEEVT SNGAALLHEKGYMD DVEALLIAEPSQDGIVYTHKGTMDIQVISKGKSA HSSMPELGFNAINPLVDFIHYLNV EYNKVDVRSKLLGTPTMNSTIINGGDQVNSIPEY AESLFNMRTIPAYDNKKFESLFNS IKEKEDNADITVNPYVNRDPVYTTGDNEFLKLAK SLGDEYFNRLDVTSSATTDASY LMKDKGEDFSFVMYGPGETGQAHQVDEYVYKDTY LTFIDLYTQMLPQYLNDFK"
gene	complement(405823..405939)	/locus-tag="SSP0369"
CDS	complement(405823..405939)	/locus-tag="SSP0369"  /note="similar to gi 27469138 ref NP-765775.1  [Staphylococcus epidermidis ATCC 12228], percent identity 72 in 37 aa, BLASTP E(): 5e-08" /codon-start=1

		/transl-table=11 /product="putative truncated succinyl-diaminopimelate desuccinylase" /protein-id="BAE17514.1" /db-xref="GI:72494193" /translation="MSVLSNEERVKILSDIIEIQ SVNEKELDVAHYLQKLFK"
gene	complement(406040..4065 31)	/locus-tag="SSP0370"
CDS	complement(406040..4065 31)	/locus-tag="SSP0370"
		/note="similar to gi 15925519 ref NP-373053.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 69 in 161 aa, BLASTP E(): 6e-61" /codon-start=1 /transl-table=11 /product="putative acetyltransferase" /protein-id="BAE17515.1" /db-xref="GI:72494194" /translation="MIRHATKSDLPNILDIYNDA ILNTTAVYSYKPQTLASREIWFEN KSQNNPIFVFEQQGEAVAFATYGSFRDWPAYQY SIEHSIYVNEHHRGKGIASQLLKQ LINHAQVEGYKTLVAGIDATNDNSIYLHKKFDFQ HSGTIQNVGYKFDKWLDLAFYQLD LSK"
gene	406754..407353	/locus-tag="SSP0371"
CDS	406754..407353	/locus-tag="SSP0371"
		/note="similar to gi 15925518 ref NP-373052.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 65 in 205 aa, BLASTP E(): 1e-72" /codon-start=1 /transl-table=11 /product="sortase A" /protein-id="BAE17516.1" /db-xref="GI:72494195" /translation="MKKWGNRLITLIGVLFILAA IYLFAPKPHIDQYLHEKESEEKIET YDKDAANKKENKQEIPKDKSEMVGYLTPDAEIK TPVYPGPATPELLDRGVSFADAE SLDDQNIAIAGHTNIGSSDYQFSNLKEAKKGSEV RFKVGNNVYKITKIFDVKPEDV QVLDEHKSSKKQLTLITCDNYNEQTNTWEDRKIF IAEAV"
gene	complement(407430..4080 98)	/locus-tag="SSP0372"
CDS	complement(407430..4080 98)	/locus-tag="SSP0372"
		/note="similar to gi 49485199 ref YP-042420.1  [Staphylococcus aureus subsp. aureus MSSA476], percent identity 81 in 221 aa, BLASTP E(): 5e-99" /codon-start=1 /transl-table=11 /product="putative N-acetylmannosamine-6-phosphate

		epimerase"
		/protein-id="BAE17517.1"
		/db-xref="GI:72494196"
		/translation="MLPQGLIVSCQALPDEPLHS SFIMSKMALAAYEGGAVGIRANSK ADIIEIKKEVDLPVIGIVKRDYAHSDFITATSK EIDELIESNCEVIALDATKQTRPK ESLSELVSYIRNKAPNVEIMADISTLEEAKNADE LGFDYVGTTLRGYTSYTKGHILYE NNYQFLKDVLAHVNAKVIAEGNVITPEMFKDVTD LGVHCTVVGGAITRPKEITKRFIN AFDK"
gene	408265..409062	/locus-tag="SSP0373"
CDS	408265..409062	/locus-tag="SSP0373"
		/note="similar to gi 57285427 gb AAW37521.1  [Staphylococcus aureus subsp. aureus COL], percent identity 73 in 264 aa, BLASTP E(): e-108" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator"
		/protein-id="BAE17518.1"
		/db-xref="GI:72494197"
		/translation="MKFENRIQRYHHLFTKTDKQ IVEYIQSNHFDDSFSTINSLAHAI GTSPATITRFSNKLDDYDNFQDLKFNLLQEMTDKV IENSPLIQRIHKYHQDIIQQTGEF ISDEKIQSFVNQIMRSRQIIYAGLGSSGLSATEF YYRMMRMGLKGSVSTDAHQMKIFG SLLTTSDTFLAISNSGETAELIAAAEVAHARGAY VVAITNYEGSTLTECADLVLITTD QSRINDSRFINTQIATLFLIDIVSYLLDDDDYMH NVYQHTKKTVLNE"
gene	complement(409147..410019)	/locus-tag="SSP0374"
CDS	complement(409147..410019)	/locus-tag="SSP0374"
		/note="similar to gi 49482548 ref YP-039772.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 57 in 284 aa, BLASTP E(): 7e-90" /codon-start=1 /transl-table=11 /product="putative ROK family protein"
		/protein-id="BAE17519.1"
		/db-xref="GI:72494198"
		/translation="MTDYKVAIDIGGTDIKAAYL DNGLNFVDYQKIPTPNNINEYIVD KVYDIVKHFQMTYKLSPLHVGISSAGVIDETNGV IDYTGPTIPNFRGTNFPKLLASLN ADVKIYNDVNAALLGELYFHQYDVDNIFCLTLGT GIGGAFYNQTLGLYNGTRHRANEI GYLLYRSEDQLTFEQRSTTALKSLMKSFSFPYS DDVPMLFKLADQDNELALDILNEW SFNVAEGLAQIIYDPLILIGGGISAQDQTL KYIVPKIQNFLPPEYGHAEIKTTH TKNHASLFGAVSQF"
gene	410343..411161	/locus-tag="SSP0375"
CDS	410343..411161	/locus-tag="SSP0375"

gene	411187..412716	/note="similar to gi 57285425 gb AAW37519.1  [Staphylococcus aureus subsp. aureus COL], percent identity 82 in 272 aa, BLASTP E(): e-126" /codon-start=1 /transl-table=11 /product="N-acetylneuraminate lyase subunit" /protein-id="BAE17520.1" /db-xref="GI:72494199" /translation="MKEEGLAQIAKNAIETEKLD GLYVNGSSGENFLLSKEQKKQVFK VAKEAVNDDVKMIAQVGSDDLNEAIELGKYATEL GYDAISAVTPFYYPFSFEEIKDYY FELIEATQNNLIIYAIPDLTGVNISIEQFGELFN HEKIIIGVKYTAPNFFLLERIRKAF PDKLILSGFDEMLVQAAVSGVDGAIGSTYNVNGV RARQIFEKAQNGNIAEAYEIQHET NNIIENVLSMGIYSTLKEILASRGIDGSVPKRPF KPFNEANRSKLDKLIKDYNL"
CDS	411187..412716	/locus-tag="SSP0376" /locus-tag="SSP0376" /note="similar to gi 57285424 gb AAW37518.1  [Staphylococcus aureus subsp. aureus COL], percent identity 81 in 510 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="sodium:solute symporter family protein" /protein-id="BAE17521.1" /db-xref="GI:72494200" /translation="MQQVGFGTWNWVAVIVYLVL MLLVGAYFTKRASQNTDSFFTASG RLPSWAVGFSTIYATTLSAITFMSTPEKAFLTDWS YIAGNIAIVAIIPLLIYFYVPFFK KLKVTSAYEYLEARFRPSVRVIGSLLFVLFHLGR VAIVIYLPPLAITAVSDLNPYVVA SLVGILCILYTFLLGGFEGVWVSDFIQGIILLGGA AAIIILGIIHIKGGMGTVVTDALD HKKLISADNWKFNNTAAAIPFIIFLGNIFNNLHQY TASQDVVQRYQASESMSETKKSLW MNGVLALISAPLFYGMGTMLYSFYTHESALPEGF NTSSIVPYLILTEMPFFIAGLLIA TIFAAQSTISSSLNSISACLSVDIKHRIFGKKG EKDEVTFARWMIILSGLFGFGMSI YLIASDSNDLWDLFLLITGLVGVPLAGVFAVGIF TKRTNTLGVICGLALGIIIFAYIFN GIGGGNSPFFVSIISFLVAFIFSYLIRIVIPDKK KDIVGLTIFDIKEKSNYVSKIHVK K"
gene	413085..413615	/locus-tag="SSP0377"
CDS	413085..413615	/locus-tag="SSP0377" /note="similar to gi 42525870 ref NP-970968.1  [Treponema denticola ATCC 35405], percent identity 45 in 182 aa, BLASTP E(): 2e-43" /codon-start=1 /transl-table=11 /product="putative NADPH-quinone

		reductase" /protein-id="BAE17522.1" /db-xref="GI:72494201" /translation="MSTLVIIAHPDISNSTVNKH WRDALSKIGESVTVHEIYPEYPHG KIDIEKEQKLEAHDHIIIFQYPLYWYSSPPLMKQ YLDEVFTHGWAYGSKGDALKGKNI GLAISIGSIAEAYTPEGNVKFTIDELVSPMIATT RFVSANYVGAHKLYSAFTIAPSQL EENTQDYLNFIQSLNK"
gene	413873..414679	/locus-tag="SSP0378"
CDS	413873..414679	/locus-tag="SSP0378" /note="similar to gi 15925515 ref NP-373049.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 67 in 266 aa, BLASTP E(): e-104" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17523.1" /db-xref="GI:72494202" /translation="MIKAIIVMDGTFLNTQKTY DEERFERIFQQLKTQQIKFIAASG NQYAKLKSIFGERAMYFVAENGAVIYEGDKLYDY QTFDRDFYQQVVDYLNIERGINNL IVCGLSSAYILKENPESFKKDAHFYRQLEEIHS LQHLPEDEYVKIAFNINRETHPTL DEDLKARFNGKLEFVSSGHDSIDIIIPGVTKGNA LKRLNLTWQLDASELMAFGDANND LDMLLLAHSYVMENSEDHSLFEAAKHVAPSNDK QGVLSVIESEVLNKPI"
gene	414769..415431	/locus-tag="SSP0379"
CDS	414769..415431	/locus-tag="SSP0379" /note="similar to gi 27468991 ref NP-765628.1  [Staphylococcus epidermidis ATCC 12228], percent identity 72 in 220 aa, BLASTP E(): 1e-90" /codon-start=1 /transl-table=11 /product="putative flavin oxidoreductase" /protein-id="BAE17524.1" /db-xref="GI:72494203" /translation="MMTQMQQTILDAFNFRHATK RFDANKKISESDFNTILETGRLSP SSLGLEPWRVVIQNREIRDKLKAISWGAQQQLD TASHFVLILARKNVTSQSDYVQHM IRNVKKYSEASIPATEKKFDDFQTNFHINDNDQS LLDWARKQTYIALGNMMTSAALLN IDSCPIEGFDLDAVTQFLTDDGIIIDEAHFAPSVM VAFGYRETEPKDKVRQTQDDIVEW LE"
gene	complement(415472..415813)	/locus-tag="SSP0380"
CDS	complement(415472..415813)	/locus-tag="SSP0380" /note="similar to gi 28379827 ref NP-786719.1  [Lactobacillus plantarum WCFS1], percent identity 70 in 114 aa,



		BLASTP E(): 2e-42" /codon-start=1 /transl-table=11 /product="truncated beta-glucosidase" /protein-id="BAE17525.1" /db-xref="GI:72494204" /translation="MWDRYNKPLFIVENGLGAKD TIEDGQIHDNYRIDYLRKHIAEAK RAVEDGVDLMGYLAWGPIDLVSMTSEITKRYGF IYVDQDDYGQGTKRIKDSFDWY KALIQSNARDL"
gene	complement(415815..416153)	/locus-tag="SSP0381"
CDS	complement(415815..416153)	/locus-tag="SSP0381"
		/note="similar to gi 15613344 ref NP-241647.1  [Bacillus halodurans C-125], percent identity 50 in 89 aa, BLASTP E(): 5e-20" /codon-start=1 /transl-table=11 /product="putative truncated transcription antiterminator" /protein-id="BAE17526.1" /db-xref="GI:72494205" /translation="MHIVNASMDENIANIYEITK ITKSILDIVRYHFNHINEDALSY SRFMTHLKFFSQRLINHESLNEVTDESLLQVLQQ KHVKSDACVDKKSLLRSIRLGLAN RFNWTQSRLK"
gene	complement(416354..416617)	/locus-tag="SSP0382"
CDS	complement(416354..416617)	/locus-tag="SSP0382"
		/note="similar to gi 15673443 ref NP-267617.1  [Lactococcus lactis subsp. lactis Il1403], percent identity 41 in 86 aa, BLASTP E(): 3e-11" /codon-start=1 /transl-table=11 /product="putative truncated beta-glucoside operon antiterminator" /protein-id="BAE17527.1" /db-xref="GI:72494206" /translation="MKITKILNNNVVISKINNEE RIVMGKGIAFGKQNGQELEKDKID KVFRLTSEEQERMLTLLNEIDQNVLLTTQDIIK ANQLYEKPM"
gene	complement(416808..417617)	/locus-tag="SSP0383"
CDS	complement(416808..417617)	/locus-tag="SSP0383"
		/note="similar to gi 57285216 gb AAW37310.1  [Staphylococcus aureus subsp. aureus COL], percent identity 60 in 268 aa, BLASTP E(): 6e-95" /codon-start=1

		/transl-table=11 /product="putative glyoxalase bleomycin resistance protein" /protein-id="BAE17528.1" /db-xref="GI:72494207" /translation="MTFHDKNATQVTNITLNVSD LKNMIKFYTQILGLTIKHETNHAV TFNVGAHGHTLTLNEIENGRRPSMRESGLFHMAL LLPTRQDLGNFLYHAASTGVQVGG GDHLVSEALYFADPEGNGIEIYYDRPKAGWIWND NKVKMDTLEVDANDLVEQRSENGW QGMPDDAKIGHLHLKAADIGQSRHYLDELGLDH VSDLPPQAVFMSTNHYHHHIAFNTW QSNMLRQNNSQLGLTHIEIYKPNAQETQFIGPE GFEILVHSNTHLVADKD"
gene	417805..418350	/locus-tag="SSP0384"
CDS	417805..418350	/locus-tag="SSP0384" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17529.1" /db-xref="GI:72494208" /translation="MTHYYFKENFFNASSSAIEI YNDKEDVVFTIELFYTSAVQQTMA YLGNNKQNFIEITDGQDITYRVLQEGAISSAIIKPF KTVWTVVEKNNQPIGLFRSKMGLKP TMYFEGTQGDIIKFQSGFFSRSVKVTESNQEIMQ TKSERFKFASRHDVYIETETETHPA MLILLFQVFYEFQEKQRKNAN"
gene	418585..420366	/locus-tag="SSP0385"
CDS	418585..420366	/locus-tag="SSP0385" /note="similar to gi 15614899 ref NP-243202.1  [Bacillus halodurans C-125], percent identity 54 in 576 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="ABC-type multidrug protein lipid transport system ATPase component" /protein-id="BAE17530.1" /db-xref="GI:72494209" /translation="MKVFLKLGWFFKQKTSYLI GLGTLLLIALLIEIVPPQIIIGRTID EMTSNRLTPRLLAIYLFILVITAILTYVLRVWR LSIFGTSQKLKILRTYLYKKYTE MSAIFFQNRRRTGDLMAHATNDIRAVQNAAGAGIL MIADSLITGGTVIITMATTVSWKL TLIAMIPLPFMVLLTSIYGSLLSKGFKKAQAAFS KLNDKTQESVAGIKVTKTFGYEPS DQADFKHLSDDVVAKNLKVSKIDALFDPTITLVI GMSYFLSIAFGAQMVFHNDISLGQ LITFNTYLGMLVWPLLALGLFFNIVQRAKASYER IEEIGELPNIDITSYVIDERPQGD IRFNINQFYFPGNEDQGIYDIHFTIKEGSTVGIV GRTGSGKSALIRLLLREFDTQHAQ DIEFGGHPIRDYNVESLRAQFGYVPQEHFLFSTT IRNNIAFSNETIDDEKIFEASKLS HIHDDIMQFSKDYQTVVGERGVSLSGGQKQRVSI ARALLVNPEILILDDSLSAVDAQT EEAILLENLERLRSGKTNIITAHMSAVKHADLII

gene	420359..422122	VMNEGRIIERGNHATLMSKKGWYY
CDS	420359..422122	DTYQAQALQEQLSRNLDSLTKGDGEND"
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		/locus-tag="SSP0386"
		/note="similar to
		gi 56419871 ref YP-147189.1
		[Geobacillus kaustophilus HTA426],
		percent identity 53 in 581 aa,
		BLASTP E(): e-177"
		/codon-start=1
		/transl-table=11
		/product="ABC-type multidrug
		protein lipid transport system
		ATPase component"
		/protein-id="BAE17531.1"
		/db-xref="GI:72494210"
		/translation="MTENANLTAKDQGSALIRLF
		KYTLPYKWIIVLAFITLILSTIAS
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		QQLRIDAFNKLKGLGMRYFDKVPGGSIVSRLTND
		TETIVDMIVGVFSTFIMAFFMMIS
		SYIMMFVLDVKLALIALIFLPIIMIILASYRKYS
		AFLFSKSRQRLSDLNSKLAESIEG
		MKIIQAFNQERRLNKEFNKINDEHYQYMLKTVKL
		DSLRLRPAISSISIFAVVMILGYF
		GVISFTTGITAGVVFVAFVQYMERFFEPINQVSQN
		LNILQQALVSASRVFALINDDTYE
		PQQEANNNDNAIETGEIEFDNVSFSDGETDVLKN
		ISLTAKPGEMIALVGHTGSGKSSI
		INLFMRFYEFNRGDIKIDGNSIKKIPKTELKEKI
		GLVLQDAFMFYGTIASNIKLYHPS
		MTFEQVKA-AAEFVHANHFIEKLPNQYQHKVIEKG
		SAFSSGERQLIAFARTIATNPKIL
		ILDEATANIDSETEEQIQQSLNKMKGRTTLAIA
		HRLSTIQDADQIFVLNKGEIVERG
		THAQLIAQKGIYHNMYLLQNG"
gene	complement(422220..4224	/locus-tag="SSP0387"
	98)	
CDS	complement(422220..4224	/locus-tag="SSP0387"
	98)	
		/note="similar to
		gi 27468987 ref NP-765624.1
		[Staphylococcus epidermidis ATCC
		12228], percent identity 65 in 91
		aa, BLASTP E(): 3e-31"
		/codon-start=1
		/transl-table=11
		/product="putative
		acetyltransferase"
		/protein-id="BAE17532.1"
		/db-xref="GI:72494211"
		/translation="MAEIKQGTNKFYIGDDENNP
		QAQITFNQQNDNQIDIDHTGVPEE
		MGGQGIGSQLVKAVVDYARDNNLKVSATCPFAKS
		VIEKHDEYQDVYVG"
gene	422676..423671	/locus-tag="SSP0388"
CDS	422676..423671	/locus-tag="SSP0388"
		/note="similar to
		gi 27468986 ref NP-765623.1
		[Staphylococcus epidermidis ATCC
		12228], percent identity 54 in 320

		aa, BLASTP E(): e-103" /codon-start=1 /transl-table=11 /product="putative ABC-type Mn Zn transport system periplasmic Mn Zn-binding protein" /protein-id="BAE17533.1" /db-xref="GI:72494212" /translation="MKKSIIIMLTTCVMMITLSAC GNINKSEKKDVSTNNKLKIYTIAF AFQSFTEQIGGKYVDVESIYPPGADMHSFEPTQK EMVNIAKSDLFIYSNQDMDPVAKK IAGSINNEHLKLPVAANLKQADLLSNHEHEHDHE HEGHEAHEEHDEHEGHDHEEGSKD PHIWLDPVLNKKMVKAIKDDLKVKDSRHKAYYEK RYKQLIADLDDINHEMKDITSNPK RDTVVISHDSIGYLANRYGFKQEGVSGMNNEEPS QRDLMAIVKRIDDTKQPYVLYEQN ISSKVTDVQKESNTTPLSFHNMATLSKKEMNDK DITYQSLMKENIKSLDKALNH"
gene	complement(423824..425248)	/locus-tag="SSP0389"
CDS	complement(423824..425248)	/locus-tag="SSP0389"  /note="similar to gi 27468985 ref NP-765622.1  [Staphylococcus epidermidis ATCC 12228], percent identity 79 in 472 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="putative aldehyde dehydrogenase" /protein-id="BAE17534.1" /db-xref="GI:72494213" /translation="MNQLFINNEFIASKSTDTMD VINPATGEKIDTITFATEAEVNDA VEKSKQAQLEWEKTPEPTRADHVKLLIPLLEQNK DTLAELYVKEQGKTLASAKGEIDK AIQFIDYMTGLSMNNKGEVLKNSRENETILLTKK PIGVTAGIVPWNAPIMVLMRKVIP AVITGCSVVIKPEATSLITLKIAELLRASTIPA GLVQILPGTGETVGTQLAQHPDIQ LISLTGSMRAGKSVYAESASTVKKVNLELGGNAP VIVTSNADLDKAVNYIVTARINNA GQVCTCPERIFVHQDIHDTFIDKLKAQMEQLTVG DPFDESTDYGAIIINQQQLDSIDDK VQNAVKNQAQLITGGHKIKRSGFFYAPTILDHIN LEDSAFKEEIFGPVLPITYSEFE HALNQANDTNAGLSSYIFSENLKEIMLATEKLKF GEVYANCEAEVVNGFHAGWRESG LGGADGIHGLEEYNTTVSYIRYD"
gene	425489..425920	/locus-tag="SSP0390"
CDS	425489..425920	/locus-tag="SSP0390"  /note="similar to gi 57285214 gb AAW37308.1  [Staphylococcus aureus subsp. aureus COL], percent identity 64 in 143 aa, BLASTP E(): 3e-45" /codon-start=1 /transl-table=11 /product="putative transcriptional

		regulator"
		/protein-id="BAE17535.1"
		/db-xref="GI:72494214"
		/translation="MDRTQISLNTFVGLNRTLDDH
		LMKIVKTDVQRYGLNVTEFAVMEL
		LYNKGQDQPIQRIGNRVLIASSSITYVVDKLEEK
		CVVRQRNEKDKRVTNASLTDKGRS
		MMDEIFPDHASTLESTFSVLTDEEITVLQTTLKK
		LSAQPIE"
gene	425990..426946	/locus-tag="SSP0391"
CDS	425990..426946	/locus-tag="SSP0391"
		/note="similar to
		gi 57285213 gb AAW37307.1
		[Staphylococcus aureus subsp.
		aureus COL], percent identity 80
		in 318 aa, BLASTP E(): e-152"
		/codon-start=1
		/transl-table=11
		/product="putative dioxygenase"
		/protein-id="BAE17536.1"
		/db-xref="GI:72494215"
		/translation="MTNNQLLGIHHVTAMTDDAE
		RNYQFFTEVLGMRLVKKTVNQDDI
		YTYHTFFADDEGSPGTDMTFFDFPNIPKGSAGTN
		SITRPSFRVPNDEALEYYEQRFDE
		FNIKHEGIQSLFGTKVLPFEEVDGQSYQLVSDEH
		NKGVAPGKPPWKNPVPMDKAIYGL
		GPIEITVSYFEDFMKILEDVFGMTVLTKEDGVVI
		LEVGEKGNGGQVILRKDTDGPEAR
		QGYGEVHHVSFRLKDHAAIVQWLEKYQTLGIGNS
		GLVDRFYFEALYARIGHILIEVST
		DGPGFMGDEPYETLGEALPPFLEPQRAYIESE
		IRPFDTSR"
gene	427028..427933	/locus-tag="SSP0392"
CDS	427028..427933	/locus-tag="SSP0392"
		/note="similar to
		gi 52141900 ref YP-084931.1
		[Bacillus cereus ZK], percent
		identity 43 in 302 aa, BLASTP E():
		2e-64"
		/codon-start=1
		/transl-table=11
		/product="putative glyoxalase
		bleomycin resistance protein"
		/protein-id="BAE17537.1"
		/db-xref="GI:72494216"
		/translation="MEAIQHIHHISAIVGNPEEN
		IRFYRDVLNLKLIKKTVNYDDPST
		YHLYFSNGNIENGITLTFNWPNAHKGRKNGQV
		ERIAFRIPKNSRDIWKAHLQAHQI
		EVVETRLFDRETLEFNDTHDLPLALVEADDDNDQ
		TDAQSIIGFHGVTLLSSHPKATLN
		TLVNDMGLHKVNEDDNVHVETKQHWQHHVVIKK
		ESAQMNVRWGVGVVHHIAWSVPTD
		KVQREWLVKMTGKGYHVTVDKDRNYFKAIYMKEQ
		GGIIFEFATEGPGFTVDERFETLG
		THLVLPQFEDRRETILQLLPPIRI"
gene	427964..428566	/locus-tag="SSP0393"
CDS	427964..428566	/locus-tag="SSP0393"
		/note="similar to
		gi 15925508 ref NP-373042.1
		[Staphylococcus aureus subsp.

		<p>aureus Mu50], percent identity 65  in 195 aa, BLASTP E(): 6e-68"  /codon-start=1  /transl-table=11  /product="putative phospholipase"  /protein-id="BAE17538.1"  /db-xref="GI:72494217"  /translation="MEHIFREGEANAPTLILLHG  TGGDESDLLPLSQLLPKYNVLSI  RGEVSENGMNRFFKRGEGQYDIEDLNFRDRLI  AFLKEAAERYGFDLSLAIPVGFSN  GSNIAISMILHQDISFQTALLYAPLYPVNDANDK  DLSGMHVLLSMGEHDPVTSKDSQ  NVIDLFENRGANVTQVWVNSHELTQAGVVAGRDL  LNNIFK"</p>
gene	428695..429249	/locus-tag="SSP0394"
CDS	428695..429249	<p>/locus-tag="SSP0394"  /note="similar to  gi 57286571 gb AAW38665.1   [Staphylococcus aureus subsp.  aureus COL], percent identity 49  in 180 aa, BLASTP E(): 2e-44"  /codon-start=1  /transl-table=11  /product="putative amidase related  to nicotinamidase"  /protein-id="BAE17539.1"  /db-xref="GI:72494218"  /translation="MNHQALIVMDMQNGIVNGLQ  QKENVIANNQKAIEHARRNSVAVI  FVRVAFTGEYMEVSPNNKMFQMKAKGVPMNKQD  ESTQIVEALNRQAKEPLVTKHRLS  AFTGSNLEVLLRGLQVDHLVLTGVSTSGVVVSTA  VEAADKDYKLTLSDAMADQDVEK  HQFLINKILTRYADVTTVEAWCNS"</p>
gene	complement(429340..430755)	/locus-tag="SSP0395"
CDS	complement(429340..430755)	<p>/locus-tag="SSP0395"  /note="similar to  gi 49487472 ref YP-044693.1   [Staphylococcus aureus subsp.  aureus MSSA476], percent identity  76 in 471 aa, BLASTP E(): 0.0"  /codon-start=1  /transl-table=11  /product="putative di- and  tricarboxylate transporter"  /protein-id="BAE17540.1"  /db-xref="GI:72494219"  /translation="MNSDIHYRKFIPIILIGIII  WLLTPIRPEGLDVGAWHMFVFAIFVA  TIIGCITQPLPIGAVAMIGFTLAVLTQTVKIDTA  VSGFGNSSIWLIAMAFFISRGFVK  TGLGRRIALQFVKLFGKKTGLGLGYSLIGVDLILA  PATPSNTARAGGIMFPIINALSRS  FGSKPEDGTQRKMGGFLIFTEFHGNLITAAMFLT  AMAGNPLAQSLAKHQGVDITWMQW  FIAALIPGIISLILVPLIIYKMPPEIKETANAK  SWAQNELKDMGKMATSEKFMVSIF  LVALALWVLGSTLNINATLTAFIALSLLLITGVV  TWSVDVLKETGAWNTLVWFSILVMM"</p>

		ANQLNELGFISWLSKSI SGSLGGLSWPIVLVLLI LFYFYSHYLFASSTAHVSAMYSAL LGVAIATGAPPLFSALMLGFFGNLMASSTHYSSG PAPILYSAGYVSQNRWWTMNAVLA IFYFIVWLGIGSLWMKLIGLM"
gene	complement (431075..4321 24)	/locus-tag="SSP0396"
CDS	complement (431075..4321 24)	/locus-tag="SSP0396"
		/note="similar to gi 27468984 ref NP-765621.1  [Staphylococcus epidermidis ATCC 12228], percent identity 68 in 349 aa, BLASTP E(): e-138" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17541.1" /db-xref="GI:72494220" /translation="MTSLKEIIIVAFVGVVVG AGFATGQEIFQFFTSNGNYSIWGV IITGCIVTLGGIFVLQTYKLNHNHTGPIKYYL PKRIATLFDIILTFLLLALAMIMT AGGVSTIHESFNIPYALSSVLLISIIITLFLKF ERLIAILGMVTPFLVIVTIIAMY YLMTGSLSFSDPNQYANTGTRSDQWWFDAINYG SLQIAAASFSLVSMGGRLKFKSSS VYGGMIGGLIITFLLMLNLGMVSQFSLIKDVAL PSLLLAKEISPMIGLFMSIVMILV IYNTVVGLMYAFASRFRPYSKHYIIMICMAVL TFATTFIGFIDLIGKVFVPMGIFG FILLFPILIKGISRK"
gene	432446..434245	/locus-tag="SSP0397"
CDS	432446..434245	/locus-tag="SSP0397"
		/note="similar to gi 27468982 ref NP-765619.1  [Staphylococcus epidermidis ATCC 12228], percent identity 72 in 592 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="Na+ H+ exchanger" /protein-id="BAE17542.1" /db-xref="GI:72494221" /translation="MTLLNLPLTLLIVIFLALGI FSQWFADKIKWPSIVVMAIVGLLV GPIFGLINPQESLGQEVFSPLVSLAVAILFEFS SNLDFRELKGIKAVIRIITVGAV IAWILGSMALHFVLGFSVTISLVLGGLFLITGPT VIQPLLKQAKVRKSVDSILRWESI ILDPIGPMLALGAFYVFQIVEQGFIEIQIILSFAL RFVIAIVIGFGASYLFMMLIKRDL IPQNLMPPIQLVFILLIFAICDEILHESGLLAVT IFGLMMARMKRHDLIFKESDHFIE NASSIMVSTVFILITSSLTLNVLESIIISWKLFIF CAVMIILVRPISILLSTMNTEISK RERAMVSMMAPRGIVVLTVAQFFGGFVEKGT PM AEYITPVTFGLVFITVVIYGFSL PLSKMMHLSSTEPPGVIIVGESEFSFHLGAKLRE HHIPVMTFNLFNNTSKRAQELDFE VFEGNLLSSNDRIYADMTRYNKCLLMTQSFVFN

		LAFNELVPEFGLKKNVNMMPVSFSD EHARSNLDGPIRNHILFSDFTSHWFNRYIVEHN ILEMPVSSKDNLTAYDMVLYHIDD NNEVTFKRDNQNITNSEEGMIGYLKDAYLHSNI"
gene	complement (434306..4362 58)	/locus-tag="SSP0398"
CDS	complement (434306..4362 58)	/locus-tag="SSP0398"
		/note="similar to gi 27468981 ref NP-765618.1  [Staphylococcus epidermidis ATCC 12228], percent identity 77 in 653 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="fructose-bisphosphatase" /protein-id="BAE17543.1" /db-xref="GI:72494222" /translation="MQKSADKSLKDRYLDLLSQQ FNTKEELATEIINLESILELPKGT EHFVSDLHGEFHAFQHVLNRNGSGNVRSKINDIFQ DTLTRKEINEFSALVYYPEEKLKI IKNSFSSKSELNEWYITTINRLIKLITYASSKYT RTKLRKSLPKNYVFIIEELLYKSN KYNNKHSYYETLINQIIIELEQSDDLIIIGLSFTVQ HLVVDHLHVVGDIYDRGPEPDKIM ETLIDYPSVDIQWGNHDVLWIGAYAGSKVCLANL LRICARYDNLDIIEDAYGINLRPL LTLAEKHYDGKNKAFRPKNAEGLTELELEQITKI HQAIAIIQFKLEAPIIKRRPTFEM EERLVLESINYEKNEATLYGKTYPLENTCFQTID PNGPNKLTDEESEVMDKLLLSVQQ SEKLKRHMTFLMQGTLYLPYNGNLLIHGCIPVD ENGEMESMVINDVKCYGRDLLDHF EDYVREAFDHKDIQDDLATDLVWYLWTGKYSSLF GKRAMTTFERFIKDKTAHKETKN PYYHLREDVNMCKMKLKDFGLDPEQGHIINGHTP VKEIDGEDPIKAEGKMIVIDGGFS KAYQSTTGIAGYTLLYNSFGMQLVAHQHFNSKKH VLLNGADELSIRRVVDKELQRQKI RHTNTGQDIQEKIDILKELMHDRYVN"
gene	436760..438304	/locus-tag="SSP0399"
CDS	436760..438304	/locus-tag="SSP0399"
		/note="similar to gi 27468505 ref NP-765142.1  [Staphylococcus epidermidis ATCC 12228], percent identity 75 in 510 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="high affinity proline permease" /protein-id="BAE17544.1" /db-xref="GI:72494223" /translation="MFTLGTSLSSQVDPNWQTYI MLVVYFVVLVIGYYGFKQSTGNV SEYMLGGRNIGPYVTALSAGASDMSGWMIMGLPG EVYTTGLSAAWLAIGLTLGAYINY IVVAPRLRVYTEKAGDAITLPDFFKNRLDDKSNS IKIISGAIIVVFFTLYTHSGMVSG GVLFEAFGVNYHIGMLLVAVIVIAYTFFGGYLA VSLTDFFGQGVVMIIAMVMVPIVAM"



		<p>LQLSGLDTFTQTAELKPTNLDLFKGTTVIGIISF  FAWGLGYFGQPHIIVRFMSIKSVK  QLPTARRFGIGWMAISLLGAVGVGLTGITFINQS  GTDIENPETLFVLMGQILFHPLVG  GFLLAAILAAIMSTISSQLLVTSSSLTEDFYKLI  RGEEAAKEHEKEFVLVGRLSVIIV  AIVSIWIAWSPNDTILGLVGNWAGFGAAFGPLV  LLSLYWKGLSRTGAVSGMLSGAIV  VIIWIAFVKPLGDVNDFFNLYEIIIPGFLTSLIVT  VVVSKFTKKPQIDVEADLTDVRRRL VKTGED"</p>
gene	complement(438504..4391 12)	/locus-tag="SSP0400"
CDS	complement(438504..4391 12)	<p>/note="similar to  gi 27468980 ref NP-765617.1   [Staphylococcus epidermidis ATCC  12228], percent identity 76 in 200  aa, BLASTP E(): 2e-82"  /codon-start=1  /transl-table=11  /product="putative alkaline  phosphatase"  /protein-id="BAE17545.1"  /db-xref="GI:72494224"  /translation="MEQILTDFISTWGYAAITIL  ILLENILPFIPSEIILTFAGLMSV  KSDLSIPVLFTISTIASLIGLLVLYYISRLVSEE  RLYRFVDKYGKWIKLKGKDVARAN  DWFKKYGAIADFICRFIPVLRVLITIPAGINRMN  VMLFAILSLIGTTIWNFALIYLGK  MLSGSWDMLMNLHTYSYIMYVIIILAVIFIVYR  LFKKNRAQ"</p>
gene	439380..440657	/locus-tag="SSP0401"
CDS	439380..440657	<p>/locus-tag="SSP0401"  /note="similar to  gi 27468974 ref NP-765611.1   [Staphylococcus epidermidis ATCC  12228], percent identity 72 in 423  aa, BLASTP E(): 0.0"  /codon-start=1  /transl-table=11  /product="putative permease of the  major facilitator superfamily"  /protein-id="BAE17546.1"  /db-xref="GI:72494225"  /translation="MDQKRTNIRWYFAIAFFIIG  VIAYMDRSNISIIAGPMMEDLHLN  KTQFGLLASFFSLGYALMQVPSGFLAEKFGSKKM  LTIALVWWSAFTILTGVVKNHGML  YAVRFLFGIGEAPMYPNSAVFNTNWFAGEKGR  SSALLAGSYFGPVIAPVVTIAIVN  MFGWQAVFYIFGAIGFIIAILWMVIAKDLPEQHK  MVNEAEKSYIMENRDIKTEKSNA  PWNIFLKRFSFYALAAQYFVVQFVVSFLIWLPT  YLTEQYNVKLTDPMAWAAGAPWI  AMFLLILCGGAISDKLLQSGMSRFIARASIAITG  FVVFCISLFMSIQTDNLVTNVIWL  SLCLGGIGIATGMSWAAATDLGRNFSGSVSGWMN  LWGNIGALLSPLLAGMMVDIVGWT  VTLELVIIIPVVFIIIMWFFVKPDQPLIVEKEDL"</p>
gene	440719..441003	/locus-tag="SSP0402"

CDS	440719..441003	/locus-tag="SSP0402" /note="similar to gi 27468973 ref NP-765610.1  [Staphylococcus epidermidis ATCC 12228], percent identity 51 in 90 aa, BLASTP E(): 8e-21" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17547.1" /db-xref="GI:72494226" /translation="MITINAIMKVDAAQRRNYLA LIEPLKRASNQEAGALYYEHFENT DEPNTFAFIERYKDEQALEAHNQSEHFQQFFSEV KQYLVEEPEIKVLSSN"
gene	441515..443440	/locus-tag="SSP0403"
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gene	complement(443569..444780)	/locus-tag="SSP0404"
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gene	complement(444780..445943)	/locus-tag="SSP0405"
CDS	complement(444780..445943)	/locus-tag="SSP0405"
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gene	446125..446538	/locus-tag="SSP0406"
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gene	447705..448235	/locus-tag="SSP0409"
CDS	447705..448235	/locus-tag="SSP0409" /note="similar to gi 27468966 ref NP-765603.1  [Staphylococcus epidermidis ATCC 12228], percent identity 33 in 175 aa, BLASTP E(): 4e-27" /codon-start=1 /transl-table=11 /product="putative truncated transcriptional regulator" /protein-id="BAE17554.1" /db-xref="GI:72494233" /translation="MKDIKTILNEKNKLKTVRVM LEQKELEIEKEMQSHKTLAEIRQ FKQYIGRRSEAPLEKLLETCTYVNQKPKMKQFKQ SVLYRIIPIGIFQYTALIASMVTK KWWPLLSTSPILFTYAVNFTIFTYTALSYVCPNC QATFKPNLKQWMFSAHTPKTRKLQ CPHCDQDHHCVIAIVQS"
gene	448416..449096	/locus-tag="SSP0410"

CDS	448416..449096	/locus-tag="SSP0410" /note="similar to gi 57285200 gb AAW37294.1  [Staphylococcus aureus subsp. aureus COL], percent identity 68 in 225 aa, BLASTP E(): 8e-89" /codon-start=1 /transl-table=11 /product="gluconate operon transcriptional repressor" /protein-id="BAE17555.1" /db-xref="GI:72494234" /translation="MKYDYPEQWLEGVSKGEMIA AEIRLRIVDGKIAPDTLLTENQIA KEYNVSRSRPVRDAFKLLKQDQLIHLERMGAEVL FEDKEKKELYDLRIMLESFAFSRI KNLNHEQIVKEMRKQLEMMKVAVQFEDAEAFTEH DMKFHEVTIMASKHQYLKTFWNNL RPVMESLILLSMSKRMNENLEDFERIHHNHEIFI EAIEQQDAKKLNKAFHLNFDDVGE DIDSFWLT"
gene	449133..450680	
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gene	450870..452228	
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gene	452464..452583	/locus-tag="SSP0413"
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gene	452619..453380	/locus-tag="SSP0414"
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gene	453652..454725	/locus-tag="SSP0415"
CDS	453652..454725	/locus-tag="SSP0415" /note="similar to gi 23100678 ref NP-694145.1  [Oceanobacillus iheyensis HTE831], percent identity 71 in 351 aa, BLASTP E(): e-141" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17560.1" /db-xref="GI:72494239"

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gene	455760..455951	/locus-tag="SSP0417"
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CDS	complement(456154..456423)	/locus-tag="SSP0418" /note="similar to gi 15925469 ref NP-373003.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 44 in 86 aa, BLASTP E(): 3e-16" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17563.1" /db-xref="GI:72494242" /translation="MNFDEKLEALRKSIDRTSFQ FHFEDLFDKDEWIQMPILERQQLE KTRFRKYVAQHNHLRIPYASEEHIRMRMNSLYDF NEIKHNFKDYV"
gene	456628..457332	/locus-tag="SSP0419"

CDS	456628..457332	/locus-tag="SSP0419" /note="similar to gi 49487262 ref YP-044483.1  [Staphylococcus aureus subsp. aureus MSSA476], percent identity 65 in 234 aa, BLASTP E(): 6e-79" /codon-start=1 /transl-table=11 /product="putative short chain dehydrogenase" /protein-id="BAE17564.1" /db-xref="GI:72494243" /translation="MVELQDKVAVVTGASSGIGA SIAETLANQGKVVLTGRDESRLA EVAKRIQDNKQAVVETSIVDVTHKEEVTELVEKT KEKFGQIDILVNSAGLMLSSAITE GDVEAWEAMIDVNIKGTLYTINAVLP SMLNQSSG HIINIASISGFVTKKSTLYSASK AAVHSITQGLEKELAKTGVRVTSISPGMVDTPLS GDTDWGARKKLDPKDIAEAAIYAL QQPSHVNVNEVTVRPV"
gene	457581..458081	/locus-tag="SSP0420"
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gene	complement(458177..458545)	/locus-tag="SSP0421"
CDS	complement(458177..458545)	/locus-tag="SSP0421" /note="similar to gi 15888020 ref NP-353701.1  [Agrobacterium tumefaciens str. C58], percent identity 53 in 115 aa, BLASTP E(): 2e-30" /codon-start=1 /transl-table=11 /product="putative glyoxalase family protein" /protein-id="BAE17566.1" /db-xref="GI:72494245" /translation="MFNQFLGIDHVQLAAPPHNE SLAKAFYSDKLGFKETIAKPSNLAK NGGVWFQVGDQQLHIGVQDDFKPATKAHPAFLVQ NASDIRKELEAKEIEIIYGDELEG ANRFYIYDPFGNRIEIIEWL"
gene	458758..459633	/locus-tag="SSP0422"
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39)

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64 in 685 aa, BLASTP E(): 0.0"

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12228], percent identity 57 in 264  
aa, BLASTP E(): 6e-91"  
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protein"
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		<pre> /protein-id="BAE17621.1" /db-xref="GI:72494300" /translation="MNIGVISDLHIDRHKSLKPK DYEYELIKAIQRNQVELLLIAGDI SNNYKLTQAFIKSVEAQAQIKVLFIPGNHDFWSA DTNATSAEILEEYMGMEACLIGKP YHLNDAWAIVGNTGWYDYSYASPEFSLERIARRK YYGATWQDKVKIDWPMDDRKLSRI AANQAIKDIEKVKDKQIILMTHIVTHPKFAVPMP HRLFDYFNAFIGTSDFDEIYKKYP IRYSIMGHVHFRNRFDEQGVTYICPCLGYQREWR SDDVTREIDHALNIIQI" </pre>
gene	complement(513368..513976)	/locus-tag="SSP0477"
CDS	complement(513368..513976)	/locus-tag="SSP0477"
		<pre> /note="similar to gi 57286437 gb AAW38531.1  [Staphylococcus aureus subsp. aureus COL], percent identity 65 in 202 aa, BLASTP E(): 4e-77" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17622.1" /db-xref="GI:72494301" /translation="MNSNILSVKPISQLFIPMI MGCEGVSAAMILQFNHLNIPATEI MRHWPRHRNNPYKGYVGHHLWIKLGYHQTIFPTA LVPHLRRYSNHVVDSTGQSLTDLC HIIDQGQPVVIYHTVLGKRPYRRTYKLDNQPTKL VANIHVTVLVGYDAQHYIIDPLW SHLGKSFILPAIIPTKYQLMKIKKSKLEQSYDAP GRMSFHLS" </pre>
gene	514156..514620	/locus-tag="SSP0478"
CDS	514156..514620	/locus-tag="SSP0478"
		<pre> /note="similar to gi 15925425 ref NP-372959.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 34 in 155 aa, BLASTP E(): 1e-24" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17623.1" /db-xref="GI:72494302" /translation="MNYIIIEELPTLSVIGEKKIY ATGQKAQENIFMFWMFEFDDSGKKD QLLELGNNQLPGLLGVCCKPHDSGEIHYLIGVTSE HKYDKWRNIELEGGRYLVFDAKGP VPESIKKAMQQINKDILPKLDYEIRHAPFFELYK EGAIREDDYVTEIWLPIV" </pre>
gene	complement(514944..516149)	/locus-tag="SSP0479"
CDS	complement(514944..516149)	/locus-tag="SSP0479"
		<pre> /note="similar to gi 49484651 ref YP-041875.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity </pre>

		66 in 387 aa, BLASTP E(): e-148"
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		/transl-table=11
		/product="putative permease of the
		major facilitator superfamily"
		/protein-id="BAE17624.1"
		/db-xref="GI:72494303"
		/translation="MDKTSNPRLPIMIIIMLGIM
		TTFGPLTIDMYVPSLPNVQNAFDT
		TASQVQLTLSFAMIGLAVGQFIFGPLSDAYGRKK
		VALIIISLYVIASLIAVFTTSLSI
		LLTLRLIQGLTGGGVIVIAKASIGDQHKGKALAK
		GLASLLVVNGIISIIAPLIGGYAL
		TIANWKAIFLILTIISFAILLFAFFKMEETRSH
		LSKLNFSAlFKDFGSLLKKPAFII
		PMLLQGLTYVMLFSFSSAAPFITQKIYDMTPQQF
		SILFAINGIGLIIVSQLTATLVEY
		INRYLLLILLTLIQIAGVILICFTLIFHLPLWVL
		VIAFFLNVCPTVGIGPLSFTLAME
		SRTGGSGNASSLLGLFQFILGGIMSPLVGLKGEY
		SVMPYIIILIITTTIFIVLLEISLK
		SFTFKNSSN"
gene	516423..516806	/locus-tag="SSP0480"
CDS	516423..516806	/locus-tag="SSP0480"
		/note="similar to
		gi 27468915 ref NP-765552.1
		[Staphylococcus epidermidis ATCC
		12228], percent identity 71 in 127
		aa, BLASTP E(): 3e-51"
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		/transl-table=11
		/product="conserved hypothetical
		protein"
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		/db-xref="GI:72494304"
		/translation="MSLSKTQYEVIKFIIVGGIN
		TFNYYVVYLILLKLLGINYLISHV
		SGFVVSFIISYYLNCYFVYKVKPTWRKFIQFPLT
		QVVMGMQGTGLLYVFVQWFHISV
		IAPFAGLIITIPITFVLSKYILRDE"
gene	517066..517935	/locus-tag="SSP0481"
CDS	517066..517935	/locus-tag="SSP0481"
		/note="similar to
		gi 57285147 gb AAW37241.1
		[Staphylococcus aureus subsp.
		aureus COL], percent identity 79
		in 285 aa, BLASTP E(): e-127"
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		/transl-table=11
		/product="putative cation efflux
		family protein"
		/protein-id="BAE17626.1"
		/db-xref="GI:72494305"
		/translation="MTQSENKIAQKGAYLSLIV
		YIILSIVKYFVGYYVYDAAVRADS
		LNNMTDIIIVSLAVIIGLKISIKPADKNHPYGLK
		SENISTLLVSFIIMFVGIIQVVIEN
		FPRIFGAHATPNAITIIYVSVISGVIMIIVFFIN
		QKLAKRTNSSSLNSAAKDNLSDAL
		VSIGTAIGLVFTQIGFSIVDIILATILGLLIIYT
		GFGIFKESIFTLSDFNEQELDAY
		KNYVLEIEEVIDVQSIKGRYHGSSIFVDVTIVVE

		SDLSLEEAAHHICDKVEHHMHEKGI SSVYVHPEPVSIIQ"
gene	complement(518225..518593)	/locus-tag="SSP0482"
CDS	complement(518225..518593)	/locus-tag="SSP0482"
		/note="similar to gi 2735514 gb AAB94658.1  [Staphylococcus carnosus], percent identity 50 in 114 aa, BLASTP E(): 1e-25" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17627.1" /db-xref="GI:72494306" /translation="MKKLLASFASITIAATGYG VTSTADAAETPVQQSSQNSDVYS QFIEAGGTKALWDNIVMPESGPNDAVNELGYRG LGQTKAEAWGKGSVEEQTKGMIKYA EDRYGSIDAAIDFRLANGWW" /locus-tag="SSP0483"
gene	518971..519657	/locus-tag="SSP0483"
CDS	518971..519657	/locus-tag="SSP0483"
		/note="similar to gi 49484632 ref YP-041856.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 75 in 228 aa, BLASTP E(): e-101" /codon-start=1 /transl-table=11 /product="putative phosphoglycerate mutase" /protein-id="BAE17628.1" /db-xref="GI:72494307" /translation="MPKLILCRHGQSVWNAENLF TGWADVDLSEQGENEAITSGKKLK AQGIEIDIVYTSLLERAIKTTYHLLNESNQLFIP IIKSWRLNERHYGGLQGLNKDDAR KKFGEDQVHIWRRSYDVAPPKQDEAQRESYLNDR KYEHLDRRVMPESLSKDTLVRVI PYWNDQISQQLLDGKTVLVSAHGNSLRALIKYLE NVSDEDIVGYEIKTGAPLIYELTD DLQVIDKYYL"
gene	complement(519913..520017)	/locus-tag="SSP0484"
CDS	complement(519913..520017)	/locus-tag="SSP0484"
		/note="similar to gi 57285145 gb AAW37239.1  [Staphylococcus aureus subsp. aureus COL], percent identity 91 in 34 aa, BLASTP E(): 9e-10" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17629.1" /db-xref="GI:72494308" /translation="MKLDLQTARRNLNSPNIKTR KRARKIIQQHKRSK"
gene	520237..521700	/locus-tag="SSP0485"
CDS	520237..521700	/locus-tag="SSP0485"

		<pre> /note="similar to gi 49484631 ref YP-041855.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 69 in 473 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="putative permease of the major facilitator superfamily" /protein-id="BAE17630.1" /db-xref="GI:72494309" /translation="MTQKTKIIMILMMLFGGFFG LLNETLLTTALPSIMKDFDIDYTQ VQWLTTAFLLTNGIVVPLSAMIIQRFSTRQVFLT AIFIFFIGTIIAGFSPNFTVLLCA RIVQAMGSGIMMPLMMTTILDIFEPHERGKYMGT FGLVIGLAPAIGPTLSGYLVEYFD WRSLFHVVAPIAALTFLGAIKFVKNVGTNRKAPI DILSIALSVLGFGGLLYGTSSLSR DGWNDPVVLTTVIGGLILVVLFIQRQTRLETPLL DFSVKNSQFAVGIVIMAFTMIAM IGSETVLPFMFVQNIMKDTALQSGLILLPGAIVMG IMSVASGFLYEKYGAKILAFIGML IVVVTSSYFIFMDENTSSAILATIIYAIRMIGIAL GLMPLMTHMTMQLSREMNAHGSSM TNTVQQISASIGTAGLITIMSQVAKDFSPNMSDY KGMDKKEMAMQIQHEALLSGYHAA FWFAVIISIISLISVFMLKSKRKINQEQQELEQQ QSK" </pre>
gene	522002..522196	/locus-tag="SSP0486"
CDS	522002..522196	<pre> /locus-tag="SSP0486" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17631.1" /db-xref="GI:72494310" /translation="MKVKVDNVKVDYDSFQALLQH YSNKEVGFSDEIQLSQKLASIYQI YNQTDELHLGALAIEIHLVP" </pre>
gene	complement(522300..523532)	/locus-tag="SSP0487"
CDS	complement(522300..523532)	<pre> /locus-tag="SSP0487" /note="similar to gi 57285140 gb AAW37234.1  [Staphylococcus aureus subsp. aureus COL], percent identity 68 in 407 aa, BLASTP E(): e-164" /codon-start=1 /transl-table=11 /product="fmhA protein" /protein-id="BAE17632.1" /db-xref="GI:72494311" /translation="MFFVNLTPEEFQTFTQNHS HYTQSRVNYEAQYNAHLLGVKDDN DEVIAAGMFTEARALKFFKYFYSQRGPILDYTNL SLVDFYFSELT KYLKQHNCLYVLL DPYILENLRNADGEIKKSYDNRMLISTLEKLGKY HQGYPVGYSKTSQIRWLSVLDLKD KSEQQLLKEMDYQTRNRIKRTTEEMGVKVRQLPIE ETDRFFKLFKMAEEKHGFSFRDEP YFEQLQKDYQGFASIQLAYIDLSEYVNGLKQKLD </pre>

gene	523810..524178	TLNHQMKDVEAALQESPNSKKQKT
CDS	523810..524178	KQTQLNQQIVSTQRKIDDTNKTITTDGPVLDLAA
		AIYIYNDYEVYYLSSGSNPDYNAY
		MGAYKLQWEMIKFAKNHNIDRYNFYGITGDFSED
		AIDYGVQQFKKGFNADVEEYIGDF
		VKPIKPLLYKLGKRIGKL"
		/locus-tag="SSP0488"
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		/note="similar to
		gi 27468906 ref NP-765543.1
		[Staphylococcus epidermidis ATCC
		12228], percent identity 54 in 118
		aa, BLASTP E(): 5e-35"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="BAE17633.1"
		/db-xref="GI:72494312"
		/translation="MKKIITLIVISTLMIAGCSS
		GKYADKIDKAVNKQQHYQKKLAEQ
		HKGDIERKFDKKDANIYVYEKGFVIIAYKPIKN
		DEEIHYYAYEYKDGKTTFKKDFNS
		RGYIQKHDPDYKEENMDLDE"
gene	524206..524811	/locus-tag="SSP0489"
CDS	524206..524811	/locus-tag="SSP0489"
		/note="similar to
		gi 27468905 ref NP-765542.1
		[Staphylococcus epidermidis ATCC
		12228], percent identity 53 in 199
		aa, BLASTP E(): 3e-57"
		/codon-start=1
		/transl-table=11
		/product="putative
		protein-disulfide isomerase"
		/protein-id="BAE17634.1"
		/db-xref="GI:72494313"
		/translation="MKKAWLSIVLVLTLVLATAC
		TNPEDTHKDDKTTSDGKIKIIEYG
		DFKCPYCKKVEKNVMPKCLKKHYIDTDKVDYQFVN
		MAFLGDDSIIGSRAGHAVQRLAPE
		QYLKFQELMFKQQPNSEKAWITNQIVDQQIDKLK
		INTTLKKEIKDDYKQENSKSWVAA
		KKDQKQYKDNHIETAPTFFVHGQKVEDPYDFENY
		KKILEKE"
gene	524996..526528	/locus-tag="SSP0490"
CDS	524996..526528	/locus-tag="SSP0490"
		/note="similar to
		gi 21284057 ref NP-647145.1
		[Staphylococcus aureus subsp.
		aureus MW2], percent identity 71
		in 517 aa, BLASTP E(): 0.0"
		/codon-start=1
		/transl-table=11
		/product="putative ABC-type Mn Zn
		transport system periplasmic Mn
		Zn-binding protein"
		/protein-id="BAE17635.1"
		/db-xref="GI:72494314"
		/translation="MKQITYISIMVLAFMVVLG
		CGKGESDNTKSNEKIKINTTVFPL
		KSFAEQIGGKHVEVNSIYPAGTDLHNYEPTQKDI
		INASKADLFLYTGDNLDPVAKKVA



		STIKKDDKKLALEDKLDKSQLLTDQHSHEEEEGHD HDEHHHHGGYDPHVWLDPKFDQTF AKEIKDELIKKDPKHKKTYEKNYEKLNDLKEID KDLKSITENKEGNTIFISHE SIGY LAERYDFVQKGVQNMNAEDPSQKSLSNIVKEIKD SGAKYILYEDNVS NKVTD TIRKET EAKPLKFYNMESLNKSQQQDYKLSYQSLMKKNII NMDKALSDSIQTEDDKEQSKHDKA ISDGYFKDSQVKDITLG DYKGNWQSVYPYLKDG LDEVMEHKAEDDDSMSAKAYKSY EKGYKTDISHITISNDTITFEKDGKKETGKYVYD GKDILKYEKGNRGVRYTFKLVDQN SHLPKYVQFSDHNIEPKAAHFHIFMGNNKDKIL KELDNWPTYYPNSLSSEEIKEEML AH"
gene	526702..527223	/locus-tag="SSP0491"
CDS	526702..527223	/locus-tag="SSP0491" /note="similar to gi 27467182 ref NP-763819.1  [Staphylococcus epidermidis ATCC 12228], percent identity 58 in 171 aa, BLASTP E(): 7e-56" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17636.1" /db-xref="GI:72494315" /translation="MIMTKFNFDAAHSVVEFSVK HLMISNIKGRFTEFDANIDGDIND LSTIKGDF TINASSIDTRVDDRDAHLRSGDFLDV ENNPEIKFEITKADEKSITGNVTI KGETNEETF DLSYEGQSKNPMNGATTVG FIVNGS INREKYGITFNQALETGGVMIGKD VKFQVSLEFALED"
gene	complement(527541..528161)	/locus-tag="SSP0492"
CDS	complement(527541..528161)	/locus-tag="SSP0492" /note="similar to gi 15925681 ref NP-373215.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 35 in 202 aa, BLASTP E(): 2e-34" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17637.1" /db-xref="GI:72494316" /translation="MNTPIKNYADTF SKELNLTQ GIYKYIFYFISFMIIMVIPRMLD NSFQLTLALMLYILFIFIGSLVLILFVIKKLIMT WGDSKKTYIAVGFSSAIVFGIYIL SEYLLRHYP I FIFWSPNQTTNFIIIGIILLLTMA ICLLKKKYFAGLILILSLPNIIS RIFTGGDYSNKNFLIISIVLTIISLSFIAYIVV QYYRDKKSIDNN"
gene	complement(528303..528641)	/locus-tag="SSP0493"
CDS	complement(528303..528641)	/locus-tag="SSP0493" /note="similar to gi 15925682 ref NP-373216.1

		[Staphylococcus aureus subsp. aureus Mu50], percent identity 71 in 112 aa, BLASTP E(): 1e-40" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="BAE17638.1" /db-xref="GI:72494317" /translation="MSISDQMMKGLLDGAILGLI AQGETYGYEILDKLKSQQFPEISD GSIYPVLLRLNKKGYVTSVSKKSMTGGPKHKYYSS ITDTGKNELNQFKANWHYLNNGMN NLMRSVNDVN"
gene	528738..529331	/locus-tag="SSP0494"
CDS	528738..529331	/locus-tag="SSP0494" /note="similar to gi 49484890 ref YP-042114.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 45 in 188 aa, BLASTP E(): 5e-47" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17639.1" /db-xref="GI:72494318" /translation="MTIDLKIGKIPATNALHHIG VKTLEDIAGYDRITLLAIHGVGPK AMDILEDNLKKHNMNFKEDIGFDVPFHLTGDLKC DNAPKRRVMLDFLIGSALVDKDKL QAIVAEDFKWEVVDAFQLTGFDIFYQELEDHKET IVSIDVKMNISHGKSGALHGTQIL ENGTTIYFADMFEFTSHRKDAVKKSITSYIIMNE GES"
gene	529332..529805	/locus-tag="SSP0495"
CDS	529332..529805	/locus-tag="SSP0495" /note="similar to gi 27468904 ref NP-765541.1  [Staphylococcus epidermidis ATCC 12228], percent identity 48 in 154 aa, BLASTP E(): 1e-35" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17640.1" /db-xref="GI:72494319" /translation="MSVKIVENNIIFTREFKATA EQIFKAYTDQNLFEKWFHPQGATT EVYESDVQTGGNAFFAIRAPQGTSYTVTQYTEVI QPTLIDYNDYFADKDGNIQKMG MHNTIHIEDNDNGVAKLTSVAVLPDPKAAQQLLD MGVEEGMNSTFDNLETLLLETL"
gene	529892..530068	/locus-tag="SSP0496"
CDS	529892..530068	/locus-tag="SSP0496" /note="similar to gi 49484620 ref YP-041844.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 46 in 58 aa, BLASTP E(): 5e-09" /codon-start=1 /transl-table=11

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                                /product="hypothetical protein"
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                                /db-xref="GI:72494320"
                                /translation="MNKRYMKVLGLYSFSTLIPT
                                VLLNEKTLSSHTFKWFLRTLGYG
                                IFAYGLHFLSKFKQ"
gene      complement(530387..5306 /locus-tag="SSP0497"
11)
CDS       complement(530387..5306 /locus-tag="SSP0497"
11)

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                                /note="partial similar to
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                                [Exiguobacterium sp. 255-15],
                                percent identity 80 in 61 aa,
                                BLASTP E(): 3e-24"
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                                /transl-table=11
                                /product="putative truncated
                                Beta-glucosidase"
                                /protein-id="BAE17642.1"
                                /db-xref="GI:72494321"
                                /translation="MIIFKNAYVTYFLMGYTPWG
                                IIDIIISFTTGEMKKRYGLIYVDRD
                                NEGHGTLERKKKASFDWYRNVIKTNGESLN"

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gene      complement(530598..5309 /locus-tag="SSP0498"
99)
CDS       complement(530598..5309 /locus-tag="SSP0498"
99)

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                                /note="similar to
                                gi|50591017|ref|ZP-00332350.1|
                                [Streptococcus suis 89/1591],
                                percent identity 39 in 134 aa,
                                BLASTP E(): 5e-20"
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                                /transl-table=11
                                /product="conserved hypothetical
                                protein"
                                /protein-id="BAE17643.1"
                                /db-xref="GI:72494322"
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                                PVSSQYIADSINSNATLVRKICRY
                                LRDGHYIQSSQGISGYSLSSSANEIHLGDLYQLI
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                                SHALDEIYSEVDTTIINKLNTYTIQSVIDHF"

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gene      531194..532018
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=> d hist

(FILE 'HOME' ENTERED AT 16:31:09 ON 16 DEC 2008)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:31:20 ON 16 DEC 2008  
SEA (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

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-----
1  FILE IFIPAT
2  FILE USPATFULL
1  FILE WPIDS
1  FILE WPINDEX

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L1 QUE (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

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FILE 'USPATFULL, IFIPAT' ENTERED AT 16:32:25 ON 16 DEC 2008
L2      3 S L1

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:33:15 ON 16 DEC 2008
      SEA ENTEROCOCCUS DURANS STRAIN 141-1
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L3      QUE ENTEROCOCCUS DURANS STRAIN 141-1
      SEA ENTEROCOCCUS DURANS STRAIN 152
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L4      QUE ENTEROCOCCUS DURANS STRAIN 152
      SEA ENTEROCOCCUS DRANS 141-1
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L5      QUE ENTEROCOCCUS DRANS 141-1
      SEA ENTEROCOCCUS DURANS 141-1
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L6      2 FILE USPATFULL
      QUE ENTEROCOCCUS DURANS 141-1
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FILE 'USPATFULL' ENTERED AT 16:36:57 ON 16 DEC 2008
L7      2 S L6

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:37:29 ON 16 DEC 2008
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      1 FILE AGRICOLA
      1 FILE BIOENG
      1 FILE BIOSIS
      1 FILE CABA
      2 FILE CAPLUS
      1 FILE FROSTI
      1 FILE FSTA
      1 FILE HEALSAFE
      1 FILE LIFESCI
      1 FILE MEDLINE
      1 FILE PASCAL
      1 FILE SCISEARCH
      2 FILE USPATFULL
L8      QUE ENTEROCOCCUS DURANS 152
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FILE 'AGRICOLA, BIOENG, BIOSIS, CABA, CAPLUS, FROSTI, FSTA, HEALSAFE,
LIFESCI, MEDLINE, PASCAL, SCISEARCH, USPATFULL' ENTERED AT 16:38:26 ON 16
DEC 2008
L9      15 S L8
L10     3 DUP REM L9 (12 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:40:04 ON 16 DEC 2008

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SEA LACTOCOCCUS LACTIS C-1-92

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 1 FILE CAPLUS  
 11 FILE GENBANK  
 1 FILE PROMT  
 2 FILE USPATFULL

L11 QUE LACTOCOCCUS LACTIS C-1-92  
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L12 15 S L11  
 L13 14 DUP REM L12 (1 DUPLICATE REMOVED)

=> d 113 1

L13 ANSWER 1 OF 14 CAPLUS COPYRIGHT 2008 ACS on STN DUPLICATE 1  
 AN 2006:299263 CAPLUS  
 DN 144:306860  
 TI Foaming composition of benign microbes for competitive exclusion of  
 undesired microbes  
 IN Podtburg, Teresa C.; Schmidt, Bruce; Cords, Bruce; Grab, Lawrence A.;  
 Halsrud, David A.  
 PA USA  
 SO U.S. Pat. Appl. Publ., 21 pp.  
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 DT Patent  
 LA English  
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	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 20060067915	A1	20060330	US 2005-233922	20050922
PRAI	US 2004-612882P	P	20040924		

=> d 113 2

L13 ANSWER 2 OF 14 USPATFULL on STN  
 AN 2006:86130 USPATFULL  
 TI Composition and method for inhibition of microorganisms  
 IN Doyle, Michael P, Peachtree City, GA, UNITED STATES  
 Zhao, Tong, Peachtree City, GA, UNITED STATES  
 PI US 20060073129 A1 20060406  
 AI US 2003-535357 A1 20031124 (10)  
 WO 2003-US37526 20031124  
 20050518 PCT 371 date  
 PRAI US 2002-428863P 20021125 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 1238  
 INCL INCLM: 424/093.450  
 NCL NCLM: 424/093.450  
 IC IPCI A61K0035-74 [I,A]; A61K0035-66 [I,C\*]  
 IPCR A61K0035-66 [I,C]; A61K0035-74 [I,A]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 113 3

L13 ANSWER 3 OF 14 PROMT COPYRIGHT 2008 Gale Group on STN  
 ACCESSION NUMBER: 2003:81217 PROMT

TITLE: Natural Additives Kill Listeria.  
 SOURCE: Food Ingredient News, (March 2003) Vol. 11, No. 3.  
 ISSN: 1070-1788.  
 PUBLISHER: Business Communications Company, Inc.  
 DOCUMENT TYPE: Newsletter  
 LANGUAGE: English  
 WORD COUNT: 391  
 \*FULL TEXT IS AVAILABLE IN THE ALL FORMAT\*

=> d 113 4

L13 ANSWER 4 OF 14 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AM286415 GenBank (R)  
 GenBank ACC. NO. (GBN): AM286415  
 GenBank VERSION (VER): AM286415.1 GI:122087364  
 CAS REGISTRY NO. (RN): 917704-63-3  
 SEQUENCE LENGTH (SQL): 4615899  
 MOLECULE TYPE (CI): DNA; circular  
 DIVISION CODE (CI): Bacteria  
 DATE (DATE): 29 Oct 2008  
 DEFINITION (DEF): Yersinia enterocolitica subsp. enterocolitica 8081  
 complete genome.  
 KEYWORDS (ST): complete genome  
 SOURCE: Yersinia enterocolitica subsp. enterocolitica 8081  
 ORGANISM (ORGN): Yersinia enterocolitica subsp. enterocolitica 8081  
 Bacteria; Proteobacteria; Gammaproteobacteria;  
 Enterobacteriales; Enterobacteriaceae; Yersinia  
 PROJECT (PJID): GenomeProject:190  
 REFERENCE: 1  
 AUTHOR (AU): Delihhas,N.  
 TITLE (TI): Annotation and evolutionary relationships of a small  
 regulatory RNA gene micF and its target ompF in  
 Yersinia species  
 JOURNAL (SO): (er) BMC Microbiol., 3, 13 (2003)  
 REFERENCE: 2  
 AUTHOR (AU): Thomson,N.R.; Howard,S.; Wren,B.W.; Holden,M.T.;  
 Crossman,L.; Challis,G.L.; Churcher,C.; Mungall,K.;  
 Brooks,K.; Chillingworth,T.; Feltwell,T.; Abdellah,Z.;  
 Hauser,H.; Jagels,K.; Maddison,M.; Moule,S.;  
 Sanders,M.; Whitehead,S.; Quail,M.A.; Dougan,G.;  
 Parkhill,J.; Prentice,M.B.  
 TITLE (TI): The complete genome sequence and comparative genome  
 analysis of the high pathogenicity Yersinia  
 enterocolitica strain 8081  
 JOURNAL (SO): PLoS Genet., 2 (12), E206 (2006)  
 REFERENCE: 3 (bases 1 to 4615899)  
 AUTHOR (AU): Thomson,N.R.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (30-JUN-2006) Thomson N.R., Pathogen  
 Sequencing Unit, The Wellcome Trust Sanger Institute,  
 Genome Campus, Hinxton, Cambridge, CB10 1SA, UNITED  
 KINGDOM

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..4615899	/organism="Yersinia enterocolitica subsp. enterocolitica 8081" /mol-type="genomic DNA" /strain="8081"

		/sub-species="enterocolitica"
gene	complement(270..710)	/db-xref="taxon:393305"
CDS	complement(270..710)	/locus-tag="YE0001"
		/locus-tag="YE0001"
		/codon-start=1
		/transl-table=11
		/product="putative flavoprotein"
		/protein-id="CAL10146.1"
		/db-xref="GI:122087365"
		/db-xref="GOA:A1JHQ8"
		/db-xref="InterPro:IPR001094"
		/db-xref="InterPro:IPR008254"
		/db-xref="InterPro:IPR015702"
		/db-xref="UniProtKB/TrEMBL:A1JHQ8"
		/translation="MADITLISGSTLGSAEYVAE HLAEKLEEAGFTTETLHGPELDEL TLDGMWLIITSTHGAGDLPDNLQPLLEQIEQQRP DLSQVRFGAVGLGSSEYDTFCGAV RKLDQQLLIIQGAIRVGDILEIDVIKHEIPEDPAE IWVKNWINLL"
misc-feature	complement(273..704)	/locus-tag="YE0001"
		/inference="protein"
		motif:PFAM:PF00258"
		/note="Pfam match to entry PF00258 flavodoxin, Flavodoxin, score 117.3, E-value 1.9e-32"
gene	complement(802..1263)	/gene="asnC"
		/locus-tag="YE0002"
CDS	complement(802..1263)	/gene="asnC"
		/locus-tag="YE0002"
		/codon-start=1
		/transl-table=11
		/product="regulatory protein"
		/protein-id="CAL10147.1"
		/db-xref="GI:122087366"
		/db-xref="GOA:A1JHQ9"
		/db-xref="InterPro:IPR000485"
		/db-xref="InterPro:IPR011991"
		/db-xref="UniProtKB/TrEMBL:A1JHQ9"
		/translation="MSEIYQIDNLDRGILNALME NARTPYAELAKNFGVSPGTIHVRV EKMRQAGIITAACVHVNPKQLGYDVCCFIGIILK SAKDYP SALKKLESLEEVVEAYYT TGHYSIFIKVMCKSIDALQQVLINKIQTIDEIQS TETLISLQNPIMRTIVP"
misc-feature	complement(868..1173)	/gene="asnC"
		/locus-tag="YE0002"
		/inference="protein"
		motif:PFAM:PF01037"
		/note="Pfam match to entry PF01037 ASNC-trans-reg, AsnC family, score 61.4, E-value 1.2e-15"
misc-feature	complement(1111..1191)	/gene="asnC"
		/locus-tag="YE0002"
		/inference="protein"
		motif:Prosites:PS00519"
		/note="PS00519 Bacterial regulatory proteins, asnC family signature."
misc-feature	complement(1129..1194)	/gene="asnC"
		/locus-tag="YE0002"
		/note="Predicted helix-turn-helix"

		motif with score 1765.000, SD 5.20 at aa 24-45, sequence TPYAELAKNFGVSPGTIHVRVE"
gene	1449..2441	/gene="asnA" /locus-tag="YE0003"
CDS	1449..2441	/gene="asnA" /locus-tag="YE0003" /codon-start=1 /transl-table=11 /product="aspartate-ammonia ligase" /protein-id="CAL10148.1" /db-xref="GI:122087367" /db-xref="GOA:A1JHR0" /db-xref="InterPro:IPR004618" /db-xref="InterPro:IPR006195" /db-xref="UniProtKB/Swiss-Prot:A1J HR0" /translation="MKKQFIQKQQQISFVKSFFS RQLEQQQLGLIEVQAPILSRVGDGT QDNLSGSEKAVQVKVKS LPDATFEVVHSLAKWKR KTLGRFDFGADQGIYTHMKALRPD EDRLSAIHSVYVDQWDWERVMGDGERNLAYLKST VNKIYAAIKETEA AISAEFDIKPF LPEQIHFIHSESLRAKFPDLDAKGRERAI AKELG AVFLIGIGGKLADGKSHDVRAPDY DDWTSPSAEGFAGLNGDIIVWNPVLEDAFEISSM GIRVDAEALKRQLALTSDEDRCLKL EWHQSLLNGEMPQTIGGGIGQSRLVMLLLQQQHI GQVQCGVWGPEISEKVEGLL"
misc-feature	1455..2186	/gene="asnA" /locus-tag="YE0003" /inference="protein motif:PFAM:PF03590" /note="Pfam match to entry PF03590 AsnA, Aspartate-ammonia ligase, score 597.7, E-value 4.6e-177"
misc-feature	2055..2078	/gene="asnA" /locus-tag="YE0003" /inference="protein motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	2595..3266	/locus-tag="YE0004"
CDS	2595..3266	/locus-tag="YE0004" /inference="similar to sequence:INSDC:AE001895" /inference="similar to sequence:INSDC:AL646078" /note="Similar to Ralstonia solanacearum probable transmembrane protein RSP0410 or RS00867 SWALL:Q8XSQ7 (EMBL:AL646078) (224 aa) fasta scores: E(): 7.3e-36, 46.54 38d in 217 aa, and to Deinococcus radiodurans hypothetical protein DR0351 SWALL:Q9RXG2 (EMBL:AE001895) (227 aa) fasta scores: E(): 3.7e-17, 31.67 38d in 221 aa" /codon-start=1



		/transl-table=11 /product="putative membrane protein" /protein-id="CAL10149.1" /db-xref="GI:122087368" /db-xref="InterPro:IPR009781" /db-xref="UniProtKB/TrEMBL:A1JHR1" /translation="MARFHPLRHYSHARPRLLS VGAGIIAYFLLPSHFTVLLRVMVS WNIFAWLYLLFLWLQLLRNDPKKIRLIARVQDES ASMVLSIVSMACLASILVILFELS TANQLSGSAKAFHLVLTGMTLLVSWLLPTAFTM HYAHLFYLSRDESDAVLPLIFPKE VTEPTYWDFLYFSFTIGVASQTADVSTGTSDIR VVLLQSVLSFIFNMILGLSINVG AGLLN" /locus-tag="YE0004"
misc-feature	join(2643..2711, 2721..2777,2838..2906, 2934..3002,3192..3260)	/inference="protein motif:TMHMM:2.0" /note="5 probable transmembrane helices predicted for YE0004 by TMHMM2.0 at aa 17-39, 43-61, 82-104, 114-136 and 200-222"
gene	complement(3276..4742)	/locus-tag="YE0005"
CDS	complement(3276..4742)	/locus-tag="YE0005" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10150.1" /db-xref="GI:122087369" /db-xref="InterPro:IPR002035" /db-xref="UniProtKB/Swiss-Prot:A1J HR3" /translation="MLSLATLDLLLSISESELIE EMVVGLLASPQLAIFFEKFPRIKR ALMKDIPGWKQNLQQRIREAKVPAGLANEFALYQ QSQLEDSPLFYAHLPQIVVQLQQW HSPFATQAKTLLHTADLERNPQTGDSFQTLFLQR WRVSLTLQTITIIHQLEQEREQL LAELQQRLLALSGALEPILATNDGAAGRLWDMSQG HLQRGDYQLLLQYGDFLQQQPELQ QLAEQLGRSRSKAQPTPDARFEPYTMVVRQPD VPVEEVSGIHQSNLILRLLPTELVM LGMSELEFEFYRRLLERRLLTYRLQGDNWQEKTL QRPISLKSHDEQPRGPFIVCVDTS GSMGGFSEQCAKAFCLALLRIALEDNRRCYIMLF ATEIIHYELSSASGIEQAIRFLSQ HFRGGTDLAACLSSTLSKMEERDWDADAVIISD FIAQRLPEELIRKIKIQQAQHR FHAVAMSAYGKPGIMRIFDHIWRFDGLKSRLIR RWKR"
misc-feature	complement(4035..4100)	/locus-tag="YE0005" /note="Predicted helix-turn-helix motif with score 997.000, SD 2.58 at aa 215-236, sequence PELQQLAELGRSRSKAQPTP"
gene	complement(4746..6254)	/locus-tag="YE0006"
CDS	complement(4746..6254)	/locus-tag="YE0006" /codon-start=1 /transl-table=11

		/product="conserved hypothetical protein" /protein-id="CAL10151.1" /db-xref="GI:122087370" /db-xref="GOA:A1JHR5" /db-xref="InterPro:IPR003593" /db-xref="InterPro:IPR011704" /db-xref="UniProtKB/Swiss-Prot:A1J HR5" /translation="MAQSSQLAERISRLSSALES GLYERQEAIRLCLLAALSGESVFL LGPPGIAKSIIARRLKFAFRNARAFEYLMTRFST PEEVFGPLSIQALKEEGRYQRMGTG GYLPEAEIVFLDEIWKAGPAILNTLLTAINERRF RNGDREDSIPMRLLVITASNELPDA DSSLEALYDRMLIRLWLDREVQEKQNFRLLSRQ NENHNPVAENLSISDEEFYQWQPL IDKIALPDNCFELIFQLRQQLSAQEQAPYVSDRR WKKALRLLQASAFFSGRDEITPID LILLKDCLWHDLSLKLQQQLEQLLTHEGYQQQ SLLMKLQHIHAQWLKHQQQQSDHQ ALTVTKQSGMFSRKPQYSLPDHLTDSTLTFLQK PLSLHDIQVNHQLIEKEMLVQWLN KGGVLRKLNQVGYAQSIDAEVDDQLHITVLVDS RQSSILSQPGASTASVPPELLVEL AELENSLAEQRRFLSQHQPCLFPTSSWLAKIEAS LLNVAEQVKQLQQKLRGH"
gene	6708..8435	/gene="kup" /locus-tag="YE0007" /note="synonym: trkD"
CDS	6708..8435	/gene="kup" /locus-tag="YE0007" /codon-start=1 /transl-table=11 /product="potassium transport protein" /protein-id="CAL10152.1" /db-xref="GI:122087371" /db-xref="GOA:A1JHR6" /db-xref="InterPro:IPR003855" /db-xref="UniProtKB/Swiss-Prot:A1J HR6" /translation="MVFGFLSLIFWMLILIVSVK YLTYVMRADNAGEGGILTLMSLAG RNTSSRATSILVILGLIGGSFFYGEVVITPAISV MSAIEGLEIAAPALDPYIVPCISIA VLTLLFVIQKHGTGSGVGLFAPVMLVWFLTLALL GLRSIIANPEVLAALNPKWAI SFF TEYKSVSFFALGAVVLAITGVEALYADMGHFGKF PIRLAWFTTVLPSLVNLNYFGQAL LLKNPEAIKNPFFLLAPDWALIPLLILATLATVI ASQAVISGVFSLTRQAVRLGYLPP MRIIHTSEMESGQIYIPVINWTLYLAVVLVIVGF ERSSNLAAAYGIAVTGTMVITSVL FCTVALKNWHWNRFVYFLLVALLVIDVPMFSAN ALKLFSGGWLPLSLGLVMFIIMTT WKSERFSLRRMHEHGNSLEAMIASLEKSPVVRV PGTAVYMSRAMNVIPFALLHNLKH NKVLHDRVLLTLRTEDAPYVHNVNRTIEQLSP TFWRVVASYGWRETPNVEEIFHRC GLEGLPCQMMETSFFMSHESLILTKRPWYFLRG KLFIALSRNALRAADQFEIPPNRV

misc-feature	6711..8432	IELGTQVEI" /gene="kup" /locus-tag="YE0007" /inference="protein" motif:PFAM:PF02705" /note="Pfam match to entry PF02705 K-trans, K+ potassium transporter, score 854.9, E-value 1.7e-254" /gene="kup"
misc-feature	join(6717..6785, 6870..6938,6966..7034, 7068..7136,7194..7262, 7299..7367,7425..7493, 7566..7634,7662..7730, 7749..7802,7830..7886)	/locus-tag="YE0007" /inference="protein" motif:TMHMM:2.0" /note="11 probable transmembrane helices predicted for YE0007 by TMHMM2.0 at aa 4-26, 55-77, 87-109, 121-143,163-185, 198-220, 240-262, 287-309, 319-341, 348-365 and 375-393"
gene	8606..9025	/locus-tag="YE0008"
CDS	8606..9025	/locus-tag="YE0008" /codon-start=1 /transl-table=11 /product="ribose permease" /protein-id="CAL10153.1" /db-xref="GI:122087372" /db-xref="GOA:A1JHR8" /db-xref="InterPro:IPR007721" /db-xref="UniProtKB/Swiss-Prot:A1J HR8" /translation="MKKGALLNSDISAVISRLGH TDQIVIGDAGLPIPATTTTRIDLAL TQGVPGFLQVFEVVTQEMQVESAYLAQEIVKNNP QLHETLLAQLSQLEQHQNQIALH YISHEAFKEQTKQSRAVIRSGECSPFANIILCSG VTF"
gene	9033..10535	/gene="rbsA"
CDS	9033..10535	/locus-tag="YE0009" /gene="rbsA" /locus-tag="YE0009" /inference="similar to sequence:INSDC:AL627280" /inference="similar to sequence:UniProtKB:P04983" /note="Similar to Escherichia coli ribose transport ATP-binding protein RbsA SWALL:RBSA-ECOLI (SWALL:P04983) (501 aa) fasta scores: E(): 2.7e-148, 85.83 38d in 494 aa,and to Salmonella typhi high affinity ribose transport protein STY896 SWALL:Q8Z2R4 (EMBL:AL627280) (501 aa) fasta scores: E(): 1.1e-147, 85.62 38d in 494 aa" /codon-start=1 /transl-table=11 /product="putative ribose"

		transport ATP-binding protein"
		/protein-id="CAL10154.1"
		/db-xref="GI:122087373"
		/db-xref="GOA:A1JHS1"
		/db-xref="InterPro:IPR003439"
		/db-xref="InterPro:IPR003593"
		/db-xref="InterPro:IPR015861"
		/db-xref="UniProtKB/TrEMBL:A1JHS1"
		/translation="MQPLLQLKGIDKAFPGVKAL
		SGAALSVYPGRVMALVGENGAGKS
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		GREFVNHFGGIDWKKMYAEADLLLARLNISYSSH
		RLVGELSIGDQQMVEIAKVLSFES
		KVIIMDEPTDALTDTETASLFNVIKELKAEGRI
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		FIAEKPVNLTLENALIEMMVGRKLEEQYPRNLNP
		RGEKRLQVKQLCGPGVENVNFTLY
		SGEILGVAGLMGAGRTELMKIIYGALPRKSGFVM
		LDGREVVTHSPQDGLANGIVYISE
		DRKRDGLVLGMSVKENMSLTALRYFSRSGSLKH
		ADEQQAVADFIRLFNIKTPSMEQP
		IGLLSGGNQQKVAIARGLMTRPKVLILDEPTRGV
		DVGAKKEIYQLINQFKQEGLSIIL
		VSSEMPEVLGMSDRIIVMHEGQLSGEFSIEQATQ
		EVLMAAAGVKRDLLEK"
misc-feature	9120..9683	/gene="rbsA"
		/locus-tag="YE0009"
		/inference="protein"
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		/note="Pfam match to entry PF00005
		ABC-tran, ABC transporter, score
		173.1, E-value 3e-49"
misc-feature	9141..9164	/gene="rbsA"
		/locus-tag="YE0009"
		/inference="protein"
		motif:Prosite:PS00017"
		/note="PS00017 ATP/GTP-binding
		site motif A (P-loop)."
misc-feature	9864..10445	/gene="rbsA"
		/locus-tag="YE0009"
		/inference="protein"
		motif:PFAM:PF00005"
		/note="Pfam match to entry PF00005
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		134.4, E-value 1.3e-37"
misc-feature	10218..10262	/gene="rbsA"
		/locus-tag="YE0009"
		/inference="protein"
		motif:Prosite:PS00211"
		/note="PS00211 ABC transporters
		family signature."
gene	10623..11588	/gene="rbsC"
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CDS	10623..11588	/gene="rbsC"
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		/codon-start=1
		/transl-table=11
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		system, permease protein"
		/protein-id="CAL10155.1"
		/db-xref="GI:122087374"

		/db-xref="GOA:A1JHS2" /db-xref="InterPro:IPR001851" /db-xref="UniProtKB/TrEMBL:A1JHS2" /translation="MSSQTINTKRWFSKEWLLEQ KSLIALLVLIADVSSLSNFFTLN NMFNIIQQTSVNAIMAVGMTLVILTSGIDLSVGS LLALTGAVAASIVGLEVNALVAVG AALALGAFVGGITGVIVAKGKVQAFIATLVMMLL LRGVTMVYTNGSPINTGFTDVADT FGWFGIGRPLGIPTPIWLMAIVFIAAWYMLHHTR LGRYIYALGGNESATRLSGISVDK VKIIVYSLCGLLAALAGIIEVARLSSAQPTAGTG YELDAIAAVVLGGTSLAGGKGQIV GTLIGALILGFLNNGNLNLLGVSSYYQMIVKAVVI LLAVLVDNKKQ"
sig-peptide	10623..10748	/gene="rbsC" /locus-tag="YE0010" /note="Signal peptide predicted for YE0010 by SignalP 2.0 HMM (Signal peptide probability 0.969) with cleavage site probability 0.169 between residues 42 and 43"
misc-feature	join(10686..10754, 10815..10883, 10911..10979, 10998..11066, 11124..11192, 11283..11351, 11445..11513)	/gene="rbsC"  /locus-tag="YE0010" /inference="protein motif:TMHMM:2.0" /note="7 probable transmembrane helices predicted for YE0010 by TMHMM2.0 at aa 22-44, 65-87, 97-119, 126-148,168-190, 221-243 and 275-297"
misc-feature	10746..11582	/gene="rbsC" /locus-tag="YE0010" /inference="protein motif:PFAM:PF02653" /note="Pfam match to entry PF02653 BPD-transp-2,Branched-chain amino acid transport system / permease component, score 3.4, E-value 7.7e-07"
gene	11760..12647	/gene="rbsB" /locus-tag="YE0011" /note="synonyms: prlB, rbsP"
CDS	11760..12647	/gene="rbsB" /locus-tag="YE0011" /inference="similar to sequence:UniProtKB:P02925" /inference="similar to sequence:UniProtKB:P02926" /note="Similar to Escherichia coli D-ribose-binding periplasmic protein precursor RbsB or RbsP or PrlB SWALL:RBSB-ECOLI (SWALL:P02925) (296 aa) fasta scores: E(): 1.7e-84, 84.74 38d in 295 aa, and to Salmonella

		typhimurium, and Salmonella typhi D-ribose-binding periplasmic protein precursor RbsB or RbsP or STM3884 or STY3894 SWALL:RBSB-SALTY (SWALL:P02926) (296 aa) fasta scores: E(): 5.6e-84, 84.06 38d in 295 aa" /codon-start=1 /transl-table=11 /product="putative D-ribose-binding periplasmic protein precursor" /protein-id="CAL10156.1" /db-xref="GI:122087375" /db-xref="InterPro:IPR001761" /db-xref="UniProtKB/TrEMBL:A1JHS3" /translation="MKMKKLATLISVVALSATVS ANALAKDTIALVVSTLNNPFFVSM KDGAQKEADKLGYNLVILDSQNNPAKELANVQDL TVRGTKLLLLINPTDSDAVGNAVKM ANQANIPVITLDRLANAGTVVSHVASDNRFGGKM AGDYIAKKVGSDAKVIQLEGIAGA SAARERGEFGKQSMKKNKFQLLASQPADFDRTKG LNMVQNLLTAHPDVQAVFAQNDEM ALGALRALQTAGKTDVLVVGFDGTDGDIKAVESG KMGATIAQRPDQIGVIGVQTADKV LKGEKVQAVIPVDLKLVTK" /gene="rbsB" /locus-tag="YE0011" /note="Signal peptide predicted for YE0011 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.933 between residues 25 and 26"
sig-peptide	11760..11834	
misc-feature	11835..12641	/gene="rbsB" /locus-tag="YE0011" /inference="protein motif:PFAM:PF00532" /note="Pfam match to entry PF00532 Peripla-BP-like, Periplasmic binding proteins and sugar binding domain of the LacI family, score 63.4, E-value 3.3e-16"
misc-feature	12432..12455	/gene="rbsB" /locus-tag="YE0011" /inference="protein motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)." /gene="rbsK" /locus-tag="YE0012" /gene="rbsK" /locus-tag="YE0012" /codon-start=1 /transl-table=11 /product="ribokinase" /protein-id="CAL10157.1" /db-xref="GI:122087376" /db-xref="GOA:A1JHS4" /db-xref="InterPro:IPR002139" /db-xref="InterPro:IPR002173" /db-xref="InterPro:IPR011611"
gene	12811..13737	
CDS	12811..13737	

		/db-xref="InterPro:IPR011877" /db-xref="UniProtKB/TrEMBL:A1JHS4" /translation="METGKLVVLGSINADHILNI EQFPRPGETVVGEQYKVAFGGKGA NQAVAAGRSGANIAFIACVGEDDIGDRVRLQLAS DNIDTAPIEAVAGTTTGVALIFVN GEGENVIGIHAGANSAVTPEYLGRYQQQVIDADA LLMQLESPLGTVIAAAKLAKQHQT QVILNPAPARELPDELLSLVDMITPNETEAERLT GIHIEQDDDAAKAAQILHDKGIAT VIITLGSRGVWLSEQGQKLVAGFKVNAVDTIAA GDTFNGALLTALLEGQAMGSAVRF AHAAAAIAVTRPGAQPSIPWRAEIDSFLQDRV"
misc-feature	12817..13701	/gene="rbsK" /locus-tag="YE0012" /inference="protein" motif:PFAM:PF00294" /note="Pfam match to entry PF00294 pfkB, pfkB family carbohydrate kinase, score 298.8, E-value 4.4e-87"
misc-feature	12928..13002	/gene="rbsK" /locus-tag="YE0012" /inference="protein" motif:Prosites:PS00583" /note="PS00583 pfkB family of carbohydrate kinases signature 1."
misc-feature	13552..13593	/gene="rbsK" /locus-tag="YE0012" /inference="protein" motif:Prosites:PS00584" /note="PS00584 pfkB family of carbohydrate kinases signature 2."
gene	13740..14741	/gene="rbsR" /locus-tag="YE0012A"
CDS	13740..14741	/gene="rbsR" /locus-tag="YE0012A" /inference="similar to sequence:INSDC:AE008881" /inference="similar to sequence:UniProtKB:P25551" /note="Similar to Escherichia coli, and Escherichia coli O157:H7 ribose operon repressor RbsR or b3753 or z5254 or ecs4695 SWALL:RBSR-ECOLI (SWALL:P25551) (329 aa) fasta scores: E(): 7.1e-94, 73.17 38d in 328 aa and to Salmonella typhimurium transcriptional repressor for rbs operon RbsR or stm3886 SWALL:Q8ZKV7 (EMBL:AE008881) (332 aa) fasta scores: E(): 5.3e-95, 74.09 38d in 332 aa" /codon-start=1 /transl-table=11 /product="ribose operon repressor" /protein-id="CAL10158.1" /db-xref="GI:122087377" /db-xref="GOA:A1JHS5" /db-xref="InterPro:IPR000843" /db-xref="InterPro:IPR001761"

		/db-xref="UniProtKB/TrEMBL:A1JHS5" /translation="MATMKDVARLAGVSTSTVSH VINKNRFVSDPIRDKVLAAIKQLN YAPSALARSLKLNETRTIGMLVTASSNPFYAEV RGVERSCYERGYSLILCNTEGDID RMSRSIETLMQKRVDGLLLMCTESHRPSQDILRC YPSLPIIMMDWAPFEGVNDVIQDN SLLGGEMATSYLIARGYTRIACIAGPQDKTPAKE RLQGFRQAMDRAGLPVLDPYEVAS DFEFGGGLVAMKQLLALPQPPEAVFTSNDAMAVG VYQALHQAGLSIPQDMAVIGYDDI EIAQYMTPLTTIHQPKDSLGLAIDTLIHLNS PEAEPQVLILTPELIERGSVATR"
gene	complement(14738..16162)	/locus-tag="YE0013"
CDS	complement(14738..16162)	/locus-tag="YE0013"  /codon-start=1 /transl-table=11 /product="putative membrane transport protein" /protein-id="CAL10159.1" /db-xref="GI:122087378" /db-xref="GOA:A1JHS6" /db-xref="InterPro:IPR001411" /db-xref="InterPro:IPR007114" /db-xref="InterPro:IPR011701" /db-xref="UniProtKB/TrEMBL:A1JHS6" /translation="MIKSARSMAGLPWIAAMAFF MQALDATILNTALPSIAESLNRSP LTMQSAIISYTLTVAMLIPVSGWLADRFGTRRIF ILAVSLFTLGSLLCALSGSLPFLV ASRVIQGVGGAMMPVARLALIRAYPRSELLPVL NFVTIPGLIGPVMGPLLGGLLVTY ATWHWIFILNIPIGLLGIFYARKYMPDFTMPKRA FDIIGFLLFGSSSLVMISVSLEIMG RPDIASYLPAAVLLGGLLMLLFYIFHAKGHPNPL IGLPLFKTRTFSGGIAGNVASRLG TGCVPFLMPLMLQVGFGYSIIAGCMMAPTAIGS MMAKSAVTQVLRSLGYRTVLVGIT AIIGVLIALFAFQSPGMSPWLMILPLFILGMAMS TQFTAMNTITLADLTDNNASSGNS VLAVTQQLAISFGVAISAVVLRFYDGLSFGNNID HFHYTFITMGAVTLLSSMVFLLLK PRDGDNLIQGRNVKKVTQPAKSEV"
sig-peptide	complement(16052..16162)	/locus-tag="YE0013"  /note="Signal peptide predicted for YE0013 by SignalP 2.0 HMM (Signal peptide probability 0.994) with cleavage site probability 0.740 between residues 37 and 38"
misc-feature	complement(join(14816..14884,14927..14995,15032..15100,15128..15196,15233..15301,15344..15412,15431..15499,15527..15583,15620..15679,15689..15757,	/locus-tag="YE0013"



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15791..15859,
15869..15937,
15956..16015,
16058..16126))

/inference="protein
motif:TMHMM:2.0"
/note="14 probable transmembrane
helices predicted for YE0013 by
TMHMM2.0 at aa 13-35, 50-69,
76-98, 102-124,136-158, 162-181,
194-212, 222-244, 251-273,
288-310,323-345, 355-377, 390-412
and 427-449"
misc-feature complement(15830..16132 /locus-tag="YE0013"
)

/inference="protein
motif:PFAM:PF00083"
/note="Pfam match to entry PF00083
sugar-tr, Sugar (and other)
transporter, score 20.7, E-value
2.1e-06"
gene complement(16237..16926 /locus-tag="YE0014"
)
CDS complement(16237..16926 /locus-tag="YE0014"
)

/codon-start=1
/transl-table=11
/product="putative GntR-family
transcriptional regulator"
/protein-id="CAL10160.1"
/db-xref="GI:122087379"
/db-xref="GOA:A1JHS7"
/db-xref="InterPro:IPR000524"
/db-xref="InterPro:IPR011711"
/db-xref="InterPro:IPR011991"
/db-xref="UniProtKB/TrEMBL:A1JHS7"
/translation="MQLNTQQQAAQRNLSYLLAE
KIGQRILAGEYEAGSILPGEIELG
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PQTNWNFLDQELLTWMMTRENFDQ
VMQHFLILRRSLEPQACSLAAINVSGKQKALLTS
LMTEMCELHAHFNRRERWQVDAQF
HQLIYEASGNPFLTSFANLFSSVYHSYFRSITGD
EVIKLQHHQNIVDTILAGDSQGAL
VACQVLLKEKD"
misc-feature complement(16696..16875 /locus-tag="YE0014"
)

/inference="protein
motif:PFAM:PF00392"
/note="Pfam match to entry PF00392
gntR, Bacterial regulatory
proteins, gntR family, score 79.0,
E-value 6.6e-21"
misc-feature complement(16744..16818 /locus-tag="YE0014"
)

/inference="protein
motif:Prosite:PS00043"
/note="PS00043 Bacterial
regulatory proteins, gntR family
signature."
misc-feature complement(16750..16815 /locus-tag="YE0014"
)

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		/note="Predicted helix-turn-helix motif with score 1101.000, SD 2.94 at aa 38-59, sequence PGEIELGEQFGVSRTAVREAVK"
gene	17506..18994	/gene="16S rRNA"
rRNA	17506..18994	/gene="16S rRNA"
		/product="16S ribosomal RNA"
		/note="match to 16S-rRNA 1..1461 (Y.enterocolitica 16S)"
gene	19220..19295	/gene="tRNA-Glu (TTC)"
tRNA	19220..19295	/gene="tRNA-Glu (TTC)"
		/product="tRNA-Glu"
		/note="codon recognized: GAA"
gene	19674..22667	/gene="23S rRNA"
rRNA	19674..22667	/gene="23S rRNA"
		/product="23S ribosomal RNA"
		/note="match to 23S-rRNA 1..2994 (Y. enterocolitica 23S EMBL:U77925, Y.pestis KIM 98 38identity, Citrobacter freundii 23S EMBL:U77928 94 38identity)"
gene	22667..22908	/gene="5S rRNA"
rRNA	22667..22908	/gene="5S rRNA"
		/product="5S ribosomal RNA"
		/note="match to 5SrRNA 1..240 Y.enterocolitica"
gene	complement(23194..23721)	/gene="mobB"
		/locus-tag="YE0016"
CDS	complement(23194..23721)	/gene="mobB"
		/locus-tag="YE0016"
		/codon-start=1
		/transl-table=11
		/product="probable molybdopterin-guanine dinucleotide biosynthesis protein B"
		/protein-id="CAL10161.1"
		/db-xref="GI:122087380"
		/db-xref="GOA:A1JHS8"
		/db-xref="InterPro:IPR004435"
		/db-xref="UniProtKB/TrEMBL:A1JHS8"
		/translation="MSRKTPPLLGIAAYSGTGKT TLKSLIPLLQQRQIRVGLIKHTH HNMEIDTPGKDSYELRKAGAYQTLVASDCRWALM TETPEQKPLDLHYLASRLDAATID LILVEGFKHEPINKIALYREAVGKPYTDLIDEYV IALASDELIETAVEQLDINQPEQI ADFICSWLQINPSQP"
misc-feature	complement(23299..23703)	/gene="mobB"
		/locus-tag="YE0016"
		/inference="protein"
		motif:PFAM:PF03205"
		/note="Pfam match to entry PF03205 MobB, Molybdopterin guanine dinucleotide synthesis protein B, score 184.3,E-value 1.3e-52"
misc-feature	complement(23662..23685)	/gene="mobB"
		/locus-tag="YE0016"
		/inference="protein"

		motif:Prosites:PS00017"
		/note="PS00017 ATP/GTP-binding
		site motif A (P-loop)."
gene	complement (23718..24317	/gene="mobA"
	)	
		/locus-tag="YE0017"
		/note="synonyms: chlB, mob, nar"
CDS	complement (23718..24317	/gene="mobA"
	)	
		/locus-tag="YE0017"
		/codon-start=1
		/transl-table=11
		/product="molybdopterin-guanine
		dinucleotide biosynthesis protein
		A"
		/protein-id="CAL10162.1"
		/db-xref="GI:122087381"
		/db-xref="GOA:A1JHS9"
		/db-xref="InterPro:IPR013482"
		/db-xref="UniProtKB/TrEMBL:A1JHS9"
		/translation="MIEMQPNITGVILAGGRSSR
		MGGNDKGLTLLHDKPLFQYVIDRL
		KPQVNDLLINANRNQELYQASGVPVVSIIITGFV
		GPLAGMHAGLSYSPTIEWVVFAPCD
		VPALPSNLVSQLWQGGKQALAAVVDGERAHPTL
		ALMHVSLKSLLAEYLAKSDRKLM
		FMDSVNAQPIIFRGQKQFSLNLTNPADCDLWEQS
		KRGEL"
gene	24462..24731	/locus-tag="YE0018"
CDS	24462..24731	/locus-tag="YE0018"
		/codon-start=1
		/transl-table=11
		/product="conserved hypothetical
		protein"
		/protein-id="CAL10163.1"
		/db-xref="GI:122087382"
		/db-xref="InterPro:IPR009383"
		/db-xref="UniProtKB/TrEMBL:A1JHT0"
		/translation="MKCHRVNELIELLHPAQQE
		PDLNLVQFLQKLSEEAGFEGEFAE
		LTDDILIIYHLKMRGSASTEVIPGLKKDYEDFKT
		AILRARGIIKD"
gene	24823..25809	/locus-tag="YE0019"
CDS	24823..25809	/locus-tag="YE0019"
		/codon-start=1
		/transl-table=11
		/product="conserved hypothetical
		protein"
		/protein-id="CAL10164.1"
		/db-xref="GI:122087383"
		/db-xref="InterPro:IPR002575"
		/db-xref="UniProtKB/TrEMBL:A1JHT1"
		/translation="MNSSAFNFQTLSPDLIMDAL
		EGVGLRVDSGLTALNSYENRVYQF
		MDEDRKRYVVKFYRPERWSSEQILEEHQFSLDLA
		ESEIPVIAPLQLDGRTLHTHGGFF
		FTVFPVSVGGRQYEIDNLDQLEWVGRYLGRIHQVG
		SDALFVARSTIGIEEYLTETPRQLL
		ASSELVPAKQRDKFLAATDLLISTIKQYWHTDWQ
		PLRLHGDCHPGNILLWRDGPMPFVDL
		DDARNGPAVQDLWMLLHGERREQLIQDLILLEAY
		GEFADFQRELALIEPLRAMRMVY

		YLAWVARRWQDPAPFKSFPWMAESDFWLQQTASF TEQVKLLQAPPLQLMPMY"
gene	25856..26479	/gene="dsbA" /locus-tag="YE0020"
CDS	25856..26479	/gene="dsbA" /locus-tag="YE0020" /codon-start=1 /transl-table=11 /product="secreted thiol:disulfide interchange protein DsbA" /protein-id="CAL10165.1" /db-xref="GI:122087384" /db-xref="GOA:A1JHT2" /db-xref="InterPro:IPR001853" /db-xref="InterPro:IPR006662" /db-xref="InterPro:IPR012335" /db-xref="UniProtKB/TrEMBL:A1JHT2" /translation="MKNVWLALVGMVMAFSASAA QFTDGTQYQTLNKPVTGEPQVLEF FSFYCPHCYQFEEVYHVPQAVKKALPEGTKMTRY HVEFLGPLGKQLTQAWAVAMALGV EEKITPLMFEGVQKTQTVQTPDDIRNVFIKAGVS GEEFDAALNSFVVKSLVVQQQKAA EDLELRGVPAMFVNGKYMINKNDGMDTSSMDTYVK QYADVVKFLLTQK"
sig-peptide	25856..25912	/gene="dsbA" /locus-tag="YE0020" /note="Signal peptide predicted for YE0020 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.992 between residues 19 and 20"
misc-feature	25856..26476	/gene="dsbA" /locus-tag="YE0020" /inference="protein motif:PFAM:PF01323" /note="Pfam match to entry PF01323 DSBA, DSBA oxidoreductase, score 486.2, E-value 1.7e-143"
misc-feature	25976..26032	/gene="dsbA" /locus-tag="YE0020" /inference="protein motif:Prosite:PS00194" /note="PS00194 Thioredoxin family active site."
gene	27070..29868	/gene="polA" /locus-tag="YE0021"
CDS	27070..29868	/note="synonym: resA" /gene="polA" /locus-tag="YE0021" /codon-start=1 /transl-table=11 /product="DNA polymerase I" /protein-id="CAL10166.1" /db-xref="GI:122087385" /db-xref="GOA:A1JHT3" /db-xref="InterPro:IPR001098" /db-xref="InterPro:IPR002298" /db-xref="InterPro:IPR002421" /db-xref="InterPro:IPR002562" /db-xref="InterPro:IPR003583" /db-xref="InterPro:IPR008918"

		/db-xref="UniProtKB/TrEMBL:A1JHT3" /translation="MAQIAENPLILVDGSSYLRY AYHAFPLTNSKGEPTGAMYGVLN MLRSLLLQYRPSHVAVVFDAGKGTFRDELFAEYK SHRPPMPDDLRAQIEPLHQMVKAM GLPLLVSVEADDVIGTLAQEAEGAGHAVLIST GDKDMAQLVTPNITLINTMNNAIL GPQEVCEKYGVPELIIIDFLALMGDSSDNIPGVP GVGEKTAQALLQGLGGLDSLNFHL DKIPTLTFRGAKTMSAKLEQNKDVAYLSYKLATI KTDVELDITCDELNVSA PDDEQLH QLFSRYEFKRWLADVEAGKWL DGKKDRPTAQASN KAFVAPESAPVAEVTAVLSQENYQ TILDEKSLSDWIERLKKA EVFAFD TETDGLDTLS SNLIGLSFAVAPGEAAYLPLAHDY LDAPAQLDRDWVLAQLKPLLEDDKALKVGQNLKF DQSM LARYGIDLRGIAFDTMLESY VLDSVAGRHDMDSLAERYLNHKTITFEEIAGKKG NQLTFNQIALEQAGPYAAEDADVT LQLHLVLWPKLQQSEGLKRVFQEIEMPLLPILSR IERTGV LIDQNILAAH SKELTIRL DELEKQAH ELAEEP FN LASPKQLQVILYEKQKLP ILKKT PGGAAS TNEEV LAELALDY PLPKVILEYRGLAKLKSTYTDKLPLMINPVSGRV HTSYHQAVTATGRLSSRDPNLQNI PVRNEEGRRIRQAFIAPEGYRIMAADYSQIELRI MAHLSQDKGLLAFAAGKDIHRAT AAEVFGLSLEKVTNEQRRSAKAINFGLIYGMSAF GLARQLNIPRGEAQRYMDLYFERY PGVLEYMERTRKQAAEQGYVTTL DGRRLYLPDIH SRNATRRKAAEREAINAPMQGTAA DIIKRAMIAVD AWLQQQPEPLVRVIMQVHDELVF EVHESVLES AEQKIRELM EQSMQL AVPLKVDVG VGYNWDQAH"
misc-feature	27088..27576	/gene="pola" /locus-tag="YE0021" /inference="protein" motif:PFAM:PF02739" /note="Pfam match to entry PF02739 5-3-exonuc-N, 5'-3' exonuclease, N-terminal resolvase-like domain, score 316.3, E-value 2.4e-92"
misc-feature	27580..27900	/gene="pola" /locus-tag="YE0021" /inference="protein" motif:PFAM:PF01367" /note="Pfam match to entry PF01367 5-3-exonuclease, 5'-3' exonuclease, C-terminal SAM fold, score 194.5, E-value 1.1e-55"
misc-feature	28048..28629	/gene="pola" /locus-tag="YE0021" /inference="protein" motif:PFAM:PF01612" /note="Pfam match to entry PF01612 3-5-exonuclease, 3'-5' exonuclease, score 229.0, E-value 4.4e-66"
misc-feature	28717..29862	/gene="pola" /locus-tag="YE0021" /inference="protein" motif:PFAM:PF00476"

		/note="Pfam match to entry PF00476 DNA-pol-A, DNA polymerase family A, score 698.2, E-value 2.6e-207"
misc-feature	29338..29397	/gene="polA" /locus-tag="YE0021" /inference="protein motif:Prosite:PS00447" /note="PS00447 DNA polymerase family A signature."
misc-RNA	30017..30134	/note="Spot 42 RNA (RF00021) as predicted by Rfam, score 91.54, positions 1 to 118"
gene	complement(30302..30955	/locus-tag="YE0022"
	)	
CDS	complement(30302..30955	/locus-tag="YE0022"
	)	
		/codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10167.1" /db-xref="GI:122087386" /db-xref="GOA:A1JHT4" /db-xref="InterPro:IPR002917" /db-xref="InterPro:IPR005289" /db-xref="UniProtKB/Swiss-Prot:A1J HT4" /translation="MTIRNFNYHMTHFVISAPDI RHLPRDEGIEVAFAGRSNAGKSSA LNTLTGQKSLARTSKTPGRTQLINLFEVVEGVRL VDLPGYGYAEVPEEMKCLKWQRALG EYLQKRNCCLKGLVVLMDIRHPLKDLDDQMITWAV AVGTPVMLLLTKADKLASGARKAQ LNMVREAIIPFMGDIQVEAFSSLKKIGVDKLREK LDTWFSEIPPEVMIDEYDDEEGK"
misc-feature	complement(30830..30853	/locus-tag="YE0022"
	)	
		/inference="protein motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-RNA	31382..31582	/note="CsrC family RNA (RF00084) as predicted by Rfam, score 35.38, positions 1 to 254"
gene	31718..32284	/locus-tag="YE0023"
CDS	31718..32284	/locus-tag="YE0023"
		/codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10168.1" /db-xref="GI:122087387" /db-xref="InterPro:IPR007336" /db-xref="UniProtKB/Swiss-Prot:A1J HT5" /translation="MKQPNKAPRADRAAPKGTAT PKRHKKTRELDIEARERKRQKRH SGNRSGARTNIEGSNKTGSTQAQEKDPRIGSKVP VPLVVESKAKAKLTTKPVAKVEAK PRLTPEEELTKLENDERLDALLDRLDNDEVL SKE DQAYVDLTLDRIDALMEQLGIELG DDEDDEEREKPEDILKLLKSGNPKDTF"

gene	32467..33840	/gene="hemN"
		/locus-tag="YE0024"
CDS	32467..33840	/gene="hemN"
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		/codon-start=1
		/transl-table=11
		/product="oxygen-independent
		coproporphyrinogen III oxidase"
		/protein-id="CAL10169.1"
		/db-xref="GI:122087388"
		/db-xref="GOA:A1JHT6"
		/db-xref="InterPro:IPR004558"
		/db-xref="InterPro:IPR006638"
		/db-xref="InterPro:IPR007197"
		/db-xref="InterPro:IPR010723"
		/db-xref="UniProtKB/TrEMBL:A1JHT6"
		/translation="MSENAVVWDLSLIQKYNYSG
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		VKRYPQRPLSLYVHIPFCHKLCYFCGCNKLVTRQ
		QHKADEYLAVLEKEIRQRAALFAG
		RQVSQMHWGSGTPTYLNKTQITHLMNLLRENDFD
		LPGAEQSIEVDPREIELDVLDHLR
		AEGFNRLSMGVQDFNKEVQRLVNREQDEDFIFAL
		IARAKALGFNSTNIDLIYGLPKQT
		PESFAFTLKRVAELNPDRLSVFNYAHLPSLFAAQ
		RKIKDADLPTAEQRLDILQHTISF
		LTESGYQFIGMDHFARPDDDELAIQREGKLHRNF
		QGYTTQGESDLLGLGVSAISMLGD
		SYAQNEKDLKTYIYAVVEQRGNALWRGLTMTEDDC
		LRRDVIKTLICNFQISYQPIEQHY
		GIRFADYFAEDFELLTPFEHDGLVERDDKSIRVT
		PRGRLLIRNICMCFDIYLRKQARK QQFSRVI"
misc-feature	32761..33522	/gene="hemN"
		/locus-tag="YE0024"
		/inference="protein
		motif:PFAM:PF02473"
		/note="Pfam match to entry PF02473
		Coprogen-an-ox,Oxygen-independent
		Coproporphyrinogen III oxidase,
		score 555.2, E-value 2.8e-164"
gene	complement(33989..35401	/gene="ntrC"
	)	
		/locus-tag="YE0025"
		/note="synonyms: glnG, glnT"
CDS	complement(33989..35401	/gene="ntrC"
	)	
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		/transl-table=11
		/product="nitrogen regulation
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		/protein-id="CAL10170.1"
		/db-xref="GI:122087389"
		/db-xref="GOA:A1JHT7"
		/db-xref="InterPro:IPR001789"
		/db-xref="InterPro:IPR002078"
		/db-xref="InterPro:IPR002197"
		/db-xref="InterPro:IPR003593"
		/db-xref="InterPro:IPR010114"
		/db-xref="UniProtKB/TrEMBL:A1JHT7"
		/translation="MQRGIVWIVDDDSSIRWVLE
		RALTGAGLNCATFDTGNQVLDALA

		TQTPDVLLSDIRMPGMDGLALLKQIKQRHPMLPV IIMTAHSDLDAAVSAYQQGAFDYL PKPFDIDEAVALVERAISHYQEQQQPARTQPASG PTADIIGEAPAMQDVFRIGRLSR SSISVLINGESGTGKELVAHALHRHSPRAKAPFI ALNMAAIPKDLIESELFGEKGAF TGANQVRQGRFEQADGGTLFLDEIGDMPLDVQTR LLRVLADGQFYRVGGYAPVKVDVR IIAATHQNLELRVQEGKFREDLFHRLNVIRVHLP PLRERREDIPRLARYFLQVAAKEL GVEAKNLHPETEVALTRLPWPGNVRQLENTCRWL TVMAAGQEVLVQDLPSELFETNTP DASGQRMPCDNWSTLLAQWADRALRSQHQLLSEA QPEMERTLLTTALRHTQGHKQEA RLLGWGRNTLTRKLKELGME"
misc-feature	complement(34001..34123)	/gene="ntrC"  /locus-tag="YE0025" /inference="protein" motif:PFAM:PF02954" /note="Pfam match to entry PF02954 HTH-8, Bacterial regulatory protein, Fis family, score 64.1, E-value 2e-16"
misc-feature	complement(34007..34072)	/gene="ntrC"  /locus-tag="YE0025" /note="Predicted helix-turn-helix motif with score 1763.000, SD 5.19 at aa 444-465, sequence GHKQEAARLLGWGRNTLTRKLK"
misc-feature	complement(34313..34342)	/gene="ntrC"  /locus-tag="YE0025" /inference="protein" motif:Prosites:PS00688" /note="PS00688 Sigma-54 interaction domain C-terminal part signature."
misc-feature	complement(34316..34981)	/gene="ntrC"  /locus-tag="YE0025" /inference="protein" motif:PFAM:PF00158" /note="Pfam match to entry PF00158 Sigma54-activat,Sigma-54 interaction domain, score 496.8, E-value 1.1e-146"
misc-feature	complement(34676..34723)	/gene="ntrC"  /locus-tag="YE0025" /inference="protein" motif:Prosites:PS00676" /note="PS00676 Sigma-54 interaction domain ATP-binding region B signature."
misc-feature	complement(34868..34909)	/gene="ntrC"  /locus-tag="YE0025" /inference="protein" motif:Prosites:PS00675" /note="PS00675 Sigma-54



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interaction domain ATP-binding
region A signature."
misc-feature    complement(35033..35392 /gene="ntrC"
)
                /locus-tag="YE0025"
                /inference="protein
                motif:PFAM:PF00072"
                /note="Pfam match to entry PF00072
                response-reg, Response regulator
                receiver domain, score 148.5,
                E-value 7.8e-42"
gene            complement(35409..36458 /gene="ntrB"
)
                /locus-tag="YE0026"
                /note="synonyms: gln1, glnR"
CDS             complement(35409..36458 /gene="ntrB"
)
                /locus-tag="YE0026"
                /codon-start=1
                /transl-table=11
                /product="Two component regulatory
                protein involved in nitrogen
                assimilation"
                /protein-id="CAL10171.1"
                /db-xref="GI:122087390"
                /db-xref="GOA:A1JHT8"
                /db-xref="InterPro:IPR000014"
                /db-xref="InterPro:IPR003594"
                /db-xref="InterPro:IPR003661"
                /db-xref="InterPro:IPR004358"
                /db-xref="InterPro:IPR005467"
                /db-xref="InterPro:IPR013767"
                /db-xref="UniProtKB/TrEMBL:A1JHT8"
                /translation="MATGTLPDAGQILNSLINSI
                LLLDDSLAIHYANPAAQQLLAQSS
                RKLFGTLPPELLGYFSLNMEMLMRESLASGQSFTD
                NEVTLVVDGRAHILSLTAQSLAEG
                FILLEMAPMDNQRRLSQEQLOHAQQIAARDLVRG
                LAHEIKNPLGGGLRGAAQLLSKALP
                DPALLEYTKVIEQADRLRNLVDRLLGPQRPQG
                VTQSIHQVAERVCQLVSLEKPDNV
                TLIRDYDPSLPPELAHDPDQIEQVLLNITRNALQA
                LGEAGGTITLRTTAFQITLHGVR
                YRLAARIDIEDDGGPVPTQLQDTLFFYPMVSGREG
                GTGLGLSIARSLIDQHSGKIEFNS
                WPGHTEFSVYLPIRQ"
misc-feature    complement(35415..35762 /gene="ntrB"
)
                /locus-tag="YE0026"
                /inference="protein
                motif:PFAM:PF02518"
                /note="Pfam match to entry PF02518
                HATPase-c, Histidine kinase-, DNA
                gyrase B-, and HSP90-like ATPase,
                score 104.0, E-value 1.9e-28"
misc-feature    complement(35877..36074 /gene="ntrB"
)
                /locus-tag="YE0026"
                /inference="protein
                motif:PFAM:PF00512"
                /note="Pfam match to entry PF00512
                HisKA, His Kinase A

```

```

        (phosphoacceptor) domain, score
        64.0, E-value 2.1e-16"
gene      complement(36607..38016 /gene="glnA"
)
        /locus-tag="YE0027"
CDS       complement(36607..38016 /gene="glnA"
)
        /locus-tag="YE0027"
        /codon-start=1
        /transl-table=11
        /product="glutamine synthetase"
        /protein-id="CAL10172.1"
        /db-xref="GI:122087391"
        /db-xref="GOA:A1JHT9"
        /db-xref="InterPro:IPR001637"
        /db-xref="InterPro:IPR004809"
        /db-xref="InterPro:IPR008146"
        /db-xref="InterPro:IPR008147"
        /db-xref="InterPro:IPR014746"
        /db-xref="UniProtKB/TrEMBL:A1JHT9"
        /translation="MSAEHVLTMLNEHEVKFVDL
RFTDTKGKEQHITIPAHQVNADFF
EEGKMFDGSSIGGWKGINESDMVLMPDASTAVMD
PFFEDSTLIIRCDILEPGTLQGYD
RDPRSISKRAEEFLKSSGIADTVLFGPEPEFFLF
DDVRFGSSIRGSHVAID DIEAWN
SSTKYEGGNKGHRPAVKGGYFPVPPVDSSQDLRS
TMCLTMEEMGLVVEAHHHEVATAG
QNEVATRFNTMTKKADEIQIYKYVVHNVAHAFGK
TATFMPKPMFGDNGSGMHCHMSLS
KNGTNLFAGDKYAGLSEMAIFYIGGIKHAKAIN
ALANPTTNSYKRLVPGYEAPVMLA
YSARNRSASIRIPVVASPKARRIEARFPDPAANP
YLCFAALLMAGLDGIINKIHPGDA
MDKNLYDLPPEEEAEIPKVAGSLDEAMAALNEDR
EFLTRGGVFTDDAIDAYIELRKEE
MDRVRMTPHPVEFELYYSV"
misc-feature complement(36823..36861 /gene="glnA"
)
        /locus-tag="YE0027"
        /inference="protein
motif:Prosite:PS00182"
        /note="PS00182 Glutamine
synthetase class-I adenylation
site."
misc-feature complement(36868..37713 /gene="glnA"
)
        /locus-tag="YE0027"
        /inference="protein
motif:PFAM:PF00120"
        /note="Pfam match to entry PF00120
gln-synt, Glutamine synthetase,
catalytic domain, score 563.6,
E-value 8.6e-167"
misc-feature complement(37195..37242 /gene="glnA"
)
        /locus-tag="YE0027"
        /inference="protein
motif:Prosite:PS00181"
        /note="PS00181 Glutamine
synthetase putative ATP-binding
region signature."

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misc-feature    complement(37729..37977 /gene="glnA"
)
                /locus-tag="YE0027"
                /inference="protein
motif:PFAM:PF03951"
                /note="Pfam match to entry PF03951
gln-synt-N, Glutamine synthetase,
beta-Grasp domain, score 169.3,
E-value 4.1e-48"
misc-feature    complement(37813..37869 /gene="glnA"
)
                /locus-tag="YE0027"
                /inference="protein
motif:Prosite:PS00180"
                /note="PS00180 Glutamine
synthetase signature 1."
gene            complement(38201..38311 /locus-tag="YE0028"
)
CDS             complement(38201..38311 /locus-tag="YE0028"
)
                /inference="similar to
sequence:INSDC:AJ414141"
                /note="Poor database matches.
Similar to the N-terminal region
of Yersinia pestis possible
membrane protein YPO0025
SWALL:Q8ZJR4 (EMBL:AJ414141) (52
aa) fasta scores: E(): 1.8e-12,
80.55 38d in 36 aa. Doubtful CDS"
                /codon-start=1
                /transl-table=11
                /product="hypothetical protein"
                /protein-id="CAL10173.1"
                /db-xref="GI:122087392"
                /db-xref="UniProtKB/TrEMBL:A1JHU0"
                /translation="MHTDYQQTPMIWHKWGVWVKV
GIDFAIDFMTQFSMNN"
gene            38529..40352
                /gene="bipA"
                /locus-tag="YE0029"
                /note="synonym: typA"
CDS             38529..40352
                /gene="bipA"
                /locus-tag="YE0029"
                /codon-start=1
                /transl-table=11
                /product="putative GTPase"
                /protein-id="CAL10174.1"
                /db-xref="GI:122087393"
                /db-xref="GOA:A1JHU1"
                /db-xref="InterPro:IPR000640"
                /db-xref="InterPro:IPR000795"
                /db-xref="InterPro:IPR004161"
                /db-xref="InterPro:IPR005225"
                /db-xref="InterPro:IPR006298"
                /db-xref="UniProtKB/TrEMBL:A1JHU1"
                /translation="MIENLRNIAIIAHVDHGKTT
LVDKLLQQSGTFGERAEATERVMD
SNDLEKERGITILAKNTAIKWKDYRINIVDTPGH
ADFGGEVERVMSMVDSVLLVVDAM
DGPMPQTRFVTKKAFANGLKPIVVINKVDRPGAR
PDWVVDQVFDLFDVNLDTDEQLDF
PIIYASALMGIAGNDHNDMAADMTPLYQAIVDHV
SPPQVEPDAPFQMQISQLDYNMYV

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		GVIGIGRIKRGKVKPNQQVTIVDSEGKTRNGKVG KVLTHMGLERIEATEAEAGDIVAI TGLGELNISDTICDVNAVEALPALSVDEPTVSMY FCVNTSPFCGKEGKYVTSRQILER LNKELIHNVALRVEETEDADAFRVSGRGELHLSV LIENMRREGFELAVSRPKVIVREI DGRKQEPFENVTLDIEEQHQGSVMQAMGERKADL KNMDPDGKGRVRLDYLPARGLIG FRTEFMTMTSGTGLLYSTFSHYDDVRPGEIGQRQ NGVLI SNGQGKAVAFALFKLQDRG KLFIGHGTEVYEGQIIIGIHSRNDLTVNCLTGKQ LTNMRASGTDEATTLPFLKKTLE QALEFIDDDDELVEVTPQSIRIRKRHLTENDRKRA GRGPKED"
misc-feature	38535..39122	/gene="bipA" /locus-tag="YE0029" /inference="protein motif:PFAM:PF00009" /note="Pfam match to entry PF00009 GTP-EFTU, Elongation factor Tu GTP binding domain, score 258.2, E-value 7.1e-75"
misc-feature	38562..38585	/gene="bipA" /locus-tag="YE0029" /inference="protein motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-feature	38658..38705	/gene="bipA" /locus-tag="YE0029" /inference="protein motif:Prosite:PS00301" /note="PS00301 GTP-binding elongation factors signature."
misc-feature	39147..39395	/gene="bipA" /locus-tag="YE0029" /inference="protein motif:PFAM:PF03144" /note="Pfam match to entry PF03144 GTP-EFTU-D2, Elongation factor Tu domain 2, score 71.9, E-value 8.8e-19"
misc-feature	39711..39977	/gene="bipA" /locus-tag="YE0029" /inference="protein motif:PFAM:PF00679" /note="Pfam match to entry PF00679 EFG-C, Elongation factor G C-terminus, score 112.3, E-value 6e-31"
gene	40648..41235	/locus-tag="YE0030"
CDS	40648..41235	/locus-tag="YE0030" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10175.1" /db-xref="GI:122087394" /db-xref="GOA:A1JHU2" /db-xref="InterPro:IPR005834" /db-xref="InterPro:IPR006402" /db-xref="UniProtKB/TrEMBL:A1JHU2"

		/translation="MLYIFDLGNVIVDIDFKRVL GVWSKLSSVPLATLSERFTMGEVF QQHERGEISDEDFARQLSDEMGLSLSFEQFAEGW QAVFVALRPEVISIMQKLRAEGHR VVVLSTNTNRLHCNYWPQHYPEVAAAADHMYLSQD LGMRKPEARIYQHVLSAENIPAEQ AVFFDDVEANIVAARIEGITGIHVTDRKVIPAYF S"
misc-feature	40648..41208	/locus-tag="YE0030" /inference="protein motif:PFAM:PF00702" /note="Pfam match to entry PF00702 Hydrolase, haloacid dehalogenase-like hydrolase, score 61.6, E-value 1.1e-15"
gene	41328..42218	/gene="rbn"
CDS	41328..42218	/locus-tag="YE0031" /gene="rbn" /locus-tag="YE0031" /codon-start=1 /transl-table=11 /product="ribonuclease BN" /protein-id="CAL10176.1" /db-xref="GI:122087395" /db-xref="GOA:A1JHU3" /db-xref="InterPro:IPR004664" /db-xref="InterPro:IPR017039" /db-xref="UniProtKB/Swiss-Prot:A1J HU3" /translation="MASFLRFRLSASLKPYITFG RMLYTRIDKDGLTMLAGHLAYVSL LSLVPLVTIVIFALFAAFPMFADISIKLKAFIFTN FMPATGDI IQNYLEQFVANSNRMT VVGTCGLIVTALLLIYSVDSVLNIIWRSKVHRS L VFSFAVYWMVLTLPILVGASMVI SSYLLSLQWLANARVDSMIDETLRLFPLLISWVS FWLLYSVVP TVRVPAQDALIGALV AALFFELGKKGFTMYITLFPSYQLIYGVLA VIPI LFLWVYWSWCIVLLGAEITVTLGE YRAQRHQAITEKSPSQSQEI"
misc-feature	41409..42161	/gene="rbn" /locus-tag="YE0031" /inference="protein motif:PFAM:PF03631" /note="Pfam match to entry PF03631 Ribonuclease-BN,Ribonuclease BN-like family, score 289.2, E-value 3.5e-84"
misc-feature	join(41442..41510, 41628..41687, 41748..41816, 41874..41933, 41967..42035, 42063..42131)	/gene="rbn" /locus-tag="YE0031" /inference="protein motif:TMHMM:2.0" /note="6 probable transmembrane helices predicted for YE0031 by TMHMM2.0 at aa 39-61, 101-120, 141-163, 183-202,214-236 and 246-268"

gene	42225..42662	/locus-tag="YE0032"
CDS	42225..42662	/locus-tag="YE0032"
		/codon-start=1
		/transl-table=11
		/product="conserved hypothetical protein"
		/protein-id="CAL10177.1"
		/db-xref="GI:122087396"
		/db-xref="GOA:A1JHU4"
		/db-xref="InterPro:IPR003732"
		/db-xref="UniProtKB/Swiss-Prot:A1JHU4"
		/translation="MIALIQRALSANVVVDGEVV GEIGPGLLILLGVEQQDTEQKAQR LCEKVLGYRIFGDENDKMNLNVKQAGGSVLVVSQ FTLVADTQKGMRPSFSRGASPAEA DRLYQYFVAQCREHGVKTETGLFAADMKVSLVND GPVTFWLQI"
misc-feature	42306..42659	/locus-tag="YE0032"
		/inference="protein"
		motif:PFAM:PF02580"
		/note="Pfam match to entry PF02580 DUF154, Uncharacterized ACR, COG1490, score 261.8, E-value 6e-76"
gene	42914..43837	/locus-tag="YE0033"
CDS	42914..43837	/locus-tag="YE0033"
		/codon-start=1
		/transl-table=11
		/product="conserved membrane protein"
		/protein-id="CAL10178.1"
		/db-xref="GI:122087397"
		/db-xref="GOA:A1JHU5"
		/db-xref="InterPro:IPR000182"
		/db-xref="InterPro:IPR012660"
		/db-xref="InterPro:IPR016181"
		/db-xref="UniProtKB/TrEMBL:A1JHU5"
		/translation="MYHLRVPTTEQELKDYYQFR WEMLRKPLHQPIGSEKDAYDAMAH HQMVDDEQGKPVAIGRLYINADNEAAIRFLAVDP SVRSKGLGTLVAMTLESVARQEGV KRVVCSAREDAVDFFSKLGFVSQGEITAPQTTTPV RHFLMIKPVVTMDDILHRPDWCGQ LQQAWYDHIPLSEKMGVRISQYTGQRFVTTMPEA GNQNPHTLTFAGSLFSLATLTGWG LIWLLLRERHLGGTIIILADAHIRYSAPVTGRPRA VAELSSLSGDLDRDLARGRRARVQL DVNLFGNEEAGAVFSGTYMVLPVDAEGDGVN"
misc-feature	43052..43282	/locus-tag="YE0033"
		/inference="protein"
		motif:PFAM:PF00583"
		/note="Pfam match to entry PF00583 Acetyltransf,Acetyltransferase (GNAT) family, score 63.3, E-value 3.3e-16"
misc-feature	43184..43249	/locus-tag="YE0033"
		/note="Predicted helix-turn-helix motif with score 1005.000, SD 2.61 at aa 91-112, sequence MTLESVARQEGVKRVVCSARED"
misc-feature	43517..43585	/locus-tag="YE0033"

		/inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted for YE0033 by TMHMM2.0 at aa 202-224"
repeat-region	44408..45116	/note="repeat unit encoding a LuxR-family transcriptional regulator"
gene	44431..45117	/locus-tag="YE0035"
CDS	44431..45117	/locus-tag="YE0035" /inference="similar to sequence:INSDC:AE004433" /inference="similar to sequence:INSDC:AE004564" /note="Similar to Pseudomonas aeruginosa probable transcriptional regulator PA1347 SWALL:Q9I3Z7 (EMBL:AE004564) (230 aa) fasta scores: E(): 3e-09, 30.43 id in 207 aa, and to the C-terminal region of Vibrio cholerae LuxR family transcriptional regulator VCA1078 SWALL:Q9KKM5 (EMBL:AE004433) (319 aa) fasta scores: E(): 2.2e-10, 27.53 38d in 207 aa" /codon-start=1 /transl-table=11 /product="LuxR family transcription regulatory protein" /protein-id="CAL10179.1" /db-xref="GI:122087398" /db-xref="GOA:A1JHU6" /db-xref="InterPro:IPR000792" /db-xref="InterPro:IPR011991" /db-xref="InterPro:IPR013656" /db-xref="UniProtKB/TrEMBL:A1JHU6" /translation="MEASLFNSLKMLIKFWECSS EPWGVKDNQSRVYVYANNRLHKLFA LPDKFSMEGRTDGELPTPISEFELEFQEHDCKVK LLQDRVTSVEIHAWNGHSYYQPYF FDKYPLIDEHGVSQGIISHSRPVEDVILTHLNKI KVPISLILTPPSDLFSKREWEVLF YILHSFSSMEIATKLHLSSITVDNIIQKIYKKIG ISGRQQLVDYCYENKINNYVPQSF FEYSGSFPLV"
misc-feature	44872..45069	/locus-tag="YE0035" /inference="protein motif:PFAM:PF00196" /note="Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 41.3, E-value 1.4e-09"
misc-feature	44926..44991	/locus-tag="YE0035" /note="Predicted helix-turn-helix motif with score 1060.000, SD 2.80 at aa 166-187, sequence FSSMEIATKLHLSSITVDNIIQ"
repeat-region	45117..45833	/note="repeat unit encoding a LuxR-family transcriptional regulator"
gene	45147..45833	/locus-tag="YE0036"

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CDS                45147..45833
                    /locus-tag="YE0036"
                    /inference="similar to
sequence:INSDC:AE004433"
                    /inference="similar to
sequence:INSDC:AE004564"
                    /note="Similar to Pseudomonas
aeruginosa probable
transcriptional regulator PA1347
SWALL:Q9I3Z7 (EMBL:AE004564) (230
aa) fasta scores: E():
2.2e-09,30.37 38d in 214 aa, and
to the C-terminal region of Vibrio
cholerae LuxR family
transcriptional regulator VCA1078
SWALL:Q9KKM5 (EMBL:AE004433) (319
aa) fasta scores: E(): 6.6e-13,
30.43 38d in 207 aa"
                    /codon-start=1
                    /transl-table=11
                    /product="LuxR family
transcription regulatory protein"
                    /protein-id="CAL10180.1"
                    /db-xref="GI:122087399"
                    /db-xref="GOA:A1JHU7"
                    /db-xref="InterPro:IPR000792"
                    /db-xref="InterPro:IPR011991"
                    /db-xref="UniProtKB/TrEMBL:A1JHU7"
                    /translation="MDKPLKNQLEILIRFWERSS
EPWGARDNQSRFIYSNDRHHKLLG
LSDKYNLEGRLDSELPSPATAAFQMEFQAHDRKVE
LSQERITSVEIHEWDGLSYLKPNE
CDKYPLIDESGVSQGIIFHVRPVEDIILSRLTKI
KAPTSLTFTPPSKLFTKREWEVLF
YILHSYSSKDIKKLHISPRTVSNITQSVYRKVG
VSNKRQIVDYCYENKINNYVPQSF
FEYSGSFPLM"
misc-feature       45588..45785
                    /locus-tag="YE0036"
                    /inference="protein
motif:PFAM:PF00196"
                    /note="Pfam match to entry PF00196
GerE, Bacterial regulatory
proteins, luxR family, score 49.3,
E-value 5.5e-12"
misc-feature       45642..45707
<-----User Break----->
                    /locus-tag="YE0036"
                    /locus-tag="YE0067"
                    /note="synonym: kdtB"
CDS                complement(75792..76271
                    /gene="coaD"
                    /locus-tag="YE0067"
                    /codon-start=1
                    /transl-table=11
                    /product="phosphopantetheine
adenylyltransferase"
                    /protein-id="CAL10209.1"
                    /db-xref="GI:122087428"
                    /db-xref="GOA:A1JHR9"
                    /db-xref="InterPro:IPR001980"
                    /db-xref="InterPro:IPR004820"
                    /db-xref="InterPro:IPR004821"
                    /db-xref="InterPro:IPR014729"

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                                /db-xref="UniProtKB/Swiss-Prot:A1J
                                HR9"
                                /translation="MITKAIYPGTFDPITNGHLD
                                LVTRASEMFSHVILAIADSSSKKP
                                MFTLAERVILAKQVTAPLKNVEVLGFSELMAEFA
                                KKHNNANILVRGLRSVSDFEYEWQL
                                ANMNRHLMPKLESVFLMPSEKWSFISSSLVKEVA
                                RHGGDITPFLPAPVTKALMTKLA"
misc-feature    complement(75870..76268 /gene="coaD"
                )
                                /locus-tag="YE0067"
                                /inference="protein
                                motif:PFAM:PF01467"
                                /note="Pfam match to entry PF01467
                                CTP-transf-2,Cytidylyltransferase,
                                score 151.3, E-value 1.1e-42"
gene            complement(76268..77050 /gene="kdtX"
                )
                                /locus-tag="YE0068"
                                /note="synonym: waaE"
CDS             complement(76268..77050 /gene="kdtX"
                )
                                /locus-tag="YE0068"
                                /codon-start=1
                                /transl-table=11
                                /product="lipopolysaccharide core
                                biosynthesis glycosyl transferase"
                                /protein-id="CAL10210.1"
                                /db-xref="GI:122087429"
                                /db-xref="GOA:A1JHS0"
                                /db-xref="InterPro:IPR001173"
                                /db-xref="UniProtKB/TrEMBL:A1JHS0"
                                /translation="MSAKKRLSVVMIVKNEASLL
                                ADCLASVTWADEIVVLDSGSEDET
                                VALAEQYGAKVYSNTEWPGYGKQRQLAQQYATGD
                                YILMLDADERVTPELKSAIETVLL
                                APEEGAVYSCARRNLFGRFMRHSGWYPDRVTRL
                                YPREQYRYNDDLHVHESLDSGSAKV
                                ILLAGDLLHLTCRDFFAFQRKQLNYAQAWANQRH
                                QQGKSCRYFAIISHTLGAFCKTWL
                                LRAGFLDGKQGLLLAVVNAQYTFNKYAALWALSH
                                QQYQKSENS"
sig-peptide     complement(76961..77050 /gene="kdtX"
                )
                                /locus-tag="YE0068"
                                /note="Signal peptide predicted
                                for YE0068 by SignalP 2.0 HMM
                                (Signal peptide probability 0.844)
                                with cleavage site probability
                                0.843 between residues 30 and 31"
misc-feature     complement(76565..77029 /gene="kdtX"
                )
                                /locus-tag="YE0068"
                                /inference="protein
                                motif:PFAM:PF00535"
                                /note="Pfam match to entry PF00535
                                Glycos-transf-2,Glycosyl
                                transferase, score 88.5, E-value
                                8.8e-24"
gene            complement(77051..78328 /gene="kdtA"
                )
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LOCUS (LOC): AM236080 GenBank (R)  
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 CAS REGISTRY NO. (RN): 906734-09-6  
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 group; Rhizobium  
 REFERENCE: 1  
 AUTHOR (AU): Young, J.W.; Crossman, L.C.; Johnston, A.W.B.;  
 Thomson, N.R.; Ghazoui, Z.F.; Hull, K.H.; Wexler, M.;  
 Curson, A.R.J.; Todd, J.D.; Poole, P.S.; Mauchline, T.H.;  
 East, A.K.; Quail, M.A.; Churcher, C.; Arrowsmith, C.;  
 Cherevach, A.; Chillingworth, T.; Clarke, K.; Cronin, A.;  
 Davis, P.; Fraser, A.; Hance, Z.; Hauser, H.; Jagels, K.;  
 Moule, S.; Mungall, K.; Norbertczak, H.; Rabinowitsch, E.;  
 Sanders, M.; Simmonds, M.; Whitehead, S.; Parkhill, J.  
 TITLE (TI): The genome of Rhizobium leguminosarum has recognizable  
 core and accessory components  
 JOURNAL (SO): Genome Biol., 7, R4-R4 (2006)  
 OTHER SOURCE (OS): CA 145:307927  
 REFERENCE: 2 (bases 1 to 5057142)  
 AUTHOR (AU): Crossman, L.C.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (21-FEB-2006) Crossman L.C., Pathogen  
 Sequencing Unit, The Wellcome Trust Sanger Institute,  
 Hinxton, Cambridge, Cambridgeshire, CB10 1SA, UNITED  
 KINGDOM

FEATURES (FEAT):

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		subject 1-192 aa similarity: fasta;
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		Rhizobium meliloti; dephospho-coa kinase; coaE; length 194 aa; 192 aa overlap; query 1-192 aa; subject 1-192 aa" /codon-start=1 /transl-table=11 /product="putative dephospho-CoA kinase" /protein-id="CAK05492.1" /db-xref="GI:115254418" /db-xref="GOA:Q1MNF3" /db-xref="UniProtKB/TrEMBL:Q1MNF3" /translation="MLKIGLTGSIGMGKSTAAKL FADAGIPVNDSDAVVHDL YAGEAA PLVNAAFPGTMKDGAVDRRELGRQLALDPDGFKC LEAIVHPLVRKRETEFLKRQRATG ADMVLLDIPLL FETGAEARVDVVVVSTDPQIQR QRVLAREGMTEEFDMILSRQTPD AEKRRRADYLDITSHSIATTRERVFEIVADLKTR IAKGDFRNA" /locus-tag="RL0004" /inference="protein motif: Pfam: PF01121.8" /note="Pfam match to entry PF01121.8 CoaE"
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CDS	3382..4104	
misc-feature	3388..3870	/locus-tag="RL0005" /inference="protein

		motif: Pfam: PF00929.11"
		/note="Pfam match to entry PF00929.11 Exonuc-X-T"
gene	complement(4172..4654)	/gene="secB"
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CDS	complement(4172..4654)	/gene="secB"
		/locus-tag="RL0006"
		/inference="similar to sequence: INSDC: AE008975"
		/inference="similar to sequence: UniProtKB: P15040"
		/note="similarity: fasta; SWALL: SECB-ECOLI (SWALL: P15040); Escherichia coli, Escherichia coli O6, Escherichia coli O157:H7, and Shigella flexneri; protein-export protein SecB; secB; length 155 aa; 151 aa overlap; query 1-151 aa; subject 1-145 aa similarity: fasta; SWALL: Q8UJC2 (EMBL: AE008975); Agrobacterium tumefaciens; protein-export protein; secB; length 160 aa; 160 aa overlap; query 1-160 aa; subject 1-160 aa"
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		/transl-table=11
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		/inference="protein motif: Pfam: PF02556.4"
		/note="Pfam match to entry PF02556.4 SecB"
gene	complement(4756..5271)	/locus-tag="RL0007"
CDS	complement(4756..5271)	/locus-tag="RL0007"
		/inference="similar to sequence: INSDC: AE007943"
		/inference="similar to sequence: INSDC: ECUW93"
		/note="similarity: fasta; with=UniProt: FXSA-ECOLI (EMBL: ECUW93); Escherichia coli.; fxsA; FxsA protein (Suppressor of F exclusion of phage T7).; length=158; id 36.364; 132 aa overlap; query 4-132; subject 1-129 similarity: fasta; with=UniProt: Q8UJC1 (EMBL: AE007943); Agrobacterium tumefaciens (strain C58/ATCC 33970).; fxsA; Hypothetical

		protein fxsA (AGR-C-11p).; length=178; id 48.521; 169 aa overlap; query 4-167; subject 1-169" /codon-start=1 /transl-table=11 /product="putative transmembrane FxsA-family protein" /protein-id="CAK05495.1" /db-xref="GI:115254421" /db-xref="GOA:Q1MNF0" /db-xref="UniProtKB/TrEMBL:Q1MNF0" /translation="MTDMRFSILPAFILLLPFAE IAGFVVVGQAIGLWLTLLVLMGLF VLGVVLLRRQGIGILRRMSSEGRNGVMPGRDLLR PAMNVIASLLLLIIPGFLTDIIAIL ILIPPVRDLVWRAIAKRFVVVNAKGGSSSGPQPD FRDRKPNKSVVDLEEEDYHREPDR NSPWSGRHLGD"
misc-feature	complement(4879..5244)	/locus-tag="RL0007" /inference="protein motif: Pfam:PF04186.2" /note="Pfam match to entry PF04186.2 FxsA"
misc-feature	complement(join(4957..5025,5116..5184,5194..5253))	/locus-tag="RL0007" /inference="protein motif: TMHMM:2.0" /note="3 probable transmembrane helices predicted at aa 7-26, 30-52 and 83-105"
gene	5394..6098	/locus-tag="RL0008"
CDS	5394..6098	/locus-tag="RL0008" /inference="similar to sequence: INSDC:AL591782" /note="similarity: fasta; SWALL:Q92TE6 (EMBL:AL591782); Rhizobium meliloti; putative translocase transmembrane protein; length 233 aa; 234 aa overlap; query 1-233 aa; subject 1-233 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05496.1" /db-xref="GI:115254422" /db-xref="GOA:Q1MNE9" /db-xref="UniProtKB/TrEMBL:Q1MNE9" /translation="MSSNDFITLFFLVAAVLIFF QLRSVLGRRTGNEKPPRDLYTPRD AAPAEAADAGKVVTLPRRDATTEDRFAAIDAF AAPGTPLNESLRALNKADPAFSPK EFLNGARMAYEMIVMAYADGDRKTLKNLLSREVV DGFDAAIGEREARGEKVKSTFVGI DKAEITHAETKGSEAQITVRIASQLISATYDKAD VLIEGDAENVAEVNDVWTFARDTR SRDPNWKLVAESEHE"
misc-feature	5646..6086	/locus-tag="RL0008" /inference="protein motif: Pfam:PF04280.4"

		/note="Pfam match to entry PF04280.4 Tim44"
gene	6091..7209	/gene="mltA"
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CDS	6091..7209	/gene="mltA"
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		/inference="similar to sequence:INSDC:AL591782"
		/inference="similar to sequence:UniProtKB:P46885"
		/note="similarity:fasta; SWALL:MLTA-ECOLI (SWALL:P46885); Escherichia coli, and Escherichia coli O157:H7; membrane-bound lytic murein transglycosylase a precursor; mltA; length 365 aa; 282 aa overlap; query 92-369 aa; subject 112-360 aa similarity:fasta; SWALL:Q92TE5 (EMBL:AL591782); Rhizobium meliloti; putative lytic murein transglycosylase a protein; length 372 aa; 365 aa overlap; query 8-371 aa; subject 3-365 aa"
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misc-feature	6310..6936	/gene="mltA"
		/locus-tag="RL0009"
		/inference="protein motif:Pfam:PF03562.4"
		/note="Pfam match to entry PF03562.4 MltA"
misc-feature	6946..7179	/gene="mltA"
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		/note="similarity:fasta;
		with=UniProt:Q92KV6
		(EMBL:SME591782); Rhizobium
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		meliloti).; Hypothetical protein
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		/db-xref="UniProtKB/TrEMBL:Q1MNE7"
		/translation="MARDRKLSADERILWGKVAR
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		LVQSEAHTILLDFLIRAHERSMRHVLVITGKGSS
		MGSDGALKRAVPLWFSKPEFRYLI
		SSYESAAQHGGEGALYIRLSRRHGERP"
misc-feature	7500..7751	/locus-tag="RL0010"
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		motif: Pfam:PF01713.8"
		/note="Pfam match to entry
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CDS	7772..8149	/locus-tag="RL0011"
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		/note="similarity:fasta;
		SWALL:Q8UJB7 (EMBL:AE008975);
		Agrobacterium tumefaciens;
		transcriptional regulator; length
		121 aa; 121 aa overlap; query
		1-121 aa; subject 1-121 aa"
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		/db-xref="UniProtKB/TrEMBL:Q1MNE6"
		/translation="MTPFGEAVRRLRARKGVSQK
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		TFDLLQRIAGYFNIIWDEAEELFLLARSSDP RVV
		IDTSGLPPEYTEFANRLARRIRNL
		DSAEIGRLSALLENGGKG DGKAS"
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		/note="Pfam match to entry
		PF01381.9 HTH-3"
gene	8285..10720	/gene="gyrB"
		/locus-tag="RL0012"
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subunit B (EC 5.99.1.3).;
length=EC 5.99.1 ( 803; id 58.612;
807 aa overlap; query 12-811;
subject 1-803 similarity:fasta;
with=UniProt:Q8UJB6
(EMBL:AE007943); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; gyrB; DNA gyrase subunit
B (AGR-C-19p).; length=AGR-C-19p;
id 86.190; 811 aa overlap; query
1-811; subject 6-816"
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SVWLKCLKIRRHDKIHEMSFTHGVA
DAPLKVTGDAPNETGTEVSFMPSTDTFTMTEFDY
GTLEHRLRELAFNLNGVRILLTDK
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ENQAILPLRGKILNVERARFDKMLSSQEIGTLIT
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CDS		
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CDS		
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		/inference="protein motif: Pfam:PF00043.11"
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		/inference="similar to sequence:INSDC:AF169302"
		/note="similarity:fasta; with=UniProt:Q8VUC7 (EMBL:AF169302); Burkholderia cepacia (Pseudomonas cepacia).; DntG.; length=281; id 38.267; 277 aa overlap; query 5-279; subject 13-279 similarity:fasta; with=UniProt:Q8UJB4"

		(EMBL:AE007944); Agrobacterium tumefaciens (strain C58/ATCC 33970).; hpcE; 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (AGR-C-22p).; length=280; id 87.097; 279 aa overlap; query 1-279; subject 1-279"
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misc-feature	13286..13783	/locus-tag="RL0016"
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		motif: Pfam:PF01557.8"
		/note="Pfam match to entry PF01557.8 FAA-hydrolase"
gene	14079..15356	/locus-tag="RL0017"
CDS	14079..15356	/locus-tag="RL0017"
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		/note="similarity:fasta; with=UniProt:Q71KW6 (EMBL:AF474374); Azospirillum brasilense.; phaZ; PHB depolymerase.; length=603; id 57.471; 348 aa overlap; query 61-406; subject 257-602 similarity:fasta; with=UniProt:Q92TD3 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; Hypothetical protein SMc02770.; length=424; id 76.000; 425 aa overlap; query 1-424; subject 1-423 Codons 60 to the C-terminus are similar to codons 255 to the C-terminus of Azospirillum brasilense PHB depolymerase phaZ UniProt:Q92TD3 (EMBL:SME591782) (603 aa), and entire protein is similar to Rhizobium meliloti (Sinorhizobium meliloti) Hypothetical protein SMc02770 UniProt:Q92TD3 (EMBL:SME591782) (424 aa)"

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CDS	15502..15936	
misc-feature	15544..15612	
gene	16044..16802	
CDS	16044..16802	

		with=UniProt:Q8UJB2 (EMBL:HS360250); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0016 (AGR-C-25p).; length=AGR-C ( 255; id 68.482; 257 aa overlap; query 1-252; subject 1-255" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05507.1" /db-xref="GI:115254433" /db-xref="UniProtKB/TrEMBL:Q1MND8" /translation="MFSLKTRSKARKPAPPEMR TLDVAGRLMPLTIKQHDRATRITL RIEPGGRALKMTVPKGLAAREVNAFLDRHQGWLL TKLAKFSTDTGLRDGGEILLRGVS HRIQHSGSLRGLTEAVSIDGRPVLRVSGMPEHVG RRIAAFLKKEARADLARLATMHAA TIRAPIRSISMKDTRSRWGSSEGNLSFSWRIV MAPPSVIDYLA AEVAHLKEMNHG PHFWALCRKLCPGMEEAKSWLKRHGSQ LHAIDFD "
misc-feature	16131..16778	/locus-tag="RL0019" /inference="protein motif: Pfam: PF01863.6" /note="Pfam match to entry PF01863.6 DUF45"
gene	16969..17637	/locus-tag="RL0020"
CDS	16969..17637	/locus-tag="RL0020" /inference="similar to sequence: UniProtKB: Q8UJB1" /inference="similar to sequence: UniProtKB: Q9X4E3" /note="similarity: fasta; SWALL: TRPF-RHOSH (SWALL: Q9X4E3); Rhodobacter sphaeroides; n-(5'-phosphoribosyl)anthranilate; trpF; length 212 aa; 206 aa overlap; query 5-209 aa; subject 6-210 aa similarity: fasta; SWALL: TRPF-AGRT5 (SWALL: Q8UJB1); Agrobacterium tumefaciens; n-(5'-phosphoribosyl)anthranilate; trpF; length 220 aa; 210 aa overlap; query 1-210 aa; subject 1-210 aa" /codon-start=1 /transl-table=11 /product="putative N-(5'-phosphoribosyl)anthranilate" /protein-id="CAK05508.1" /db-xref="GI:115254434" /db-xref="GOA: Q1MND7" /db-xref="UniProtKB/TrEMBL: Q1MND7" /translation="MRPDIKICGLKTPEAVDRAL KRGATHIGFIFFEKSPRYIEPDLA AKLAEARGKAKIVAVVVDPTNDELDEIVSLLKP DMLQLHGNE SPEHVLTIKALYGLP VMKVFSVRTADDLKRVEAYIGIADRFLFDAKAPK GSELPGGNGISFDWSLLSWLDGSV

		DYMLSGGLNKDNVAEALFVTKAPGIDVSSGVETA PGVKSVAKIDEFFDAVEKANAPMM ASGS"
misc-feature	16981..17595	/locus-tag="RL0020" /inference="protein motif: Pfam: PF00697.10" /note="Pfam match to entry PF00697.10 PRAI"
gene	17640..18860	/gene="trpB" /locus-tag="RL0021"
CDS	17640..18860	/gene="trpB" /locus-tag="RL0021" /EC-number="4.2.1.20" /inference="similar to sequence: UniProtKB: P56929" /inference="similar to sequence: UniProtKB: Q9X4E5" /note="similarity: fasta; SWALL: TRPB-RHOSH (SWALL: Q9X4E5); Rhodobacter sphaeroides; tryptophan synthase beta chain; trpB; length 409 aa; 401 aa overlap; query 8-406 aa; subject 7-407 aa similarity: fasta; SWALL: TRPB-RHIET (SWALL: P56929); Rhizobium etli; tryptophan synthase beta chain; trpB; length 406 aa; 406 aa overlap; query 1-406 aa; subject 1-406 aa" /codon-start=1 /transl-table=11 /product="putative tryptophan synthase beta chain" /protein-id="CAK05509.1" /db-xref="GI:115254435" /db-xref="GOA:Q1MND6" /db-xref="UniProtKB/TREMBL:Q1MND6" /translation="MNETPKPNSFRSGPDEDGRF GIYGGRFVAETLMPLILDLDQDEWN RAKNDPAFQAEKHLGAHYIGRPSPLYFAERLTA ELGGAKIYFKREELNHTGSHKINN CIGQILLAKRMGKTRIIAETGAGQHGVASATVAA RFGLPCVVYMGATDVERQAPNVFR MKLLGAEVKPVTAGSGTLKDAMNEALRDWVTNVE DTYYLIGTAAGPHPYPEMVRDFQS VIGIEAKEQMLAAEGRPLDLVIAAVGGGSNAIGI FHPFLDDPSVKIVGVEAGGKGLQG DEHCASITAGSPGVLHGNRTYLLQSDGQIKEGH SISAGLDYPGIGPEHSWLNDTGRV DYVPIMDHEALEAFQTLTRLEGIIPALEPSHAIA EVIKRAPTMGKDEIILMNLSGRGD KDIFTVGKILGMGL"
misc-feature	17820..18809	/gene="trpB" /locus-tag="RL0021" /inference="protein motif: Pfam: PF00291.10" /note="Pfam match to entry PF00291.10 PALP"
gene	18864..19703	/gene="trpA" /locus-tag="RL0022"
CDS	18864..19703	/gene="trpA" /locus-tag="RL0022" /inference="similar to

		sequence:INSDC:AE007944" /inference="similar to sequence:INSDC:AF107094" /note="similarity:fasta; with=UniProt:TRPA-RHOSH (EMBL:AF107094); Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).; trpA; Tryptophan synthase alpha chain (EC 4.2.1.20).; length=263; id 62.214; 262 aa overlap; query 4-265; subject 3-259 similarity:fasta; with=UniProt:TRPA-AGRT5 (EMBL:AE007944); Agrobacterium tumefaciens (strain C58/ATCC 33970).; trpA; Tryptophan synthase alpha chain (EC 4.2.1.20).; length=279; id 84.229; 279 aa overlap; query 1-279; subject 1-279; putative tryptophan synthase, alpha subunit" /codon-start=1 /transl-table=11 /product="Tryptophan synthase alpha chain." /protein-id="CAK05510.1" /db-xref="GI:115254436" /db-xref="GOA:Q1MND5" /db-xref="UniProtKB/TrEMBL:Q1MND5" /translation="MTARMDKRFAELKAEGRPAL VTYFMGGDPDYDTSLGIMKALPEA GSDIIELGMPFSDPMADGPAIQLAGQRALKGGQT LKKTLQLAADFRKTNDATPIVMMG YYNPIYIYGVEKFLDDALLAGIDGLIVVDLPPEM DDELCIPAIRKGINFIRLATPTTD EKRLPKVLKNTSGFVYYVSMNGITGSALPDPSLV SGAVERIKQHTKLPVCVGVFGVKTA EHAKVIGGSADGVVVGTAIVNQVATSLTHDGKAT ADTVQAVATLVRGLSTGTRSARLV AAE" /gene="trpA" /locus-tag="RL0022" /inference="protein motif:Pfam:PF00290.9" /note="Pfam match to entry PF00290.9 Trp-syntA" /locus-tag="RL0023" /locus-tag="RL0023" /inference="similar to sequence:INSDC:HS028244" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:ACCD-ECOLI (EMBL:HS028244); Escherichia coli O157:H7.; accD; Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta (EC 6.4.1.2) (ACCase beta chain).; length=304; id 46.831; 284 aa overlap; query 1-283; subject 1-281 similarity:fasta; with=UniProt:Q92TC7
misc-feature	18888..19676	
gene	19845..20750	
CDS	19845..20750	

		(EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PROBABLE ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA PROTEIN (EC 6.4.1.2).; length=304; id 85.526; 304 aa overlap; query 1-301; subject 1-304; putative acetyl-coenzyme A carboxylase carboxyl transferase subunit" /codon-start=1 /transl-table=11 /product="Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta (ACCase beta chain)." /protein-id="CAK05511.1" /db-xref="GI:115254437" /db-xref="GOA:Q1MND4" /db-xref="UniProtKB/TrEMBL:Q1MND4" /translation="MNWITNYVRPRINSMLGRRE VPENLWIKCPETGEMVFHKDLEGN KWVIPASGYHMKMPAKARLADLFDNGEFESLPQP KVAQDPLKFRDSKKYSDRLRDSRL KTEQEDTILAGVGKVQGLKLVAVVHEFNFIGGSL GMAAGEAIVKAFERATAEKCP LVM FPASGGARMQEGILSLMQLPRTTVAVDMLKESGQ PYIVVLTNPTTGGVTASYAMLGDI HLAEPGAIEIGFAGKRVIEQTLREKLPEGFQTAEY LLEHGMVDMVVKRHDIPETLARLL KILTKKPVSAANDMNGGAIALAASA" /locus-tag="RL0023" /inference="protein motif: Pfam: PF01039.9" /note="Pfam match to entry PF01039.9 Carboxyl-trans"
misc-feature	20172..20372	
gene	20778..22130	/gene="folC" /locus-tag="RL0024"
CDS	20778..22130	/gene="folC" /locus-tag="RL0024" /inference="similar to sequence: INSDC: ECD862" /inference="similar to sequence: INSDC: SME591782" /note="similarity: fasta; with=UniProt: FOLC-ECOLI (EMBL: ECD862); Escherichia coli.; folC; FolC bifunctional protein [Includes: Folylpolyglutamate synthase (EC 6.3.2.17) (Folylpoly-gamma-glutamate synthetase) (FPGS); Dihydrofolate synthase (EC 6.3.2.12)].; length=422; id 31.757; 444 aa overlap; query 1-442; subject 2-411 similarity: fasta; with=UniProt: Q92TC6 (EMBL: SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PROBABLE FOLC BIFUNCTIONAL PROTEIN INCLUDES: FOLYLPOLYGLUTAMATE SYNTHASE AND DIHYDROFOLATE SYNTHASE (EC



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6.3.2.17) (EC 6.3.2.12).;
length=447; id 75.901; 444 aa
overlap; query 7-450; subject
4-447"
/codon-start=1
/transl-table=11
/product="putative FolC
bifunctional protein [Includes:
Folylpolyglutamate synthase (EC
6.3.2.17)
(Folylpoly-gamma-glutamate
synthetase) (FPGS); Dihydrofolate
synthase] ."
/protein-id="CAK05512.1"
/db-xref="GI:115254438"
/db-xref="GOA:Q1MND3"
/db-xref="UniProtKB/TrEMBL:Q1MND3"
/translation="MIPRGQTAVSEAAQEIDKLM
GLHPKGFDSLDRITRLLDV LGNP
HRKLPPVIHVAGTNGKGSVTAFCRALLEAGGYSA
HVHTSPHLVNWHERYRIGVKGGRG
QLVDDAVFAEAVRRVADANAGQHITVFEILTAVT
FILFSEHPADAAIIEVGLGGRFDA
TNVISDPAVSVIMPISLDHQPYLGDRVELIAAEK
AGIMKPGFPVVIGHQEYDAALDVL
MSTAERLHCPSAVFGQDFMAHEEYGR LVYQDEFG
LADLPLPRLPGRHQYANAAAAIRA
VKAAGFTVTETMMEKAMSSVEWPGRLQRLSEGR L
LSHAPAGAEIWI DGGHNP GAGEVI
AEAMANFEERQSRPLFLIIGMINTKDPVG YFKAF
AGLVEKVFCVPIRGSEAMIDPVIL
SNAAYDAGLVAEPMSTVGDAL EAIKAVADPEALP
PRILVGGS LYLVDVLADNGTPPK
/misc-feature 20877..21641 /gene="folC"
/locus-tag="RL0024"
/inference="protein
motif: Pfam: PF01225.11"
/note="Pfam match to entry
PF01225.11 Mur-ligase"
gene complement(22203..22523 /locus-tag="RL0025"
)
CDS complement(22203..22523 /locus-tag="RL0025"
)
/inference="similar to
sequence: INSDC: A35135"
/inference="similar to
sequence: INSDC: AE008976"
/note="similarity: fasta;
with=UniProt: THIO-RHOSH
(EMBL: A35135); Rhodobacter
sphaeroides (Rhodopseudomonas
sphaeroides).; trxA; Thioredoxin
(TRX).; length=TRX; id 57.692; 104
aa overlap; query 2-105; subject
1-104 similarity: fasta;
with=UniProt: Q8UJA6
(EMBL: AE008976); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; trxA; Thioredoxin C-1.;
length=133; id 91.509; 106 aa
overlap; query 1-106; subject
28-133 Similar to entire protein

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of Rhodobacter sphaeroides
(Rhodopseudomonas sphaeroides)
Thioredoxin (TRX) trxA (104 aa),
and similar, but truncated at the
N-terminus, to Agrobacterium
tumefaciens (strain C58/ATCC
33970) Thioredoxin C-1 trxA (133
aa) "
/codon-start=1
/transl-table=11
/product="putative thioredoxin"
/protein-id="CAK05513.1"
/db-xref="GI:115254439"
/db-xref="GOA:Q1MND2"
/db-xref="UniProtKB/TrEMBL:Q1MND2"
/translation="MATVKVDINNFQSEVLESAE
PVVVDFWAEWCGPCKMIAPSLEEI
AVEMEGKVKVAKLNIDENPELAAQFGVRSIPTLA
IFKGGEVADISVGAKPKTALSNI SSAA"
misc-feature    complement(22206..22520 /locus-tag="RL0025"
)
                /inference="protein
                motif: Pfam:PF00085.8"
                /note="Pfam match to entry
                PF00085.8 Thioredoxin"
gene            complement(22599..26150 /locus-tag="RL0026"
)
CDS             complement(22599..26150 /locus-tag="RL0026"
)
                /inference="similar to
                sequence: INSDC:AE008977"
                /note="similarity: fasta;
                with=UniProt:Q8UJA5
                (EMBL:AE008977); Agrobacterium
                tumefaciens (strain C58/ATCC
                33970).; uvrD; ATP-dependant DNA
                helicase.; length=1185; id 62.203;
                1180 aa overlap; query 6-1183;
                subject 8-1185"
                /codon-start=1
                /transl-table=11
                /product="putative ATP-dependent
                UvrD family DNA helicase"
                /protein-id="CAK05514.1"
                /db-xref="GI:115254440"
                /db-xref="GOA:Q1MND1"
                /db-xref="UniProtKB/TrEMBL:Q1MND1"
                /translation="MSDVTALPNDDDPGAWIGWT
                TIQQAIASDPLRSAWVSANAGSGK
                THVLTQRVIRLLLSGARPSAILCLTYTKAAASEM
                SNRVFERLAEWVVLDDDLRRIT
                QIEGMAPDGLKLAEARRLFAKALETPGGLKIQTI
                HAFCEALLHQFPLEANVAGHFSVL
                DDRAAVALLSDARRALLTATAPDEDSALAEAFAY
                VLNLGDESGLENLLGDIVANRNAI
                RRFTAAAEQQGGVEMVLRKRLGLAVGDTEDRIEA
                QYWPLPELSGSLVLELYLSLADQKG
                GAKAQEVAYGLRLAGRERDDARRAQFLEKIFLTV
                KGEPKADSQFFVKAMLAEAPQLAE
                AIAIARAHVAASRDRLKLMRYGATHAALVLADR
                LNHDEELKKQRSQDLDFEDLITRT
                ADLLTKSGVGPWIIHYKLDRGIDHILVDEAQDTSP

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pantothenate kinase"
/codon-start=1
/transl-table=11
/product="Pantothenate kinase
(Pantothenic acid kinase) (Rts
protein)."
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misc-feature      complement(43080..43742

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)
/locus-tag="RL0040"
/inference="protein
motif: Pfam:PF00485.7"
/note="Pfam match to entry
PF00485.7 PRK"
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gene              complement(44048..44371

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)
/locus-tag="RL0041"
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CDS               complement(44048..44371

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)
/locus-tag="RL0041"
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sequence:INSDC:AE007946"
/inference="similar to
sequence:INSDC:ECRFBM"
/note="similarity:fasta;
with=UniProt:HIS2-ECOLI
(EMBL:ECRFBM); Escherichia coli.;
hisI; Histidine biosynthesis
bifunctional protein hisIE
[Includes: Phosphoribosyl-AMP
cyclohydrolase (EC 3.5.4.19)
(PRA-CH); Phosphoribosyl-ATP
pyrophosphatase (EC 3.6.1.31)
(PRA-PH)].; length=203; id 47.126;
87 aa overlap; query 6-92; subject
115-201 similarity:fasta;
with=UniProt:HIS2-AGRT5
(EMBL:AE007946); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; hisE; Phosphoribosyl-ATP
pyrophosphatase (EC 3.6.1.31)
(PRA-PH).; length=107; id 71.698;
106 aa overlap; query 1-106;
subject 1-106"
/codon-start=1
/transl-table=11
/product="putative histidine
biosynthesis bifunctional protein"
/protein-id="CAK05529.1"
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/db-xref="GI:115254455"
/db-xref="GOA:Q1MNF9"
/db-xref="UniProtKB/TrEMBL:Q1MNF9"
/translation="MSGFSLSDLESIVAERSKAP
PEQSWTAKLVAGGQPKAAKKLGEE
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EIPLENVMAELERRTAQSGLKEKA SRQSS"
misc-feature      complement(44090..44356
)
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                    /inference="protein
motif: Pfam:PF01503.6"
                    /note="Pfam match to entry
PF01503.6 PRA-PH"
gene              complement(44389..45177
)
                    /gene="hisF"
                    /locus-tag="RL0042"
CDS               complement(44389..45177
)
                    /gene="hisF"
                    /locus-tag="RL0042"
                    /inference="similar to
sequence: INSDC:ABHISHAFE"
                    /inference="similar to
sequence: INSDC:AE007946"
                    /note="similarity:fasta;
with=UniProt:HIS6-AZOBR
(EMBL:ABHISHAFE); Azospirillum
brasilense.; hisF; Imidazole
glycerol phosphate synthase
subunit hisF (EC 4.1.3.-) (IGP
synthase cyclase subunit) (IGP
synthase subunit hisF) (ImGP
synthase subunit hisF) (IGPS
subunit hisF).; length=261; id
69.767; 258 aa overlap; query
3-260; subject 2-251
similarity:fasta;
with=UniProt:HIS6-AGRT5
(EMBL:AE007946); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; hisF; Imidazole glycerol
phosphate synthase subunit hisF
(EC 4.1.3.-) (IGP synthase cyclase
subunit) (IGP synthase subunit
hisF) (ImGP synthase subunit hisF)
(IGPS subunit hisF).; length=258;
id 82.129; 263 aa overlap; query
1-262; subject 1-258"
                    /codon-start=1
                    /transl-table=11
                    /product="putative imadazole
glycerol phosphate synthase
sununit"
                    /protein-id="CAK05530.1"
                    /db-xref="GI:115254456"
                    /db-xref="GOA:Q1MNF7"
                    /db-xref="UniProtKB/TrEMBL:Q1MNF7"
                    /translation="MTLKARVIPCLDVKDGRVVK
GVNFLNLVDAGDPVEAAKAYDAAG
ADELCFLDITASSDNRETIFDVVSRTADQCFMPL
TVGGGVRTIADIRKLLLCGADKVS
INSAAVSNPDFVTEAADKFGDQCIVVSIDAKRRR
TOAVGGDNLSAWEIYTHGGRNATG

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IDAVEFAQKMVARGAGELLVTSMDRDGTVGYDL
ELTRAIADAVRVPVIASGGVGDLD
DLVAGVKEGHANAVLAASIFHFGTYSVSEAKHYM
SKCGIDMRDL"
misc-feature    complement(44446..45162 /gene="hisF"
)
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                /inference="protein
                motif: Pfam: PF00977.8"
                /note="Pfam match to entry
                PF00977.8 His-biosynth"
gene            complement(45178..45924 /gene="hisA"
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CDS             complement(45178..45924 /gene="hisA"
)
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                sequence: INSDC: ECD840"
                /inference="similar to
                sequence: INSDC: SME591782"
                /note="similarity: fasta;
                with=UniProt: HIS4-ECOLI
                (EMBL: ECD840); Escherichia coli.;
                hisA;
                1-(5-phosphoribosyl)-5-[(5-phospho
                ribosylamino)methylidene amino]
                imidazole-4-carboxamide isomerase
                (EC 5.3.1.16)
                (Phosphoribosylformimino-5-aminoim
                idazole carboxamide ribotide
                isomerase).;
                length=5-phosphoribosyl; id
                35.081; 248 aa overlap; query
                2-242; subject 1-245
                similarity: fasta;
                with=UniProt: HIS4-RHIME
                (EMBL: SME591782); Rhizobium
                meliloti (Sinorhizobium
                meliloti).; hisA;
                1-(5-phosphoribosyl)-5-[(5-phospho
                ribosylamino)methylidene amino]
                imidazole-4-carboxamide isomerase
                (EC 5.3.1.16)
                (Phosphoribosylformimino-5-aminoim
                idazole carboxamide ribotide
                isomerase).;
                length=5-phosphoribosyl; id
                88.066; 243 aa overlap; query
                1-243; subject 1-243"
                /codon-start=1
                /transl-table=11
                /product="putative
                imidazole-4-carboxamide isomerase"
                /protein-id="CAK05531.1"
                /db-xref="GI:115254457"
                /db-xref="GOA:Q1MNC1"
                /db-xref="UniProtKB/TrEMBL:Q1MNC1"
                /translation="MILFPAIDLKGGQCVRLKLG
                DMQQATVYNTDPAAQARSFEDQGF
                EWLHVVDLDGAFAGHSANGDAVEAILKATDNPVQ
                LGGGIRTLDHIEAWLSRGLRRVIL

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		GTVAVRNPDLVIEACRKFPDHSVAVGIDAKGGKVA VEGWAEASELGIIELARKFEGAGV AAIIYTDIDRDGILAGINWSSTLELADAVSIPVI ASGGLASLDDIRRMLEPDARKLEG AISGRALYDGRIDPKEALALIKAAKAKETA"
misc-feature	complement(45232..45921 )	/gene="hisA"  /locus-tag="RL0043" /inference="protein motif: Pfam:PF00977.8" /note="Pfam match to entry PF00977.8 His-biosynth"
gene	complement(45931..46488 )	/locus-tag="RL0044"
CDS	complement(45931..46488 )	/locus-tag="RL0044"  /note="no significant database hits" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAK05532.1" /db-xref="GI:115254458" /db-xref="UniProtKB/TrEMBL:Q1MNC0" /translation="MIHDSFPANDGSSRRQNGVS AGDIAEAVLEFYIEGEDDLIGLLA YALYERQKRDFVLSHRKRNAGRSPDEAELAAVNS NYLSTDLRNTLRDRASQILSSYAE TYVEAMEPQIRLTAVNSDALRQVRSIEKSIKRL GFWRQVRAGFAVTL L L L L L L F G A A A IAAVFFQSDIVDAWNALMVPTTLRM"
misc-feature	complement(45991..46059 )	/locus-tag="RL0044"  /inference="protein motif: TMHMM:2.0" /note="1 probable transmembrane helix predicted at aa 144-166"
gene	complement(46485..46676 )	/locus-tag="RL0045"
CDS	complement(46485..46676 )	/locus-tag="RL0045"  /note="no significant database hits" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAK05533.1" /db-xref="GI:115254459" /db-xref="UniProtKB/TrEMBL:Q1MNB9" /translation="MRSMPASRKSGKV FYTLRPS REGLPPFSDIKLPGGTVIRRVDEA IHRKALSNAAKALKERLDR"
gene	complement(46921..47571 )	/gene="hisH"  /locus-tag="RL0046"
CDS	complement(46921..47571 )	/gene="hisH"  /locus-tag="RL0046" /inference="similar to sequence: INSDC:ECD840" /inference="similar to sequence: INSDC:SME591782"

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/feature "misc-feature" complement(46927..47562)
    /note="similarity:fasta;
    with=UniProt:HIS5-ECOLI
    (EMBL:ECD840); Escherichia coli.;
    hisH; Imidazole glycerol phosphate
    synthase subunit hisH (EC 2.4.2.-)
    (IGP synthase glutamine
    amidotransferase subunit) (IGP
    synthase subunit hisH) (ImGP
    synthase subunit hisH) (IGPS
    subunit hisH).; length=196; id
    36.792; 212 aa overlap; query
    1-212; subject 1-194
    similarity:fasta;
    with=UniProt:HIS5-RHIME
    (EMBL:SME591782); Rhizobium
    meliloti (Sinorhizobium
    meliloti).; hisH; Imidazole
    glycerol phosphate synthase
    subunit hisH (EC 2.4.2.-) (IGP
    synthase glutamine
    amidotransferase subunit) (IGP
    synthase subunit hisH) (ImGP
    synthase subunit hisH) (IGPS
    subunit hisH).; length=216; id
    81.944; 216 aa overlap; query
    1-216; subject 1-216"
    /codon-start=1
    /transl-table=11
    /product="putative imadazole
    glycerol phosphate synthase
    subunit"
    /protein-id="CAK05534.1"
    /db-xref="GI:115254460"
    /db-xref="GOA:Q1MNB8"
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dehydratase (EC 4.2.1.19) (IGPD)..
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 CAS REGISTRY NO. (RN): 843924-26-5  
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 MOLECULE TYPE (CI): DNA; circular  
 DIVISION CODE (CI): Bacteria  
 DATE (DATE): 23 Oct 2008  
 DEFINITION (DEF): Bacteroides fragilis NCTC 9343, complete genome.  
 KEYWORDS (ST): complete genome  
 SOURCE: Bacteroides fragilis NCTC 9343  
 ORGANISM (ORGN): Bacteroides fragilis NCTC 9343  
 Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales;  
 Bacteroidaceae; Bacteroides  
 PROJECT (PJID): GenomeProject:46  
 REFERENCE: 1 (bases 1 to 5205140)  
 AUTHOR (AU): Cerdeno-Tarraga, A.M.; Patrick, S.; Crossman, L.C.;  
 Blakely, G.; Abratt, V.; Lennard, N.; Poxton, I.;  
 Duerden, B.; Harris, B.; Quail, M.A.; Barron, A.; Clark, L.;  
 Corton, C.; Doggett, J.; Holden, M.T.; Larke, N.; Line, A.;  
 Lord, A.; Norbertczak, H.; Ormond, D.; Price, C.;  
 Rabbinowitsch, E.; Woodward, J.; Barrell, B.; Parkhill, J.  
 TITLE (TI): Extensive DNA inversions in the B. fragilis genome  
 control variable gene expression  
 JOURNAL (SO): Science, 307 (5714), 1463-1465 (2005)  
 OTHER SOURCE (OS): CA 142:234199  
 REFERENCE: 2 (bases 1 to 5205140)  
 AUTHOR (AU): Cerdeno-Tarraga, A.M.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (29-JUL-2004) Cerdeno-Tarraga A.M., submitted  
 on behalf of the Pathogen Sequencing Unit, Sanger  
 Institute, Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA E-mail: amct@sanger.ac.uk

FEATURES (FEAT):

Feature Key	Location	Qualifier
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3424841..3424900, 1011-1033"
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3737299..3737367, 227-249, 254-276, 297-319,
3737428..3737496, 347-369, 376-398 and 438-460"
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3753109..3753168))
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3841494..3841550, 268-290, 302-319, 323-341,
3841560..3841613, 348-370, 385-404 and 411-433"
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3905850..3905906, 231-253, 273-295, 308-326,
3905943..3906011, 341-363, 376-398 and 402-424"
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3937648..3937716, 222-244, 274-293, 300-322,
3937855..3937923, 358-380, 427-449, 459-481, 502-524
3938029..3938097, and 529-548"
3938116..3938175,
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3938365..3938433,
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4088311..4088379, 335-357, 370-392 and 397-419"
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4089574..4089633, 197-219, 228-247, 262-284, 316-335
4089658..4089726, and 339-356"
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4608603..4608656, 232-249, 259-278, 285-302,
4608675..4608734, 381-400, 413-435 and 445-464"
4608762..4608815,
4608834..4608902,
4608930..4608998,
4609059..4609112,
4609254..4609313,
4609332..4609385,
4609428..4609496))
misc-feature complement(order(461139 /note="4 probable transmembrane
0..4611458, helices predicted for BF3914 by
4611486..4611554, TMHMM2.0 at aa 9-31, 66-88,
4611615..4611683, 109-131 and 141-163"
4611786..4611854))
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3..4631342, helices predicted for BF3925 by
4631928..4631981)) TMHMM2.0 at aa 13-30 and 226-245"
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9..4632107, helices predicted for BF3926 by
4632117..4632185, TMHMM2.0 at aa 12-34, 54-76,

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=> d l13 4 tit

'TIT' IS NOT A VALID FORMAT

In a multifile environment, a format can only be used if it is valid in at least one of the files. Refer to file specific help messages or the STNGUIDE file for information on formats available in individual files.

REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):.

L13 ANSWER 4 OF 14 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AM286415 GenBank (R)  
GenBank ACC. NO. (GBN): AM286415  
GenBank VERSION (VER): AM286415.1 GI:122087364  
CAS REGISTRY NO. (RN): 917704-63-3  
SEQUENCE LENGTH (SQL): 4615899  
MOLECULE TYPE (CI): DNA; circular  
DIVISION CODE (CI): Bacteria  
DATE (DATE): 29 Oct 2008  
DEFINITION (DEF): *Yersinia enterocolitica* subsp. *enterocolitica* 8081 complete genome.  
KEYWORDS (ST): complete genome  
SOURCE: *Yersinia enterocolitica* subsp. *enterocolitica* 8081  
ORGANISM (ORGN): *Yersinia enterocolitica* subsp. *enterocolitica* 8081 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; *Yersinia*  
PROJECT (PJID): GenomeProject:190  
REFERENCE: 1  
AUTHOR (AU): Delihhas, N.  
TITLE (TI): Annotation and evolutionary relationships of a small regulatory RNA gene *micF* and its target *ompF* in *Yersinia* species  
JOURNAL (SO): (er) BMC Microbiol., 3, 13 (2003)  
REFERENCE: 2  
AUTHOR (AU): Thomson, N.R.; Howard, S.; Wren, B.W.; Holden, M.T.; Crossman, L.; Challis, G.L.; Churcher, C.; Mungall, K.; Brooks, K.; Chillingworth, T.; Feltwell, T.; Abdellah, Z.; Hauser, H.; Jagels, K.; Maddison, M.; Moule, S.; Sanders, M.; Whitehead, S.; Quail, M.A.; Dougan, G.; Parkhill, J.; Prentice, M.B.  
TITLE (TI): The complete genome sequence and comparative genome analysis of the high pathogenicity *Yersinia enterocolitica* strain 8081  
JOURNAL (SO): PLoS Genet., 2 (12), E206 (2006)  
REFERENCE: 3 (bases 1 to 4615899)  
AUTHOR (AU): Thomson, N.R.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (30-JUN-2006) Thomson N.R., Pathogen Sequencing Unit, The Wellcome Trust Sanger Institute, Genome Campus, Hinxton, Cambridge, CB10 1SA, UNITED KINGDOM

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..4615899	/organism=" <i>Yersinia enterocolitica</i> subsp. <i>enterocolitica</i> 8081" /mol-type="genomic DNA" /strain="8081" /sub-species="enterocolitica" /db-xref="taxon:393305"
gene	complement(270..710)	/locus-tag="YE0001"
CDS	complement(270..710)	/locus-tag="YE0001"

		/codon-start=1 /transl-table=11 /product="putative flavoprotein" /protein-id="CAL10146.1" /db-xref="GI:122087365" /db-xref="GOA:A1JHQ8" /db-xref="InterPro:IPR001094" /db-xref="InterPro:IPR008254" /db-xref="InterPro:IPR015702" /db-xref="UniProtKB/TrEMBL:A1JHQ8" /translation="MADITLISGSTLGSAEYVAE HLAEKLEEAGFTTETLHGPELDEL TLDGMWLIITSTHGAGDLPDNLQPLLEQIEQQR DLSQVRFGAVGLGSSEYDTFCGAV RKLDQQLIIQGAIRVGDILEIDVIKHEIPEDPAE IWVKNWINLL"
misc-feature	complement(273..704)	/locus-tag="YE0001" /inference="protein" motif:PFAM:PF00258" /note="Pfam match to entry PF00258 flavodoxin, Flavodoxin, score 117.3, E-value 1.9e-32"
gene	complement(802..1263)	/gene="asnC" /locus-tag="YE0002"
CDS	complement(802..1263)	/gene="asnC" /locus-tag="YE0002" /codon-start=1 /transl-table=11 /product="regulatory protein" /protein-id="CAL10147.1" /db-xref="GI:122087366" /db-xref="GOA:A1JHQ9" /db-xref="InterPro:IPR000485" /db-xref="InterPro:IPR011991" /db-xref="UniProtKB/TrEMBL:A1JHQ9" /translation="MSEIYQIDNLDRGILNALME NARTPYAELAKNFGVSPGTIHVRV EKMRQAGIITAACVHVNPKQLGYDVCCFIGIILK SAKDYP SALKKLESLEEVVEAYYT TGHYSIFIKVMCKSIDALQQVLINKIQTIDEIQS TETLISLQNPIMRTIVP"
misc-feature	complement(868..1173)	/gene="asnC" /locus-tag="YE0002" /inference="protein" motif:PFAM:PF01037" /note="Pfam match to entry PF01037 ASNC-trans-reg, AsnC family, score 61.4, E-value 1.2e-15"
misc-feature	complement(1111..1191)	/gene="asnC" /locus-tag="YE0002" /inference="protein" motif:Prosite:PS00519" /note="PS00519 Bacterial regulatory proteins, asnC family signature."
misc-feature	complement(1129..1194)	/gene="asnC" /locus-tag="YE0002" /note="Predicted helix-turn-helix motif with score 1765.000, SD 5.20 at aa 24-45, sequence TPYAELAKNFGVSPGTIHVRVE"
gene	1449..2441	/gene="asnA"

CDS	1449..2441	/locus-tag="YE0003" /gene="asnA" /locus-tag="YE0003" /codon-start=1 /transl-table=11 /product="aspartate-ammonia ligase" /protein-id="CAL10148.1" /db-xref="GI:122087367" /db-xref="GOA:A1JHR0" /db-xref="InterPro:IPR004618" /db-xref="InterPro:IPR006195" /db-xref="UniProtKB/Swiss-Prot:A1J HR0" /translation="MKKQFIQKQQQISFVKSFFS RQLEQQGLGLIEVQAPILSRVGDGT QDNLSGSEKAVQVKVKS LPDATFEVVHSLAKWKR KTLGRFDGADQGIYTHMKALRPD EDRLSAIHSVYVDQWDWERVMGDGERNLAYLKST VNKIYAAIKETEA AISAEFDIKPF LPEQIHFIHSESLRAKFPDLDAKGRERAI AKELG AVFLIGIGGKLADGKSHDVRAPDY DDWTSPSAEGFAGLNGDIIVWNPVLEDAFEISSM GIRVDAEALKRQLALTSDEDRCLKL EWHQSLLNGEMPQTIGGGIGQSRLVMLLLQQQHI GQVQCGVWGPEISEKVEGLL"
misc-feature	1455..2186	/gene="asnA" /locus-tag="YE0003" /inference="protein motif:PFAM:PF03590" /note="Pfam match to entry PF03590 AsnA, Aspartate-ammonia ligase, score 597.7, E-value 4.6e-177"
misc-feature	2055..2078	/gene="asnA" /locus-tag="YE0003" /inference="protein motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	2595..3266	/locus-tag="YE0004"
CDS	2595..3266	/locus-tag="YE0004" /inference="similar to sequence:INSDC:AE001895" /inference="similar to sequence:INSDC:AL646078" /note="Similar to Ralstonia solanacearum probable transmembrane protein RSP0410 or RS00867 SWALL:Q8XSQ7 (EMBL:AL646078) (224 aa) fasta scores: E(): 7.3e-36, 46.54 38d in 217 aa, and to Deinococcus radiodurans hypothetical protein DR0351 SWALL:Q9RXG2 (EMBL:AE001895) (227 aa) fasta scores: E(): 3.7e-17, 31.67 38d in 221 aa" /codon-start=1 /transl-table=11 /product="putative membrane protein" /protein-id="CAL10149.1"

		/db-xref="GI:122087368" /db-xref="InterPro:IPR009781" /db-xref="UniProtKB/TrEMBL:A1JHR1" /translation="MARFHPLRHYSHARPRLLLS VGAGIIAYFLLPSHFTVLLRVMVS WNIFAWLYLLFLWLQLLRNDPKKIRLIARVQDES ASMVLSIVSMACLASILVILFELS TANQLSGSAKAFHLVLTGMTLLVSWLLLPTAFTM HYAHLFYLSRDESDAVLPLIFPKE VTEPTYWDFLYFSFTIGVASQTADVSTGTSDIRR VLLQSVLSFIFNMTILGLSINVG AGLLN" /locus-tag="YE0004"
misc-feature	join(2643..2711, 2721..2777,2838..2906, 2934..3002,3192..3260)	/inference="protein motif:TMHMM:2.0" /note="5 probable transmembrane helices predicted for YE0004 by TMHMM2.0 at aa 17-39, 43-61, 82-104, 114-136 and 200-222"
gene CDS	complement(3276..4742) complement(3276..4742)	/locus-tag="YE0005" /locus-tag="YE0005" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10150.1" /db-xref="GI:122087369" /db-xref="InterPro:IPR002035" /db-xref="UniProtKB/Swiss-Prot:A1J HR3" /translation="MLSLATLDLLLSISESELIE EMVVGLLASPQLAIFFEKFPRIKR ALMKDIPGWKQNLQQRIREAKVPAGLANEFALYQ QSQLEDSPLFYAHLPPQIVVQLQQW HSPFATQAKTLLHTADLERNPQTGDSFQTLFLQR WRVSLTLQTITIIHQLEQEREQL LAELQQRLLALSGALEPILATNDGAAGRLWDMSQG HLQRGDYQLLLQYGDFLQQQPELQ QLAEQLGRSRSKAQPTPDARFEPYTMVVRQPD VPPEVSGIHQSNDILRLLPTELVM LGMSELEFEFYRLLERRLLTYRLQGDNWQEKTL QRPISLKSHEQPRGPFIVCVDTS GSMGGFSEQCAKAFCLALLRIALEDNRRCYIMLF ATEIIHYELSSASGIEQAIRFLSQ HFRGGTDLAACLSTLSKMEERDWDADAVIISD FIAQRLPEELIRKIKIQQAQHR FHAVAMSAYGKPGIMRIFDHIWRFDGLKSRLIR RWKR"
misc-feature	complement(4035..4100)	/locus-tag="YE0005" /note="Predicted helix-turn-helix motif with score 997.000, SD 2.58 at aa 215-236, sequence PELQQLAELGRSRSKAQPTP"
gene CDS	complement(4746..6254) complement(4746..6254)	/locus-tag="YE0006" /locus-tag="YE0006" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10151.1" /db-xref="GI:122087370"

		/db-xref="GOA:A1JHR5" /db-xref="InterPro:IPR003593" /db-xref="InterPro:IPR011704" /db-xref="UniProtKB/Swiss-Prot:A1JHR5" /translation="MAQSSQLAERISRLSSALES GLYERQEAIRLCLLAALSGESVFL LGPPGIAKSLIARRLKFAFRNARAFEYLMTRFST PEEVFGPLSIQALKEEGRYQRMGTG GYLPEAEIVFLDEIWKAGPAILNTLLTAINERRF RNGDREDSIPMRLLVTASNELPDA DSSLEALYDRMLIRLWLDREVQEKQNFRLLSLRQ NENHNPVAENLSISDEEFYQWQPL IDKIALPDNCFELIFQLRQQLSAQEQAPYVSDRR WKKALRLLQASAFFSGRDEITPID LILLKDCLWHDLSLKLQQLLEQLLTHEGYQQQ SLLMKLQHIHAQWLKHQQQSDHQ ALTVTKQSGMFSRKPYSLPDHLTDSTLTFLQK PLSLHDIQVNLHQIEKEMLVQWLN KGGVLRAKLNGVGYAQSIDAEVDDQLHITVLDVS RQSSILSQPGASTASVPPELLVEL AELENSLAEQRRLFSQHQPCLFTPSSWLAKIEAS LLNVAEQVKQLQQLRGH"
gene	6708..8435	/gene="kup" /locus-tag="YE0007" /note="synonym: trkD"
CDS	6708..8435	/gene="kup" /locus-tag="YE0007" /codon-start=1 /transl-table=11 /product="potassium transport protein" /protein-id="CAL10152.1" /db-xref="GI:122087371" /db-xref="GOA:A1JHR6" /db-xref="InterPro:IPR003855" /db-xref="UniProtKB/Swiss-Prot:A1JHR6" /translation="MVFGFLSLIFWMLILIVSVK YLTYVMRADNAGEGGILTLMFLAG RNTSSRATSILVILGLIGGSFFYGEVVITPAISV MSAIEGLEIAAPALDPYIVPCSA VLTLLFVIQKHGTGSVGKLFAPVMLVWFLTLALL GLRSIIANPEVLAALNPKWAISFF TEYKSVSFFALGAVVLAITGVEALYADMGHFGKF PIRLAWFTVVLP SLVLNYFGQ GAL LLKNPEAIKNPFFLLAPDWALIPLLILATLATVI ASQAVISGVFSLTRQAVRLGYLPP MRIIHTSEMESGQIYIPVINWTLYLAVVLVIVGF ERSSNLAAAYGIAVTGTMVITSVL FCTVALKNWHWNRRFFVYFLLVALLVIDVPMFSAN ALKLFGGWLPLSLGLVMFIIMTT WKSERFSLRRMHEHGNSLEAMIASLEKSPVVRV PGTAVYMSRAMNVIPFALLHNLKH NKVLHDRVVLLTLRTEDAPYVHNVNRVTIEQLSP TFWRVVASYGWRETPNVEEIFHRC GLEGLPCQMMETSFFMSHESLILTKRPWYLFRLG KLFIALSRNALRAADQFEIPPNRV IELGTQVEI"
misc-feature	6711..8432	/gene="kup" /locus-tag="YE0007" /inference="protein"

		motif:PFAM:PF02705"
		/note="Pfam match to entry PF02705
		K-trans, K+ potassium transporter,
		score 854.9, E-value 1.7e-254"
misc-feature	join(6717..6785,	/gene="kup"
	6870..6938,6966..7034,	
	7068..7136,7194..7262,	
	7299..7367,7425..7493,	
	7566..7634,7662..7730,	
	7749..7802,7830..7886)	
		/locus-tag="YE0007"
		/inference="protein
		motif:TMHMM:2.0"
		/note="11 probable transmembrane
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		TMHMM2.0 at aa 4-26, 55-77,
		87-109, 121-143,163-185, 198-220,
		240-262, 287-309, 319-341, 348-365
		and 375-393"
gene	8606..9025	/locus-tag="YE0008"
CDS	8606..9025	/locus-tag="YE0008"
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		/transl-table=11
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		/db-xref="GI:122087372"
		/db-xref="GOA:A1JHR8"
		/db-xref="InterPro:IPR007721"
		/db-xref="UniProtKB/Swiss-Prot:A1J
		HR8"
		/translation="MKKGALLNSDISAVISRLGH
		TDQIVIGDAGLPIPATTTTRIDLAL
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		QLHETLLAQLSQLEQHQQGNQIALH
		YISHEAFKEQTKQSRVIRSGECSPFANIILCSG
		VTF"
gene	9033..10535	/gene="rbsA"
		/locus-tag="YE0009"
CDS	9033..10535	/gene="rbsA"
		/locus-tag="YE0009"
		/inference="similar to
		sequence:INSDC:AL627280"
		/inference="similar to
		sequence:UniProtKB:P04983"
		/note="Similar to Escherichia coli
		ribose transport ATP-binding
		protein RbsA SWALL:RBSA-ECOLI
		(SWALL:P04983) (501 aa) fasta
		scores: E(): 2.7e-148, 85.83 38d
		in 494 aa,and to Salmonella typhi
		high affinity ribose transport
		protein STY896 SWALL:Q8Z2R4
		(EMBL:AL627280) (501 aa) fasta
		scores: E(): 1.1e-147, 85.62 38d
		in 494 aa"
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misc-feature	9120..9683	/gene="rbsA" /locus-tag="YE0009" /inference="protein" motif:PFAM:PF00005" /note="Pfam match to entry PF00005 ABC-tran, ABC transporter, score 173.1, E-value 3e-49"
misc-feature	9141..9164	/gene="rbsA" /locus-tag="YE0009" /inference="protein" motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-feature	9864..10445	/gene="rbsA" /locus-tag="YE0009" /inference="protein" motif:PFAM:PF00005" /note="Pfam match to entry PF00005 ABC-tran, ABC transporter, score 134.4, E-value 1.3e-37"
misc-feature	10218..10262	/gene="rbsA" /locus-tag="YE0009" /inference="protein" motif:Prosite:PS00211" /note="PS00211 ABC transporters family signature."
gene	10623..11588	/gene="rbsC" /locus-tag="YE0010"
CDS	10623..11588	/gene="rbsC" /locus-tag="YE0010" /codon-start=1 /transl-table=11 /product="putative sugar transport system, permease protein" /protein-id="CAL10155.1" /db-xref="GI:122087374" /db-xref="GOA:A1JHS2" /db-xref="InterPro:IPR001851" /db-xref="UniProtKB/TrEMBL:A1JHS2" /translation="MSSQTINTKRWFSKEWLLEQ



		KSLIALLVLIAVVSSLSPNFFTLN NMFNILQQTSVNAIMAVGMTLVILTSGIDLSVGS LLALTGAVAASIVGLEVNALVAVG AALALGAFVGGITGVIVAKGKVQAFIATLVMMLL LRGVTMVYTNGSPINTGFTDVADT FGWFGIGRPLGIPTPIWLMAIVFIAAWYMLHHTR LGRIYIALGGNESATRLSGISVDK VKIIVYSLCGLLAALAGIIEVARLSSAQPTAGTG YELDAIAAVVLGGTSLAGGKGQIV GTLIGALILGFLNNGLNLLGVSSYYQMIVKAVVI LLAVLVDNKKQ"
sig-peptide	10623..10748	/gene="rbsC" /locus-tag="YE0010" /note="Signal peptide predicted for YE0010 by SignalP 2.0 HMM (Signal peptide probability 0.969) with cleavage site probability 0.169 between residues 42 and 43"
misc-feature	join(10686..10754, 10815..10883, 10911..10979, 10998..11066, 11124..11192, 11283..11351, 11445..11513)	/gene="rbsC"  /locus-tag="YE0010" /inference="protein motif:TMHMM:2.0" /note="7 probable transmembrane helices predicted for YE0010 by TMHMM2.0 at aa 22-44, 65-87, 97-119, 126-148, 168-190, 221-243 and 275-297"
misc-feature	10746..11582	/gene="rbsC" /locus-tag="YE0010" /inference="protein motif:PFAM:PF02653" /note="Pfam match to entry PF02653 BPD-transp-2, Branched-chain amino acid transport system / permease component, score 3.4, E-value 7.7e-07"
gene	11760..12647	/gene="rbsB" /locus-tag="YE0011" /note="synonyms: prlB, rbsP"
CDS	11760..12647	/gene="rbsB" /locus-tag="YE0011" /inference="similar to sequence:UniProtKB:P02925" /inference="similar to sequence:UniProtKB:P02926" /note="Similar to Escherichia coli D-ribose-binding periplasmic protein precursor RbsB or RbsP or PrlB SWALL:RBSB-ECOLI (SWALL:P02925) (296 aa) fasta scores: E(): 1.7e-84, 84.74 38d in 295 aa, and to Salmonella typhimurium, and Salmonella typhi D-ribose-binding periplasmic protein precursor RbsB or RbsP or STM3884 or STY3894

		SWALL:RBSB-SALTY (SWALL:P02926)
		(296 aa) fasta scores: E():
		5.6e-84, 84.06 38d in 295 aa"
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		protein precursor"
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		/db-xref="InterPro:IPR001761"
		/db-xref="UniProtKB/TrEMBL:A1JHS3"
		/translation="MKMKKLATLISVVALSATVS
		ANALAKDTIALVVSTLNNPFFVSM
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		TVRGTKLLLINPTDSDAVGNAVKM
		ANQANIPVITLDRLANAGTVVSHVASDNRFGGKM
		AGDYIAKKVGSDAKVIQLEGIAGA
		SAARERGEFGFKQSMEKNKFQLLASQPADFDRTKG
		LNVMQNLLTAHPDVQAVFAQNDEM
		ALGALRALQTAGKTDVLVVGFDGTDGDIKAVESG
		KMGATIAQRPDQIGVIGVQTADKV
		LKGEKVQAVIPVDLKLVTK"
sig-peptide	11760..11834	/gene="rbsB"
		/locus-tag="YE0011"
		/note="Signal peptide predicted
		for YE0011 by SignalP 2.0 HMM
		(Signal peptide probability 1.000)
		with cleavage site probability
		0.933 between residues 25 and 26"
misc-feature	11835..12641	/gene="rbsB"
		/locus-tag="YE0011"
		/inference="protein
		motif:PFAM:PF00532"
		/note="Pfam match to entry PF00532
		Peripla-BP-like,Periplasmic
		binding proteins and sugar binding
		domain of the LacI family, score
		63.4, E-value 3.3e-16"
misc-feature	12432..12455	/gene="rbsB"
		/locus-tag="YE0011"
		/inference="protein
		motif:Prosite:PS00017"
		/note="PS00017 ATP/GTP-binding
		site motif A (P-loop)."
gene	12811..13737	/gene="rbsK"
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CDS	12811..13737	/gene="rbsK"
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		NQAVAAGRSGANIAFIACVGEDDIGDRVRLQLAS DNIDTAPIEAVAGTTTGVALIFVN GEGENVIGIHAGANSAVTPEYLGRYQQQVIDADA LLMQLESPLGTVIAAAKLAKQHQT QVILNPAPARELPDELLSLVDMITPNETEAERLT GIHIEQDDDAAKAAQILHDKGIAT VIITLGSRGVWLSEQQGKLVAGFKVNAVDTIAA GDTFNGALLTALLEGQAMGSAVR AHAAAAIAVTRPGAQPSIPWRAEIDSFLQDRV"
misc-feature	12817..13701	/gene="rbsK" /locus-tag="YE0012" /inference="protein motif:PFAM:PF00294" /note="Pfam match to entry PF00294 pfkB, pfkB family carbohydrate kinase, score 298.8, E-value 4.4e-87"
misc-feature	12928..13002	/gene="rbsK" /locus-tag="YE0012" /inference="protein motif:Prosites:PS00583" /note="PS00583 pfkB family of carbohydrate kinases signature 1."
misc-feature	13552..13593	/gene="rbsK" /locus-tag="YE0012" /inference="protein motif:Prosites:PS00584" /note="PS00584 pfkB family of carbohydrate kinases signature 2."
gene	13740..14741	/gene="rbsR" /locus-tag="YE0012A"
CDS	13740..14741	/gene="rbsR" /locus-tag="YE0012A" /inference="similar to sequence:INSDC:AE008881" /inference="similar to sequence:UniProtKB:P25551" /note="Similar to Escherichia coli, and Escherichia coli O157:H7 ribose operon repressor RbsR or b3753 or z5254 or ecs4695 SWALL:RBSR-ECOLI (SWALL:P25551) (329 aa) fasta scores: E(): 7.1e-94, 73.17 38d in 328 aa and to Salmonella typhimurium transcriptional repressor for rbs operon RbsR or stm3886 SWALL:Q8ZKV7 (EMBL:AE008881) (332 aa) fasta scores: E(): 5.3e-95, 74.09 38d in 332 aa" /codon-start=1 /transl-table=11 /product="ribose operon repressor" /protein-id="CAL10158.1" /db-xref="GI:122087377" /db-xref="GOA:A1JHS5" /db-xref="InterPro:IPR000843" /db-xref="InterPro:IPR001761" /db-xref="UniProtKB/TrEMBL:A1JHS5" /translation="MATMKDVARLAGVSTSTVSH VINKNRFVSDPIRDKVLAAIKQLN YAPSALARSLKLNETRTIGMLVTASSNPFYAEVV"

RGVERSCYERGYSLILCNTEGDID  
RMSRSIETLMQKRVDGLLLMCTESHRPSQDILRC

<-----User Break----->

LCEKVLGYRIFGDENDKMNLNVKQAGGSVLVVSQ  
FTLVADTQKGMRPFSFSGASPAEA

=> d l14 4 ti

L14 NOT FOUND

The L-number entered has not been defined in this session, or it has been deleted. To see the L-numbers currently defined in this session, enter DISPLAY HISTORY at an arrow prompt (=>).

=> d l13 4 ti

L13 ANSWER 4 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Annotation and evolutionary relationships of a small regulatory RNA gene micF and its target ompF in Yersinia species  
TITLE (TI): The complete genome sequence and comparative genome analysis of the high pathogenicity Yersinia enterocolitica strain 8081  
TITLE (TI): Direct Submission

=> d l13 5 ti

L13 ANSWER 5 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): The genome of Rhizobium leguminosarum has recognizable core and accessory components  
TITLE (TI): Direct Submission

=> d l13 6-14 ti

L13 ANSWER 6 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Whole genome sequence of Staphylococcus saprophyticus reveals the pathogenesis of uncomplicated urinary tract infection  
TITLE (TI): Direct Submission

L13 ANSWER 7 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): The Chlamydomophila abortus genome sequence reveals an array of variable proteins that contribute to interspecies variation  
TITLE (TI): Direct Submission

L13 ANSWER 8 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Extensive DNA inversions in the B. fragilis genome control variable gene expression  
TITLE (TI): Direct Submission

L13 ANSWER 9 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Complete genome sequence of Clostridium perfringens, an anaerobic flesh-eater  
TITLE (TI): Direct Submission

L13 ANSWER 10 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Genomic plasticity of the causative agent of  
melioidosis, Burkholderia pseudomallei  
TITLE (TI): Direct Submission

L13 ANSWER 11 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): The genome sequence of the enterobacterial  
phytopathogen Erwinia carotovora subsp. atroseptica  
SCRI1043 and functional genomic identification of novel  
virulence factors  
TITLE (TI): Direct Submission

L13 ANSWER 12 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Complete genomes of two clinical Staphylococcus aureus  
strains: evidence for the rapid evolution of virulence  
and drug resistance  
TITLE (TI): Direct Submission

L13 ANSWER 13 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Complete genomes of two clinical Staphylococcus aureus  
strains: evidence for the rapid evolution of virulence  
and drug resistance  
TITLE (TI): Direct Submission

L13 ANSWER 14 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Complete genome sequence of the model actinomycete  
Streptomyces coelicolor A3(2)  
TITLE (TI): Direct Submission

=> d hist

(FILE 'HOME' ENTERED AT 16:31:09 ON 16 DEC 2008)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:31:20 ON 16 DEC 2008  
SEA (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

-----  
1 FILE IFIPAT  
2 FILE USPATFULL  
1 FILE WPIDS  
1 FILE WPINDEX

L1 QUE (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O  
-----

FILE 'USPATFULL, IFIPAT' ENTERED AT 16:32:25 ON 16 DEC 2008

L2 3 S L1

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:33:15 ON 16 DEC 2008  
SEA ENTEROCOCCUS DURANS STRAIN 141-1

L3 QUE ENTEROCOCCUS DURANS STRAIN 141-1  
-----

```

                SEA ENTEROCOCCUS DURANS STRAIN 152
                -----
L4              QUE ENTEROCOCCUS DURANS STRAIN 152
                -----
                SEA ENTEROCOCCUS DRANS 141-1
                -----
L5              QUE ENTEROCOCCUS DRANS 141-1
                -----
                SEA ENTEROCOCCUS DURANS 141-1
                -----
L6              2   FILE USPATFULL
                QUE ENTEROCOCCUS DURANS 141-1
                -----

FILE 'USPATFULL' ENTERED AT 16:36:57 ON 16 DEC 2008
L7              2 S L6

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:37:29 ON 16 DEC 2008
                SEA ENTEROCOCCUS DURANS 152
                -----
                1   FILE AGRICOLA
                1   FILE BIOENG
                1   FILE BIOSIS
                1   FILE CABA
                2   FILE CAPLUS
                1   FILE FROSTI
                1   FILE FSTA
                1   FILE HEALSAFE
                1   FILE LIFESCI
                1   FILE MEDLINE
                1   FILE PASCAL
                1   FILE SCISEARCH
                2   FILE USPATFULL
L8              QUE ENTEROCOCCUS DURANS 152
                -----

FILE 'AGRICOLA, BIOENG, BIOSIS, CABA, CAPLUS, FROSTI, FSTA, HEALSAFE,
LIFESCI, MEDLINE, PASCAL, SCISEARCH, USPATFULL' ENTERED AT 16:38:26 ON 16
DEC 2008
L9              15 S L8
L10             3 DUP REM L9 (12 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:40:04 ON 16 DEC 2008
                SEA LACTOCOCCUS LACTIS C-1-92
                -----
                1   FILE CAPLUS
                11  FILE GENBANK
                1   FILE PROMT
                2   FILE USPATFULL
L11             QUE LACTOCOCCUS LACTIS C-1-92
                -----

FILE 'CAPLUS, GENBANK, PROMT, USPATFULL' ENTERED AT 16:41:04 ON 16 DEC
2008
L12             15 S L11
L13             14 DUP REM L12 (1 DUPLICATE REMOVED)

```

```
=> index bioscience
FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED
COST IN U.S. DOLLARS
FULL ESTIMATED COST
```

	SINCE FILE ENTRY	TOTAL SESSION
	110.65	153.92

```
INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:47:33 ON 16 DEC 2008
```

69 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view  
search error messages that display as 0\* with SET DETAIL OFF.

```
=> s Lactococcus lactis C-1-152
31 FILES SEARCHED...
7 FILE GENBANK
60 FILES SEARCHED...
2 FILE USPATFULL
1 FILE WPIDS
1 FILE WPINDEX
```

4 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L14 QUE LACTOCOCCUS LACTIS C-1-152

```
=> file genbank uspatfull
COST IN U.S. DOLLARS
FULL ESTIMATED COST
```

	SINCE FILE ENTRY	TOTAL SESSION
	2.60	156.52

FILE 'GENBANK' ENTERED AT 16:49:45 ON 16 DEC 2008

FILE 'USPATFULL' ENTERED AT 16:49:45 ON 16 DEC 2008  
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

```
=> s l14
L15 9 L14
```

```
=> rem dup l15
DUP IS NOT VALID HERE
The DELETE command is used to remove various items stored by the
system.
```

To delete a saved query, saved answer set, saved L-number list, SDI request, batch request, mailing list, or user-defined cluster, format, or search field, enter the name. The name may include ? for left, right, or simultaneous left and right truncation.

Examples:

DELETE BIO?/Q	- delete query names starting with BIO
DELETE ?DRUG/A	- delete answer set names ending with DRUG
DELETE ?ELEC?/L	- delete L-number lists containing ELEC
DELETE ANTICOAG/S	- delete SDI request
DELETE ENZYME/B	- delete batch request
DELETE .MYCLUSTER	- delete user-defined cluster
DELETE .MYFORMAT	- delete user-defined display format
DELETE .MYFIELD	- delete user-defined search field

DELETE NAMELIST MYLIST - delete mailing list

To delete an ordered document or an offline print, enter its number.

Examples:

```
DELETE P123001C      - delete print request
DELETE D134002C      - delete document order request
```

To delete an individual L-number or range of L-numbers, enter the L-number or L-number range. You may also enter DELETE LAST followed by a number, n, to delete the last n L-numbers. RENUMBER or NORENUMBER may also be explicitly specified to override the value of SET RENUMBER.

Examples:

```
DELETE L21           - delete a single L-number
DELETE L3-L6         - delete a range of L-numbers
DELETE LAST 4        - delete the last 4 L-numbers
DELETE L33-          - delete L33 and any higher L-number
DELETE -L55          - delete L55 and any lower L-number
DELETE L2-L6 RENUMBER - delete a range of L-numbers and
                      renumber remaining L-numbers
DELETE RENUMBER      - renumber L-numbers after deletion of
                      intermediate L-numbers
```

Entire sets of saved items, SDI requests, batch requests, user-defined items, or E-numbers can be deleted.

Examples:

```
DELETE SAVED/Q - delete all saved queries
DELETE SAVED/A - delete all saved answer sets
DELETE SAVED/L - delete all saved L-number lists
DELETE SAVED   - delete all saved queries, answer sets,
                  and L-number lists
DELETE SAVED/S - delete all SDI requests
DELETE SAVED/B - delete all batch requests
DELETE CLUSTER - delete all user-defined clusters
DELETE FORMAT  - delete all user-defined display formats
DELETE FIELD   - delete all user-defined search fields
DELETE SELECT  - delete all E-numbers
DELETE HISTORY - delete all L-numbers and restart the
                  session at L1
```

To delete an entire multifile SDI request, enter DELETE and the name of the request. To delete a component from the multifile SDI, enter DELETE and the name of the component.

```
=> dup rem l15
DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L15
L16          9 DUP REM L15 (0 DUPLICATES REMOVED)
```

```
=> d l16 1 ti
```

```
L16  ANSWER 1 OF 9  USPATFULL on STN
TI    Composition and method for inhibition of microorganisms
```



=> d 116 1 bib

L16 ANSWER 1 OF 9 USPATFULL on STN  
AN 2006:86130 USPATFULL  
TI Composition and method for inhibition of microorganisms  
IN Doyle, Michael P, Peachtree City, GA, UNITED STATES  
Zhao, Tong, Peachtree City, GA, UNITED STATES  
PI US 20060073129 A1 20060406  
AI US 2003-535357 A1 20031124 (10)  
WO 2003-US37526 20031124  
20050518 PCT 371 date  
PRAI US 2002-428863P 20021125 (60)  
DT Utility  
FS APPLICATION  
LREP Barnes & Thornburg, 11 South Meridian Street, Indianapolis, IN, 46204, US  
CLMN Number of Claims: 35  
ECL Exemplary Claim: 1  
DRWN 1 Drawing Page(s)  
LN.CNT 1238  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 116 2 bib

L16 ANSWER 2 OF 9 USPATFULL on STN  
AN 2006:79924 USPATFULL  
TI Foaming composition of competitive exclusion microbes and method of  
using same  
IN Podtburg, Teresa C., Waconia, MN, UNITED STATES  
Schmidt, Bruce, Apple Valley, MN, UNITED STATES  
Cords, Bruce, Inver Grove Heights, MN, UNITED STATES  
Grab, Lawrence A., Dusseldorf, GERMANY, FEDERAL REPUBLIC OF  
Halsrud, David A., Minneapolis, MN, UNITED STATES  
PI US 20060067915 A1 20060330  
AI US 2005-233922 A1 20050922 (11)  
PRAI US 2004-612882P 20040924 (60)  
DT Utility  
FS APPLICATION  
LREP MERCHANT & GOULD PC, P.O. BOX 2903, MINNEAPOLIS, MN, 55402-0903, US  
CLMN Number of Claims: 23  
ECL Exemplary Claim: 1  
DRWN 1 Drawing Page(s)  
LN.CNT 1878  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 116 3 bib

'BIB' IS NOT A VALID FORMAT

In a multifile environment, a format can only be used if it is valid  
in at least one of the files. Refer to file specific help messages  
or the STNGUIDE file for information on formats available in  
individual files.

REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):d 116 3 ti

'D' IS NOT A VALID FORMAT

In a multifile environment, a format can only be used if it is valid  
in at least one of the files. Refer to file specific help messages  
or the STNGUIDE file for information on formats available in  
individual files.

REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):ti

L16 ANSWER 3 OF 9 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): The complete genome, comparative and functional  
analysis of *Stenotrophomonas maltophilia* reveals an  
organism heavily shielded by drug resistance  
determinants  
TITLE (TI): Direct Submission

=> d l16 4-9 ti

L16 ANSWER 4 OF 9 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Annotation and evolutionary relationships of a small  
regulatory RNA gene *micF* and its target *ompF* in  
*Yersinia* species  
TITLE (TI): The complete genome sequence and comparative genome  
analysis of the high pathogenicity *Yersinia*  
*enterocolitica* strain 8081  
TITLE (TI): Direct Submission

L16 ANSWER 5 OF 9 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Complete DNA sequence of a serogroup A strain of  
*Neisseria meningitidis* Z2491  
TITLE (TI): Direct Submission

L16 ANSWER 6 OF 9 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): The genome of *Rhizobium leguminosarum* has recognizable  
core and accessory components  
TITLE (TI): Direct Submission

L16 ANSWER 7 OF 9 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Extensive DNA inversions in the *B. fragilis* genome  
control variable gene expression  
TITLE (TI): Direct Submission

L16 ANSWER 8 OF 9 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Genome sequence of *Yersinia pestis*, the causative agent  
of plague  
TITLE (TI): Annotation and evolutionary relationships of a small  
regulatory RNA gene *micF* and its target *ompF* in  
*Yersinia* species  
TITLE (TI): Direct Submission

L16 ANSWER 9 OF 9 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Complete genomes of two clinical *Staphylococcus aureus*  
strains: evidence for the rapid evolution of virulence  
and drug resistance  
TITLE (TI): Direct Submission

=> d hist

(FILE 'HOME' ENTERED AT 16:31:09 ON 16 DEC 2008)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,

DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:31:20 ON 16 DEC 2008  
SEA (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

-----  
1 FILE IFIPAT  
2 FILE USPATFULL  
1 FILE WPIDS  
1 FILE WPINDEX

L1 QUE (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

-----

FILE 'USPATFULL, IFIPAT' ENTERED AT 16:32:25 ON 16 DEC 2008

L2 3 S L1

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:33:15 ON 16 DEC 2008  
SEA ENTEROCOCCUS DURANS STRAIN 141-1

-----  
L3 QUE ENTEROCOCCUS DURANS STRAIN 141-1

-----

SEA ENTEROCOCCUS DURANS STRAIN 152

-----

L4 QUE ENTEROCOCCUS DURANS STRAIN 152

-----

SEA ENTEROCOCCUS DRANS 141-1

-----

L5 QUE ENTEROCOCCUS DRANS 141-1

-----

SEA ENTEROCOCCUS DURANS 141-1

-----

2 FILE USPATFULL

L6 QUE ENTEROCOCCUS DURANS 141-1

-----

FILE 'USPATFULL' ENTERED AT 16:36:57 ON 16 DEC 2008

L7 2 S L6

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:37:29 ON 16 DEC 2008  
SEA ENTEROCOCCUS DURANS 152

-----  
1 FILE AGRICOLA  
1 FILE BIOENG  
1 FILE BIOSIS  
1 FILE CABA  
2 FILE CAPLUS  
1 FILE FROSTI  
1 FILE FSTA  
1 FILE HEALSAFE  
1 FILE LIFESCI  
1 FILE MEDLINE  
1 FILE PASCAL  
1 FILE SCISEARCH  
2 FILE USPATFULL

L8 QUE ENTEROCOCCUS DURANS 152

-----

FILE 'AGRICOLA, BIOENG, BIOSIS, CABA, CAPLUS, FROSTI, FSTA, HEALSAFE,  
LIFESCI, MEDLINE, PASCAL, SCISEARCH, USPATFULL' ENTERED AT 16:38:26 ON 16

DEC 2008

L9 15 S L8  
L10 3 DUP REM L9 (12 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:40:04 ON 16 DEC 2008  
SEA LACTOCOCCUS LACTIS C-1-92

-----  
1 FILE CAPLUS  
11 FILE GENBANK  
1 FILE PROMT  
2 FILE USPATFULL

L11 QUE LACTOCOCCUS LACTIS C-1-92  
-----

FILE 'CAPLUS, GENBANK, PROMT, USPATFULL' ENTERED AT 16:41:04 ON 16 DEC 2008

L12 15 S L11  
L13 14 DUP REM L12 (1 DUPLICATE REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:47:33 ON 16 DEC 2008  
SEA LACTOCOCCUS LACTIS C-1-152

-----  
7 FILE GENBANK  
2 FILE USPATFULL  
1 FILE WPIDS  
1 FILE WPINDEX

L14 QUE LACTOCOCCUS LACTIS C-1-152  
-----

FILE 'GENBANK, USPATFULL' ENTERED AT 16:49:45 ON 16 DEC 2008

L15 9 S L14  
L16 9 DUP REM L15 (0 DUPLICATES REMOVED)

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
30.05	186.57

FULL ESTIMATED COST

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:55:03 ON 16 DEC 2008

69 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0\* with SET DETAIL OFF.

=> s food(p)process? and inhibit? (p)pathogen? and surface

0\* FILE ADISNEWS  
11 FILE AGRICOLA  
2\* FILE ANTE  
1\* FILE AQUALINE  
4 FILE AQUASCI  
11\* FILE BIOENG

32 FILE BIOSIS  
11\* FILE BIOTECHABS  
11\* FILE BIOTECHDS  
12\* FILE BIOTECHNO  
13 FILE CABA  
15 FILE CAPLUS  
0\* FILE CEABA-VTB

16 FILES SEARCHED...

0\* FILE CIN  
1 FILE CROPU  
6 FILE DISSABS  
12 FILE EMBASE  
16\* FILE ESBIODBASE

30 FILES SEARCHED...

0\* FILE FOMAD  
0\* FILE FOREGE  
20\* FILE FROSTI  
45\* FILE FSTA  
1 FILE GENBANK  
1 FILE HEALSAFE  
39 FILE IFIPAT  
0\* FILE KOSMET  
13 FILE LIFESCI  
12 FILE MEDLINE  
0\* FILE NTIS  
1\* FILE NUTRACEUT  
18\* FILE PASCAL

47 FILES SEARCHED...

1\* FILE PHARMAML  
24 FILE PROMT  
14 FILE SCISEARCH  
16 FILE TOXCENTER  
2042 FILE USPATFULL  
5 FILE USPATOLD  
620 FILE USPAT2

64 FILES SEARCHED...

1\* FILE WATER  
32 FILE WPIDS  
1 FILE WPIFV  
32 FILE WPINDEX

35 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L17 QUE FOOD(P) PROCESS? AND INHIBIT? (P) PATHOGEN? AND SURFACE

=> s L17 and (Enterococcus durans or Lactococcus lactis)

0\* FILE ADISNEWS  
0\* FILE ANTE  
0\* FILE AQUALINE  
0\* FILE BIOENG  
0\* FILE BIOTECHABS  
0\* FILE BIOTECHDS  
0\* FILE BIOTECHNO  
1 FILE CAPLUS  
0\* FILE CEABA-VTB  
0\* FILE CIN

22 FILES SEARCHED...

1 FILE DISSABS  
0\* FILE ESBIODBASE  
0\* FILE FOMAD  
0\* FILE FOREGE  
0\* FILE FROSTI

```

0* FILE FSTA
35 FILES SEARCHED...
0* FILE KOSMET
0* FILE NTIS
0* FILE NUTRACEUT
0* FILE PASCAL
47 FILES SEARCHED...
0* FILE PHARMAML
92 FILE USPATFULL
15 FILE USPAT2
0* FILE WATER
68 FILES SEARCHED...

```

4 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L18 QUE L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)

```

=> \file caplus dissabs uspatfull
\FILE IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

```

```

=> file caplus dissabs uspatfull
COST IN U.S. DOLLARS          SINCE FILE      TOTAL
                               ENTRY      SESSION
FULL ESTIMATED COST          5.85      192.42

```

FILE 'CAPLUS' ENTERED AT 17:00:10 ON 16 DEC 2008  
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 PLEASE SEE "HELP USAGETERMS" FOR DETAILS.  
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 CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

```

=> file baplus dissabs uspatfull uspat2
'BAPLUS' IS NOT A VALID FILE NAME
Enter "HELP FILE NAMES" at an arrow prompt (=>) for a list of files
that are available. If you have requested multiple files, you can
specify a corrected file name or you can enter "IGNORE" to continue
accessing the remaining file names entered.
ENTER A FILE NAME OR (IGNORE):.

```

```

COST IN U.S. DOLLARS          SINCE FILE      TOTAL
                               ENTRY      SESSION
FULL ESTIMATED COST          2.40      194.82

```

FILE 'DISSABS' ENTERED AT 17:00:27 ON 16 DEC 2008  
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FILE 'USPATFULL' ENTERED AT 17:00:27 ON 16 DEC 2008  
 CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'USPAT2' ENTERED AT 17:00:27 ON 16 DEC 2008  
 CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

```

=> file caplus dissabs uspatfull uspat2
COST IN U.S. DOLLARS          SINCE FILE      TOTAL
                               ENTRY      SESSION

```

FULL ESTIMATED COST

3.42

198.24

FILE 'CAPLUS' ENTERED AT 17:00:43 ON 16 DEC 2008  
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PLEASE SEE "HELP USAGETERMS" FOR DETAILS.  
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FILE 'USPATFULL' ENTERED AT 17:00:43 ON 16 DEC 2008  
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'USPAT2' ENTERED AT 17:00:43 ON 16 DEC 2008  
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

=> d 118

L18 HAS NO ANSWERS

L17 QUE FOOD(P) PROCESS? AND INHIBIT? (P) PATHOGEN? AND SURF  
ACE

L18 QUE L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)

=> s 118

L19 109 L18

=> s 119 and treat?(p)surface

L20 46 L19 AND TREAT?(P) SURFACE

=> s 120 and inhibit(p)pathogen(p)?organis?

L21 3 L20 AND INHIBIT(P) PATHOGEN(P) ?ORGANIS?

=> d 121 1-3

L21 ANSWER 1 OF 3 USPATFULL on STN

AN 2006:303630 USPATFULL

TI Proteases, nucleic acids encoding them and methods for making and using  
them

IN Cayouette, Michelle, 3812 PARK BOULEVARD #505, SAN DIEGO, CA, UNITED  
STATES 92103

Hansen, Connie Jo, San Diego, CA, UNITED STATES

McClure, Amy, San Diego, CA, UNITED STATES

Sun, May, San Diego, CA, UNITED STATES

Gramatikova, Svetlana, San Diego, CA, UNITED STATES

Dycaico, Mark, San Diego, CA, UNITED STATES

Barton, Nelson R., San Diego, CA, UNITED STATES

Stege, Justin T., San Diego, CA, UNITED STATES

Aboushadi, Nahla M., Oceanside, CA, UNITED STATES

PA DIVERSA CORPORATION (U.S. corporation)

PI US 20060259995 A1 20061116

AI US 2003-530643 A1 20031010 (10)

WO 2003-US32819 20031010

20060407 PCT 371 date

PRAI US 2002-418467P 20021010 (60)

US 2003-471423P 20030516 (60)

DT Utility

FS APPLICATION

LN.CNT 7319

INCL INCLM: 800/018.000

INCLS: 435/069.100; 435/226.000; 435/320.100; 435/325.000; 435/006.000;  
536/023.200; 800/288.000

NCL NCLM: 800/018.000

NCLS: 435/006.000; 435/069.100; 435/226.000; 435/320.100; 435/325.000;  
536/023.200; 800/288.000

IC IPCI A01K0067-027 [I,A]; C12Q0001-68 [I,A]; C07H0021-04 [I,A];  
C07H0021-00 [I,C\*]; C12P0021-06 [I,A]; C12N0009-64 [I,A];  
A01H0001-00 [I,A]

IPCR A01K0067-027 [I,C]; A01K0067-027 [I,A]; A01H0001-00 [I,C];  
A01H0001-00 [I,A]; C07H0021-00 [I,C]; C07H0021-04 [I,A];  
C12N0009-64 [I,C]; C12N0009-64 [I,A]; C12P0021-06 [I,C];  
C12P0021-06 [I,A]; C12Q0001-68 [I,C]; C12Q0001-68 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L21 ANSWER 2 OF 3 USPATFULL on STN

AN 2004:12970 USPATFULL

TI Polynucleotides, materials incorporating them, and methods for using  
them

IN Glenn, Matthew, Whenuapai, NEW ZEALAND  
Havukkala, Ilkka J., Remuera, NEW ZEALAND  
Lubbers, Mark, Palmerston North, NEW ZEALAND  
Dekker, James, Palmerston North, NEW ZEALAND

PA GENESIS RESEARCH AND DEVELOPMENT CORP. LTD., Parnell, NEW ZEALAND  
(non-U.S. corporation)

PI US 20040009490 A1 20040115  
US 7125698 B2 20061024

AI US 2002-264213 A1 20021003 (10)

RLI Continuation-in-part of Ser. No. US 2001-971536, filed on 2 Oct 2001,  
PENDING Continuation-in-part of Ser. No. US 2000-634238, filed on 8 Aug  
2000, GRANTED, Pat. No. US 6544772

PRAI US 1999-147853P 19990809 (60)  
US 1999-147852P 19990809 (60)  
US 1999-152032P 19990901 (60)  
US 1999-152031P 19990901 (60)

DT Utility

FS APPLICATION

LN.CNT 5375

INCL INCLM: 435/006.000  
INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.200

NCL NCLM: 435/193.000; 435/006.000  
NCLS: 426/534.000; 435/183.000; 435/194.000; 530/350.000; 435/069.100;  
435/252.300; 435/320.100; 536/023.200

IC [7]  
ICM C12Q001-68  
ICS C07H021-04; C12P021-02; C12N001-21; C12N015-74; C07K014-335  
IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*];  
C12P0021-02 [ICS,7]; C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7];  
C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C\*]

IPCI-2 C12N0009-10 [I,A]

IPCR C12N0009-10 [I,C]; C12N0009-10 [I,A]; A23C0019-00 [I,C\*];  
A23C0019-032 [I,A]; A61K0038-00 [N,C\*]; A61K0038-00 [N,A];  
C07K0014-195 [I,C\*]; C07K0014-335 [I,A]; C12N0001-21 [I,C\*];  
C12N0001-21 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L21 ANSWER 3 OF 3 USPAT2 on STN

AN 2004:12970 USPAT2

TI Polynucleotides, materials incorporating them, and methods for using  
them

IN Glenn, Matthew, 14 Waimarie Road, Whenuapai, Auckland, NEW ZEALAND  
Havukkala, Ilkka J., 19 Liley Place, Remuera, Auckland, NEW ZEALAND  
Lubbers, Mark, 397 Ruahine Street, Palmerston North, NEW ZEALAND  
Dekker, James, 135 Russel Street, Palmerston North, NEW ZEALAND

PI US 7125698 B2 20061024

AI US 2002-264213 20021003 (10)



RLI Continuation-in-part of Ser. No. US 2001-971536, filed on 2 Oct 2001,  
PENDING Continuation-in-part of Ser. No. US 2000-634238, filed on 8 Aug  
2000, Pat. No. US 6544772

PRAI US 1999-152032P 19990901 (60)  
US 1999-152031P 19990901 (60)  
US 1999-147853P 19990809 (60)  
US 1999-147852P 19990809 (60)

DT Utility  
FS GRANTED

LN.CNT 5273

INCL INCLM: 435/193.000  
INCLS: 435/183.000; 435/194.000; 426/534.000; 530/350.000

NCL NCLM: 435/193.000; 435/006.000  
NCLS: 426/534.000; 435/183.000; 435/194.000; 530/350.000; 435/069.100;  
435/252.300; 435/320.100; 536/023.200

IC IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*];  
C12P0021-02 [ICS,7]; C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7];  
C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C\*]  
IPCI-2 C12N0009-10 [I,A]  
IPCR C12N0009-10 [I,C]; C12N0009-10 [I,A]; A23C0019-00 [I,C\*];  
A23C0019-032 [I,A]; A61K0038-00 [N,C\*]; A61K0038-00 [N,A];  
C07K0014-195 [I,C\*]; C07K0014-335 [I,A]; C12N0001-21 [I,C\*];  
C12N0001-21 [I,A]

EXF 435/193; 435/183; 435/194; 426/534; 530/350  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d hist

(FILE 'HOME' ENTERED AT 16:31:09 ON 16 DEC 2008)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:31:20 ON 16 DEC 2008  
SEA (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

-----  
1 FILE IFIPAT  
2 FILE USPATFULL  
1 FILE WPIDS  
1 FILE WPINDEX

L1 QUE (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O  
-----

FILE 'USPATFULL, IFIPAT' ENTERED AT 16:32:25 ON 16 DEC 2008

L2 3 S L1

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:33:15 ON 16 DEC 2008  
SEA ENTEROCOCCUS DURANS STRAIN 141-1

L3 QUE ENTEROCOCCUS DURANS STRAIN 141-1  
-----

SEA ENTEROCOCCUS DURANS STRAIN 152  
-----

L4 QUE ENTEROCOCCUS DURANS STRAIN 152  
-----

SEA ENTEROCOCCUS DRANS 141-1  
-----

L5 QUE ENTEROCOCCUS DRANS 141-1

```

-----
      SEA ENTEROCOCCUS DURANS 141-1
-----
L6      2      FILE USPATFULL
      QUE ENTEROCOCCUS DURANS 141-1
-----

L7      FILE 'USPATFULL' ENTERED AT 16:36:57 ON 16 DEC 2008
      2 S L6

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:37:29 ON 16 DEC 2008
      SEA ENTEROCOCCUS DURANS 152
-----
      1      FILE AGRICOLA
      1      FILE BIOENG
      1      FILE BIOSIS
      1      FILE CABA
      2      FILE CAPLUS
      1      FILE FROSTI
      1      FILE FSTA
      1      FILE HEALSAFE
      1      FILE LIFESCI
      1      FILE MEDLINE
      1      FILE PASCAL
      1      FILE SCISEARCH
      2      FILE USPATFULL
L8      QUE ENTEROCOCCUS DURANS 152
-----

FILE 'AGRICOLA, BIOENG, BIOSIS, CABA, CAPLUS, FROSTI, FSTA, HEALSAFE,
LIFESCI, MEDLINE, PASCAL, SCISEARCH, USPATFULL' ENTERED AT 16:38:26 ON 16
DEC 2008
L9      15 S L8
L10     3 DUP REM L9 (12 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:40:04 ON 16 DEC 2008
      SEA LACTOCOCCUS LACTIS C-1-92
-----
      1      FILE CAPLUS
      11     FILE GENBANK
      1      FILE PROMT
      2      FILE USPATFULL
L11     QUE LACTOCOCCUS LACTIS C-1-92
-----

FILE 'CAPLUS, GENBANK, PROMT, USPATFULL' ENTERED AT 16:41:04 ON 16 DEC
2008
L12     15 S L11
L13     14 DUP REM L12 (1 DUPLICATE REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:47:33 ON 16 DEC 2008
      SEA LACTOCOCCUS LACTIS C-1-152
-----

```

```
7 FILE GENBANK
2 FILE USPATFULL
1 FILE WPIDS
1 FILE WPINDEX
L14 QUE LACTOCOCCUS LACTIS C-1-152
-----
```

```
FILE 'GENBANK, USPATFULL' ENTERED AT 16:49:45 ON 16 DEC 2008
L15 9 S L14
L16 9 DUP REM L15 (0 DUPLICATES REMOVED)
```

```
INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:55:03 ON 16 DEC 2008
SEA FOOD(P)PROCESS? AND INHIBIT? (P)PATHOGEN? AND SURFACE
-----
```

```
0* FILE ADISNEWS
11 FILE AGRICOLA
2* FILE ANTE
1* FILE AQUALINE
4 FILE AQUASCI
11* FILE BIOENG
32 FILE BIOSIS
11* FILE BIOTECHABS
11* FILE BIOTECHDS
12* FILE BIOTECHNO
13 FILE CABA
15 FILE CAPLUS
0* FILE CEABA-VTB
0* FILE CIN
1 FILE CROPU
6 FILE DISSABS
12 FILE EMBASE
16* FILE ESBIODBASE
0* FILE FOMAD
0* FILE FOREGE
20* FILE FROSTI
45* FILE FSTA
1 FILE GENBANK
1 FILE HEALSAFE
39 FILE IFIPAT
0* FILE KOSMET
13 FILE LIFESCI
12 FILE MEDLINE
0* FILE NTIS
1* FILE NUTRACEUT
18* FILE PASCAL
1* FILE PHARMAML
24 FILE PROMT
14 FILE SCISEARCH
16 FILE TOXCENTER
2042 FILE USPATFULL
5 FILE USPATOLD
620 FILE USPAT2
1* FILE WATER
32 FILE WPIDS
1 FILE WPIFV
32 FILE WPINDEX
L17 QUE FOOD(P) PROCESS? AND INHIBIT? (P) PATHOGEN? AND SURFACE
-----
SEA L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)
```

```

-----
0*  FILE ADISNEWS
0*  FILE ANTE
0*  FILE AQUALINE
0*  FILE BIOENG
0*  FILE BIOTECHABS
0*  FILE BIOTECHDS
0*  FILE BIOTECHNO
1   FILE CAPLUS
0*  FILE CEABA-VTB
0*  FILE CIN
1   FILE DISSABS
0*  FILE ESBIODBASE
0*  FILE FOMAD
0*  FILE FOREGE
0*  FILE FROSTI
0*  FILE FSTA
0*  FILE KOSMET
0*  FILE NTIS
0*  FILE NUTRACEUT
0*  FILE PASCAL
0*  FILE PHARMAML
92  FILE USPATFULL
15  FILE USPAT2
0*  FILE WATER
L18  QUE L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)
-----

```

FILE 'CAPLUS, DISSABS, USPATFULL' ENTERED AT 17:00:10 ON 16 DEC 2008

FILE 'DISSABS, USPATFULL, USPAT2' ENTERED AT 17:00:27 ON 16 DEC 2008

FILE 'CAPLUS, DISSABS, USPATFULL, USPAT2' ENTERED AT 17:00:43 ON 16 DEC 2008

```

L19      109 S L18
L20      46 S L19 AND TREAT?(P) SURFACE
L21      3 S L20 AND INHIBIT(P) PATHOGEN(P) ?ORGANIS?

```

=> s L21 and (Enterococcus durans)\  
MISSING OPERATOR DURANS)\  
The search profile that was entered contains terms or  
nested terms that are not separated by a logical operator.

```

=> s L21 and (Enterococcus durans or Lactococcus lactis)
L22      3 L21 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)

```

```

=> s l22 and inhibit?(p) first population of microorganism
L23      0 L22 AND INHIBIT?(P) FIRST POPULATION OF MICROORGANISM

```

```

=> s l22 and (C-1-152 or C-1-92 or 152 or 141-1)
L24      3 L22 AND (C-1-152 OR C-1-92 OR 152 OR 141-1)

```

=> d 124

```

L24  ANSWER 1 OF 3  USPATFULL on STN
AN   2006:303630  USPATFULL
TI   Proteases, nucleic acids encoding them and methods for making and using
      them
IN   Cayouette, Michelle, 3812 PARK BOULEVARD #505, SAN DIEGO, CA, UNITED
      STATES 92103
      Hansen, Connie Jo, San Diego, CA, UNITED STATES
      McClure, Amy, San Diego, CA, UNITED STATES

```

Sun, May, San Diego, CA, UNITED STATES  
Gramatikova, Svetlana, San Diego, CA, UNITED STATES  
Dycaico, Mark, San Diego, CA, UNITED STATES  
Barton, Nelson R., San Diego, CA, UNITED STATES  
Stege, Justin T., San Diego, CA, UNITED STATES  
Aboushadi, Nahla M., Oceanside, CA, UNITED STATES  
PA DIVERSA CORPORATION (U.S. corporation)  
PI US 20060259995 A1 20061116  
AI US 2003-530643 A1 20031010 (10)  
WO 2003-US32819 20031010  
20060407 PCT 371 date  
PRAI US 2002-418467P 20021010 (60)  
US 2003-471423P 20030516 (60)  
DT Utility  
FS APPLICATION  
LN.CNT 7319  
INCL INCLM: 800/018.000  
INCLS: 435/069.100; 435/226.000; 435/320.100; 435/325.000; 435/006.000;  
536/023.200; 800/288.000  
NCL NCLM: 800/018.000  
NCLS: 435/006.000; 435/069.100; 435/226.000; 435/320.100; 435/325.000;  
536/023.200; 800/288.000  
IC IPCI A01K0067-027 [I,A]; C12Q0001-68 [I,A]; C07H0021-04 [I,A];  
C07H0021-00 [I,C\*]; C12P0021-06 [I,A]; C12N0009-64 [I,A];  
A01H0001-00 [I,A]  
IPCR A01K0067-027 [I,C]; A01K0067-027 [I,A]; A01H0001-00 [I,C];  
A01H0001-00 [I,A]; C07H0021-00 [I,C]; C07H0021-04 [I,A];  
C12N0009-64 [I,C]; C12N0009-64 [I,A]; C12P0021-06 [I,C];  
C12P0021-06 [I,A]; C12Q0001-68 [I,C]; C12Q0001-68 [I,A]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 124 1 ti

L24 ANSWER 1 OF 3 USPATFULL on STN  
TI Proteases, nucleic acids encoding them and methods for making and using  
them

=> d 124 1 kwic

L24 ANSWER 1 OF 3 USPATFULL on STN  
AB . . . therapeutic, and industrial contexts. The polypeptides of the  
invention can be used as, e.g., an additive for a detergent, for  
processing foods and for chemical synthesis utilizing a reverse  
reaction. Additionally, the polypeptides of the invention can be used in  
food processing, brewing, bath additives, alcohol  
production, peptide synthesis, enantioselectivity, hide preparation in  
the leather industry, waste management and animal degradation, silver.  
SUMM . . . therapeutic, and industrial contexts. The polypeptides of the  
invention can be used as, e.g., an additive for a detergent, for  
processing foods and for chemical synthesis utilizing a reverse  
reaction. Additionally, the polypeptides of the invention can be used in  
food processing, brewing, bath additives, alcohol  
production, peptide synthesis, enantioselectivity, hide preparation in  
the leather industry, waste management and animal degradation, silver.  
SUMM . . .  
Enzymes are used within a wide range of applications in industry,  
research, and medicine. Through the use of enzymes, industrial  
processes can be carried out at reduced temperatures and  
pressures and with less dependence on the use of corrosive or toxic. .

. substances. The use of enzymes can thus reduce production costs, energy consumption, and pollution as compared to non-enzymatic products and processes. An important group of enzymes is the proteases. Proteases are carbonyl hydrolases which generally act to cleave peptide bonds of. . . The extracellular proteases are of commercial value and find multiple applications in various industrial sectors. Industrial applications of proteases include food processing, brewing, alcohol production, peptide synthesis, enantioselectivity, hide preparation in the leather industry, waste management and animal degradation, silver recovery in. . . milling. Additionally, proteases are important components of laundry detergents and other products. Within biological research, proteases are used in purification processes to degrade unwanted proteins. It is often desirable to employ proteases of low specificity or mixtures of more specific proteases. . . .

SUMM . . . in laundry detergents to aid in the removal of proteinaceous stains (e.g., Crabb, ACS Symposium Series 460:82-94, 1991). In the food processing industry, serine proteases are used to produce protein-rich concentrates from fish and livestock, and in the preparation of dairy products (Kida et al., Journal of Fermentation and Bioengineering 80:478-484, 1995; Haard and Simpson, in Martin, A. M., ed., Fisheries Processing: Biotechnological Applications, Chapman and Hall, London, 1994, 132-154; Bos et al., European Patent Office Publication 494 149 A1).

SUMM . . . 206 207-209 210  
211

C	231	232-233	234	235
D	160	161-163	164	165
E	195	196-198	199	200
F	224	225-228	229	230
G	152	153-157	158	
	159			
H	189	190-192	193	194
I	220	221	222	223
J	173	174-178	179	180
K	212	213-217	218	219
L	148. . .			

SUMM . . . acid of the invention, wherein the polypeptide has a protease activity. The protease can be a nonsurface-active protease or a surface-active protease. The protease can be formulated in a non-aqueous liquid composition, a cast solid, a granular form, a particulate form, . . .

DETD . . . defined amount of one or more polypeptides (including antibodies) or nucleic acids immobilized onto a defined area of a substrate surface, as discussed in further detail, below.

DETD . . . Cell. Probes 10:257-271) and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario); see also Berger (1987) Methods Enzymol. 152:307-316; Sambrook; Ausubel; U.S. Pat. Nos. 4,683,195 and 4,683,202; Sooknanan (1995) Biotechnology 13:563-564.

DETD Inhibition of protease expression can have a variety of industrial applications. For example, inhibition of protease expression can slow or prevent spoilage. Spoilage can occur when polypeptides, e.g., structural polypeptides, are enzymatically degraded. This. . . lead to the deterioration, or rot, of fruits and vegetables. In one aspect, use of compositions of the invention that inhibit the expression and/or activity of proteases, e.g., antibodies, antisense oligonucleotides, ribozymes and RNAi, are used to slow or prevent spoilage. . . to slow or prevent spoilage. These compositions also can be expressed by the plant (e.g., a transgenic plant) or another organism (e.g., a bacterium or other microorganism transformed with a protease gene of the

invention). The compositions of the invention for the inhibition of protease expression (e.g., antisense, iRNA, ribozymes, antibodies) can be used as pharmaceutical compositions, e.g., as anti-pathogen agents or in other therapies, e.g., anti-inflammatory or skin or digestive aid treatments. For example, proteases are attractive antimalarial targets. . . . especially in the processes of host erythrocyte rupture, invasion and hemoglobin degradation; see, e.g., Wu (2003) Genome Res. 13:601-616. Selective inhibition of the mosquito angiotensin-converting enzyme (ACE) (a dipeptidyl carboxypeptidase) involved in the activation/inactivation of a peptide regulating egg-laying activity can be an effective anti-mosquito method; see, e.g., Ekbote (2003) Comp. Biochem. Physiol. B. Biochem. Mol. Biol. 134:593-598. Inhibition of matrix metalloproteases (e.g., metalloproteinases) and collagenases, which can degrade extracellular matrices and promote cancer cell migration and metastases, can. . . .

DETD . . . include gram negative bacteria, such as Escherichia coli and Pseudomonas fluorescens; gram positive bacteria, such as Streptomyces diversa, Lactobacillus gasseri, Lactococcus lactis, Lactococcus cremoris, Bacillus subtilis. Exemplary host cells also include eukaryotic organisms, e.g., various yeast, such as Saccharomyces sp., including Saccharomyces. . . .

DETD . . . comprising a defined amount of one or more biological molecules, e.g., oligonucleotides, immobilized onto a defined area of a substrate surface for specific binding to a sample molecule, e.g., mRNA transcripts.

DETD . . . formulated as a hand or machine laundry detergent composition comprising a polypeptide of the invention. A laundry additive suitable for pre-treatment of stained fabrics can comprise a polypeptide of the invention. A fabric softener composition can comprise a protease of the. . . invention. Alternatively, a protease of the invention can be formulated as a detergent composition for use in general household hard surface cleaning operations. In alternative aspects, detergent additives and detergent compositions of the invention may comprise one or more other enzymes. . . .

DETD Treating Foods and Food Processing

DETD The proteases of the invention have numerous applications in food processing industry. For example, in one aspect, the proteases of the invention are used to improve the extraction of oil from. . . .

DETD Proteases of the present invention, in the modification of animal feed or a food, can process the food or feed either in vitro (by modifying components of the feed or food) or in vivo. Proteases can be added to animal feed or food compositions containing high amounts of arabinogalactans or galactans, e.g. feed or food containing plant material from soy bean, rape seed, lupin and the like. When added to the feed or food the protease significantly improves the in vivo break-down of plant cell wall material, whereby a better utilization of the plant. . . more digestible by the animal. Thus, proteases of the invention can contribute to the available energy of the feed or food. Also, by contributing to the degradation of galactan-comprising proteins, a protease of the invention can improve the digestibility and uptake of carbohydrate and non-carbohydrate feed or food constituents such as protein, fat and minerals.

DETD The proteases of the invention can be in paper or pulp treatment or paper deinking. For example, in one aspect, the invention provides a paper treatment process using proteases of the invention. In another aspect, paper components of recycled photocopied paper during chemical and enzymatic deinking. . . . proteases of the invention can be used in combination with cellulases, pectate lyases or other enzymes. The paper can be treated by the following three processes: 1) disintegration in the presence of

proteases of the invention, 2) disintegration with a deinking chemical and proteases of the invention, and/or 3) disintegration after soaking with proteases of the invention. The recycled paper treated with proteases can have a higher brightness due to removal of toner particles as compared to the paper treated with just cellulase. While the invention is not limited by any particular mechanism, the effect of proteases of the invention may be due to its behavior as surface-active agents in pulp suspension.

DETD . . . from the well bore; reducing the flow of production fluids from the formation below expected flow rates; formulating an enzyme treatment by blending together an aqueous fluid and a polypeptide of the invention; pumping the enzyme treatment to a desired location within the well bore; allowing the enzyme treatment to degrade the viscous, protein-containing, damaging fluid, whereby the fluid can be removed from the subterranean formation to the well surface; and wherein the enzyme treatment is effective to attack protein in cell walls.

CLM What is claimed is:

. . . polypeptide as set forth in claim 60, wherein the polypeptide has a protease activity, wherein optionally the protease is a non-surface-active protease or a surface-active protease, and optionally the protease is formulated in a non-aqueous liquid composition, a cast solid, a granular form, a particulate. . .

=> d hist

(FILE 'HOME' ENTERED AT 16:31:09 ON 16 DEC 2008)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:31:20 ON 16 DEC 2008  
SEA (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

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1 FILE IFIPAT  
2 FILE USPATFULL  
1 FILE WPIDS  
1 FILE WPINDEX

L1 QUE (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

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FILE 'USPATFULL, IFIPAT' ENTERED AT 16:32:25 ON 16 DEC 2008

L2 3 S L1

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:33:15 ON 16 DEC 2008  
SEA ENTEROCOCCUS DURANS STRAIN 141-1

L3 QUE ENTEROCOCCUS DURANS STRAIN 141-1

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SEA ENTEROCOCCUS DURANS STRAIN 152

L4 QUE ENTEROCOCCUS DURANS STRAIN 152

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SEA ENTEROCOCCUS DRANS 141-1

L5 QUE ENTEROCOCCUS DRANS 141-1

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SEA ENTEROCOCCUS DURANS 141-1



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L6      2  FILE USPATFULL
        QUE ENTEROCOCCUS DURANS 141-1
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FILE 'USPATFULL' ENTERED AT 16:36:57 ON 16 DEC 2008
L7      2 S L6

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:37:29 ON 16 DEC 2008
        SEA ENTEROCOCCUS DURANS 152
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        1  FILE AGRICOLA
        1  FILE BIOENG
        1  FILE BIOSIS
        1  FILE CABA
        2  FILE CAPLUS
        1  FILE FROSTI
        1  FILE FSTA
        1  FILE HEALSAFE
        1  FILE LIFESCI
        1  FILE MEDLINE
        1  FILE PASCAL
        1  FILE SCISEARCH
        2  FILE USPATFULL
L8      QUE ENTEROCOCCUS DURANS 152
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FILE 'AGRICOLA, BIOENG, BIOSIS, CABA, CAPLUS, FROSTI, FSTA, HEALSAFE,
LIFESCI, MEDLINE, PASCAL, SCISEARCH, USPATFULL' ENTERED AT 16:38:26 ON 16
DEC 2008
L9      15 S L8
L10     3 DUP REM L9 (12 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:40:04 ON 16 DEC 2008
        SEA LACTOCOCCUS LACTIS C-1-92
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        1  FILE CAPLUS
        11 FILE GENBANK
        1  FILE PROMT
        2  FILE USPATFULL
L11     QUE LACTOCOCCUS LACTIS C-1-92
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FILE 'CAPLUS, GENBANK, PROMT, USPATFULL' ENTERED AT 16:41:04 ON 16 DEC
2008
L12     15 S L11
L13     14 DUP REM L12 (1 DUPLICATE REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:47:33 ON 16 DEC 2008
        SEA LACTOCOCCUS LACTIS C-1-152
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        7  FILE GENBANK
        2  FILE USPATFULL

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1 FILE WPIDS  
1 FILE WPINDEX  
L14 QUE LACTOCOCCUS LACTIS C-1-152  
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FILE 'GENBANK, USPATFULL' ENTERED AT 16:49:45 ON 16 DEC 2008  
L15 9 S L14  
L16 9 DUP REM L15 (0 DUPLICATES REMOVED)

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AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:55:03 ON 16 DEC 2008  
SEA FOOD(P)PROCESS? AND INHIBIT? (P)PATHOGEN? AND SURFACE  
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0\* FILE ADISNEWS  
11 FILE AGRICOLA  
2\* FILE ANTE  
1\* FILE AQUALINE  
4 FILE AQUASCI  
11\* FILE BIOENG  
32 FILE BIOSIS  
11\* FILE BIOTECHABS  
11\* FILE BIOTECHDS  
12\* FILE BIOTECHNO  
13 FILE CABA  
15 FILE CAPLUS  
0\* FILE CEABA-VTB  
0\* FILE CIN  
1 FILE CROPU  
6 FILE DISSABS  
12 FILE EMBASE  
16\* FILE ESBIODBASE  
0\* FILE FOMAD  
0\* FILE FOREGE  
20\* FILE FROSTI  
45\* FILE FSTA  
1 FILE GENBANK  
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39 FILE IFIPAT  
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13 FILE LIFESCI  
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18\* FILE PASCAL  
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24 FILE PROMT  
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2042 FILE USPATFULL  
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620 FILE USPAT2  
1\* FILE WATER  
32 FILE WPIDS  
1 FILE WPIFV  
32 FILE WPINDEX  
L17 QUE FOOD(P) PROCESS? AND INHIBIT? (P) PATHOGEN? AND SURFACE  
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SEA L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)  
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0\* FILE ADISNEWS

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0* FILE ANTE
0* FILE AQUALINE
0* FILE BIOENG
0* FILE BIOTECHABS
0* FILE BIOTECHDS
0* FILE BIOTECHNO
1 FILE CAPLUS
0* FILE CEABA-VTB
0* FILE CIN
1 FILE DISSABS
0* FILE ESBIODBASE
0* FILE FOMAD
0* FILE FOREGE
0* FILE FROSTI
0* FILE FSTA
0* FILE KOSMET
0* FILE NTIS
0* FILE NUTRACEUT
0* FILE PASCAL
0* FILE PHARMAML
92 FILE USPATFULL
15 FILE USPAT2
0* FILE WATER

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L18 QUE L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)

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FILE 'CAPLUS, DISSABS, USPATFULL' ENTERED AT 17:00:10 ON 16 DEC 2008

FILE 'DISSABS, USPATFULL, USPAT2' ENTERED AT 17:00:27 ON 16 DEC 2008

FILE 'CAPLUS, DISSABS, USPATFULL, USPAT2' ENTERED AT 17:00:43 ON 16 DEC 2008

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L19      109 S L18
L20      46 S L19 AND TREAT?(P)SURFACE
L21      3 S L20 AND INHIBIT(P)PATHOGEN(P)?ORGANIS?
L22      3 S L21 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)
L23      0 S L22 AND INHIBIT?(P)FIRST POPULATION OF MICROORGANISM
L24      3 S L22 AND (C-1-152 OR C-1-92 OR 152 OR 141-1)

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=> s l24 and strain

L25 3 L24 AND STRAIN

=> d l25 1 kwic

L25 ANSWER 1 OF 3 USPATFULL on STN

AB . . . therapeutic, and industrial contexts. The polypeptides of the invention can be used as, e.g., an additive for a detergent, for processing foods and for chemical synthesis utilizing a reverse reaction. Additionally, the polypeptides of the invention can be used in food processing, brewing, bath additives, alcohol production, peptide synthesis, enantioselectivity, hide preparation in the leather industry, waste management and animal degradation, silver.

SUMM . . . therapeutic, and industrial contexts. The polypeptides of the invention can be used as, e.g., an additive for a detergent, for processing foods and for chemical synthesis utilizing a reverse reaction. Additionally, the polypeptides of the invention can be used in food processing, brewing, bath additives, alcohol production, peptide synthesis, enantioselectivity, hide preparation in the leather industry, waste management and animal degradation, silver.

SUMM . . . Enzymes are used within a wide range of applications in industry,

research, and medicine. Through the use of enzymes, industrial processes can be carried out at reduced temperatures and pressures and with less dependence on the use of corrosive or toxic. . substances. The use of enzymes can thus reduce production costs, energy consumption, and pollution as compared to non-enzymatic products and processes. An important group of enzymes is the proteases. Proteases are carbonyl hydrolases which generally act to cleave peptide bonds of. . . The extracellular proteases are of commercial value and find multiple applications in various industrial sectors. Industrial applications of proteases include food processing, brewing, alcohol production, peptide synthesis, enantioselectivity, hide preparation in the leather industry, waste management and animal degradation, silver recovery in. . . milling. Additionally, proteases are important components of laundry detergents and other products. Within biological research, proteases are used in purification processes to degrade unwanted proteins. It is often desirable to employ proteases of low specificity or mixtures of more specific proteases. . . .

SUMM . . . in laundry detergents to aid in the removal of proteinaceous stains (e.g., Crabb, ACS Symposium Series 460:82-94, 1991). In the food processing industry, serine proteases are used to produce protein-rich concentrates from fish and livestock, and in the preparation of dairy products (Kida et al., Journal of Fermentation and Bioengineering 80:478-484, 1995; Haard and Simpson, in Martin, A. M., ed., Fisheries Processing: Biotechnological Applications, Chapman and Hall, London, 1994, 132-154; Bos et al., European Patent Office Publication 494 149 A1).

SUMM . . . e.g., an archeal source, a bacterial source, a fungal source (e.g., filamentous ascomycetes, such as Cochliobolus heterostrophus, e.g., C. heterostrophus strain C4, having ATCC accession no. 48331), or an environmental source, e.g., a mixed environmental source, e.g., as set forth below.. . .

SUMM 187, 188Cochliobolus heterostrophus strain C4 (ATCC 48331)  
SUMM 210, 211 Cochliobolus heterostrophus strain C4 (ATCC 48331)  
SUMM 234, 235 Cochliobolus heterostrophus strain C4 (ATCC 48331)  
SUMM 164, 165 Cochliobolus heterostrophus strain C4 (ATCC 48331)  
SUMM 199, 200 Cochliobolus heterostrophus strain C4 (ATCC 48331)  
SUMM 229, 230 Cochliobolus heterostrophus strain C4 (ATCC 48331)  
SUMM 158, 159 Cochliobolus heterostrophus strain C4 (ATCC 48331)  
SUMM 193, 194 Cochliobolus heterostrophus strain C4 (ATCC 48331)  
SUMM 222, 223Cochliobolus heterostrophus strain C4 (ATCC 48331)  
SUMM 179, 180 Cochliobolus heterostrophus strain C4 (ATCC 48331)  
SUMM 218, 219Cochliobolus heterostrophus strain C4 (ATCC 48331)  
SUMM 150, 151 Cochliobolus heterostrophus strain C4 (ATCC 48331)  
SUMM 171, 172Cochliobolus heterostrophus strain C4 (ATCC 48331)  
SUMM 204, 205Cochliobolus heterostrophus strain C4 (ATCC 48331)  
SUMM 254, 255Cochliobolus heterostrophus strain C4 (ATCC 48331)  
SUMM 248, 249 Cochliobolus heterostrophus strain C4 (ATCC 48331)  
SUMM 241, 242 Cochliobolus heterostrophus strain C4 (ATCC 48331)

85, 86 Environmental  
11, 12 Environmental  
121, 122 Environmental  
117, 118 Environmental  
119, 120 Environmental  
83, 84 Environmental  
9, 10 Environmental  
93, 94. . .  
SUMM . . . 206 207-209 210  
211

C 231 232-233 234 235

D	160	161-163	164	165
E	195	196-198	199	200
F	224	225-228	229	230
G	152	153-157	158	
	159			
H	189	190-192	193	194
I	220	221	222	223
J	173	174-178	179	180
K	212	213-217	218	219
L	148.			
SUMM	. . . comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer. . . .			
SUMM	. . . comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer. . . .			
SUMM	. . . a newly engineered phenotype. In another aspect, the method can comprise culturing the selected cell, thereby generating a new cell strain comprising a newly engineered phenotype.			
SUMM	. . . acid of the invention, wherein the polypeptide has a protease activity. The protease can be a nonsurface-active protease or a surface-active protease. The protease can be formulated in a non-aqueous liquid composition, a cast solid, a granular form, a particulate form,. . . .			
DETD	. . . defined amount of one or more polypeptides (including antibodies) or nucleic acids immobilized onto a defined area of a substrate surface, as discussed in further detail, below.			
DETD	. . . as appropriate for activating promoters, selecting transformants or amplifying the genes of the invention. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter may be induced by appropriate means (e.g., temperature shift or chemical induction). . . .			
DETD	. . . Cell. Probes 10:257-271) and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario); see also Berger (1987) Methods Enzymol. 152:307-316; Sambrook; Ausubel; U.S. Pat. Nos. 4,683,195 and 4,683,202; Sooknanan (1995) Biotechnology 13:563-564.			
DETD	Inhibition of protease expression can have a variety of industrial applications. For example, inhibition of protease expression can slow or prevent spoilage. Spoilage can occur when polypeptides, e.g., structural polypeptides, are enzymatically degraded. This. . . lead to the deterioration, or rot, of fruits and vegetables. In one aspect, use of compositions of the invention that inhibit the expression and/or activity of proteases, e.g., antibodies, antisense oligonucleotides, ribozymes and RNAi, are used to slow or prevent spoilage.. . . to slow or prevent spoilage. These compositions also can be expressed by the plant (e.g., a transgenic plant) or another organism (e.g., a bacterium or other microorganism transformed with a protease gene of the invention). The compositions of the invention for the inhibition of protease expression (e.g., antisense, iRNA, ribozymes, antibodies)			

can be used as pharmaceutical compositions, e.g., as anti-pathogen agents or in other therapies, e.g., anti-inflammatory or skin or digestive aid treatments. For example, proteases are attractive antimalarial targets. . . especially in the processes of host erythrocyte rupture, invasion and hemoglobin degradation; see, e.g., Wu (2003) Genome Res. 13:601-616. Selective inhibition of the mosquito angiotensin-converting enzyme (ACE) (a dipeptidyl carboxypeptidase) involved in the activation/inactivation of a peptide regulating egg-laying activity can be an effective anti-mosquito method; see, e.g., Ekbote (2003) Comp. Biochem. Physiol. B. Biochem. Mol. Biol. 134:593-598. Inhibition of matrix metalloproteases (e.g., metalloproteinases) and collagenases, which can degrade extracellular matrices and promote cancer cell migration and metastases, can. . .

DETD . . . (SLR), recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer. . .

DETD . . . some aspects, random mutations in a sequence of interest are generated by propagating the sequence of interest in a bacterial strain, such as an E. coli strain, which carries mutations in one or more of the DNA repair pathways. Such "mutator" strains have a higher random mutation. . .

DETD . . . include gram negative bacteria, such as Escherichia coli and Pseudomonas fluorescens; gram positive bacteria, such as Streptomyces diversa, Lactobacillus gasserii, Lactococcus lactis, Lactococcus cremoris, Bacillus subtilis. Exemplary host cells also include eukaryotic organisms, e.g., various yeast, such as Saccharomyces sp., including Saccharomyces. . .

DETD . . . simultaneously quantified. Alternatively, arrays comprising genomic nucleic acid can also be used to determine the genotype of a newly engineered strain made by the methods of the invention. Polypeptide arrays" can also be used to simultaneously quantify a plurality of proteins.. . . comprising a defined amount of one or more biological molecules, e.g., oligonucleotides, immobilized onto a defined area of a substrate surface for specific binding to a sample molecule, e.g., mRNA transcripts.

DETD . . . methods of the invention provide whole cell evolution, or whole cell engineering, of a cell to develop a new cell strain having a new phenotype, e.g., a new or modified protease activity, by modifying the genetic composition of the cell. The. . .

DETD Once the metabolic network for a given strain is built, mathematic presentation by matrix notion can be introduced to estimate the intracellular metabolic fluxes if the on-line metabolome. . .

DETD . . . formulated as a hand or machine laundry detergent composition comprising a polypeptide of the invention. A laundry additive suitable for pre-treatment of stained fabrics can comprise a polypeptide of the invention. A fabric softener composition can comprise a protease of the. . . invention. Alternatively, a protease of the invention can be formulated as a detergent composition for use in general household hard surface cleaning operations. In alternative aspects, detergent additives and detergent compositions of the invention may comprise one or more other enzymes. . .

DETD . . . or one or more additional fabric processing steps. During the weaving of textiles, the threads are exposed to considerable mechanical strain. Prior to weaving on mechanical looms, warp yarns are often coated with sizing starch or starch derivatives in order to. . .

DETD Treating Foods and Food Processing

DETD The proteases of the invention have numerous applications in

food processing industry. For example, in one aspect, the proteases of the invention are used to improve the extraction of oil from. . .

DETD Proteases of the present invention, in the modification of animal feed or a food, can process the food or feed either in vitro (by modifying components of the feed or food) or in vivo. Proteases can be added to animal feed or food compositions containing high amounts of arabinogalactans or galactans, e.g. feed or food containing plant material from soy bean, rape seed, lupin and the like. When added to the feed or food the protease significantly improves the in vivo break-down of plant cell wall material, whereby a better utilization of the plant. . . more digestible by the animal. Thus, proteases of the invention can contribute to the available energy of the feed or food. Also, by contributing to the degradation of galactan-comprising proteins, a protease of the invention can improve the digestibility and uptake of carbohydrate and non-carbohydrate feed or food constituents such as protein, fat and minerals.

DETD The proteases of the invention can be in paper or pulp treatment or paper deinking. For example, in one aspect, the invention provides a paper treatment process using proteases of the invention. In another aspect, paper components of recycled photocopied paper during chemical and enzymatic deinking. . . proteases of the invention can be used in combination with cellulases, pectate lyases or other enzymes. The paper can be treated by the following three processes: 1) disintegration in the presence of proteases of the invention, 2) disintegration with a deinking chemical and proteases of the invention, and/or 3) disintegration after soaking with proteases of the invention. The recycled paper treated with proteases can have a higher brightness due to removal of toner particles as compared to the paper treated with just cellulase. While the invention is not limited by any particular mechanism, the effect of proteases of the invention may be due to its behavior as surface-active agents in pulp suspension.

DETD . . . from the well bore; reducing the flow of production fluids from the formation below expected flow rates; formulating an enzyme treatment by blending together an aqueous fluid and a polypeptide of the invention; pumping the enzyme treatment to a desired location within the well bore; allowing the enzyme treatment to degrade the viscous, protein-containing, damaging fluid, whereby the fluid can be removed from the subterranean formation to the well surface; and wherein the enzyme treatment is effective to attack protein in cell walls.

CLM What is claimed is:

. . . comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer. . .

CLM What is claimed is:

. . . polypeptide as set forth in claim 60, wherein the polypeptide has a protease activity, wherein optionally the protease is a non-surface-active protease or a surface-active protease, and optionally the protease is formulated in a non-aqueous liquid composition, a cast solid, a granular form, a particulate. . .

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(FILE 'HOME' ENTERED AT 16:31:09 ON 16 DEC 2008)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:31:20 ON 16 DEC 2008  
SEA (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

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1 FILE IFIPAT  
2 FILE USPATFULL  
1 FILE WPIDS  
1 FILE WPINDEX

L1 QUE (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O  
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FILE 'USPATFULL, IFIPAT' ENTERED AT 16:32:25 ON 16 DEC 2008

L2 3 S L1

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:33:15 ON 16 DEC 2008  
SEA ENTEROCOCCUS DURANS STRAIN 141-1

L3 QUE ENTEROCOCCUS DURANS STRAIN 141-1  
-----

SEA ENTEROCOCCUS DURANS STRAIN 152  
-----

L4 QUE ENTEROCOCCUS DURANS STRAIN 152  
-----

SEA ENTEROCOCCUS DRANS 141-1  
-----

L5 QUE ENTEROCOCCUS DRANS 141-1  
-----

SEA ENTEROCOCCUS DURANS 141-1  
-----

2 FILE USPATFULL

L6 QUE ENTEROCOCCUS DURANS 141-1  
-----

FILE 'USPATFULL' ENTERED AT 16:36:57 ON 16 DEC 2008

L7 2 S L6

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:37:29 ON 16 DEC 2008  
SEA ENTEROCOCCUS DURANS 152

-----  
1 FILE AGRICOLA  
1 FILE BIOENG  
1 FILE BIOSIS  
1 FILE CABA  
2 FILE CAPLUS  
1 FILE FROSTI  
1 FILE FSTA  
1 FILE HEALSAFE  
1 FILE LIFESCI  
1 FILE MEDLINE  
1 FILE PASCAL  
1 FILE SCISEARCH  
2 FILE USPATFULL



```

L8          QUE ENTEROCOCCUS DURANS 152
          -----

FILE 'AGRICOLA, BIOENG, BIOSIS, CABA, CAPLUS, FROSTI, FSTA, HEALSAFE,
LIFESCI, MEDLINE, PASCAL, SCISEARCH, USPATFULL' ENTERED AT 16:38:26 ON 16
DEC 2008

L9          15 S L8
L10         3 DUP REM L9 (12 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:40:04 ON 16 DEC 2008
          SEA LACTOCOCCUS LACTIS C-1-92
          -----
          1  FILE CAPLUS
          11 FILE GENBANK
          1  FILE PROMT
          2  FILE USPATFULL
L11         QUE LACTOCOCCUS LACTIS C-1-92
          -----

FILE 'CAPLUS, GENBANK, PROMT, USPATFULL' ENTERED AT 16:41:04 ON 16 DEC
2008

L12         15 S L11
L13         14 DUP REM L12 (1 DUPLICATE REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:47:33 ON 16 DEC 2008
          SEA LACTOCOCCUS LACTIS C-1-152
          -----
          7  FILE GENBANK
          2  FILE USPATFULL
          1  FILE WPIDS
          1  FILE WPINDEX
L14         QUE LACTOCOCCUS LACTIS C-1-152
          -----

FILE 'GENBANK, USPATFULL' ENTERED AT 16:49:45 ON 16 DEC 2008

L15         9 S L14
L16         9 DUP REM L15 (0 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:55:03 ON 16 DEC 2008
          SEA FOOD(P)PROCESS? AND INHIBIT? (P)PATHOGEN? AND SURFACE
          -----
          0*  FILE ADISNEWS
          11  FILE AGRICOLA
          2*  FILE ANTE
          1*  FILE AQUALINE
          4   FILE AQUASCI
          11* FILE BIOENG
          32  FILE BIOSIS
          11* FILE BIOTECHABS
          11* FILE BIOTECHDS
          12* FILE BIOTECHNO
          13  FILE CABA
          15  FILE CAPLUS

```

0\* FILE CEABA-VTB  
 0\* FILE CIN  
 1 FILE CROPU  
 6 FILE DISSABS  
 12 FILE EMBASE  
 16\* FILE ESBIODBASE  
 0\* FILE FOMAD  
 0\* FILE FOREGE  
 20\* FILE FROSTI  
 45\* FILE FSTA  
 1 FILE GENBANK  
 1 FILE HEALSAFE  
 39 FILE IFIPAT  
 0\* FILE KOSMET  
 13 FILE LIFESCI  
 12 FILE MEDLINE  
 0\* FILE NTIS  
 1\* FILE NUTRACEUT  
 18\* FILE PASCAL  
 1\* FILE PHARMAML  
 24 FILE PROMT  
 14 FILE SCISEARCH  
 16 FILE TOXCENTER  
 2042 FILE USPATFULL  
 5 FILE USPATOLD  
 620 FILE USPAT2  
 1\* FILE WATER  
 32 FILE WPIDS  
 1 FILE WPIFV  
 32 FILE WPINDEX

L17 QUE FOOD(P) PROCESS? AND INHIBIT? (P) PATHOGEN? AND SURFACE

-----  
 SEA L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)  
 -----

0\* FILE ADISNEWS  
 0\* FILE ANTE  
 0\* FILE AQUALINE  
 0\* FILE BIOENG  
 0\* FILE BIOTECHABS  
 0\* FILE BIOTECHDS  
 0\* FILE BIOTECHNO  
 1 FILE CAPLUS  
 0\* FILE CEABA-VTB  
 0\* FILE CIN  
 1 FILE DISSABS  
 0\* FILE ESBIODBASE  
 0\* FILE FOMAD  
 0\* FILE FOREGE  
 0\* FILE FROSTI  
 0\* FILE FSTA  
 0\* FILE KOSMET  
 0\* FILE NTIS  
 0\* FILE NUTRACEUT  
 0\* FILE PASCAL  
 0\* FILE PHARMAML  
 92 FILE USPATFULL  
 15 FILE USPAT2  
 0\* FILE WATER

L18 QUE L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)

-----

FILE 'DISSABS, USPATFULL, USPAT2' ENTERED AT 17:00:27 ON 16 DEC 2008

FILE 'CAPLUS, DISSABS, USPATFULL, USPAT2' ENTERED AT 17:00:43 ON 16 DEC 2008

```
L19      109 S L18
L20      46 S L19 AND TREAT?(P)SURFACE
L21      3 S L20 AND INHIBIT(P)PATHOGEN(P)?ORGANIS?
L22      3 S L21 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)
L23      0 S L22 AND INHIBIT?(P)FIRST POPULATION OF MICROORGANISM
L24      3 S L22 AND (C-1-152 OR C-1-92 OR 152 OR 141-1)
L25      3 S L24 AND STRAIN
```

```
=> s l25 and strain 152
L26      0 L25 AND STRAIN 152
```

```
=> s L25 and strain 141-1
L27      0 L25 AND STRAIN 141-1
```

```
=> s L25 and strain C-1-152
L28      0 L25 AND STRAIN C-1-152
```

```
=> s l25 and strain C-1-92
L29      0 L25 AND STRAIN C-1-92
```

```
=> d hist
```

(FILE 'HOME' ENTERED AT 16:31:09 ON 16 DEC 2008)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:31:20 ON 16 DEC 2008  
SEA (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

```
-----
1  FILE IFIPAT
2  FILE USPATFULL
1  FILE WPIDS
1  FILE WPINDEX
```

```
L1      QUE (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O
-----
```

FILE 'USPATFULL, IFIPAT' ENTERED AT 16:32:25 ON 16 DEC 2008

```
L2      3 S L1
```

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:33:15 ON 16 DEC 2008  
SEA ENTEROCOCCUS DURANS STRAIN 141-1

```
L3      QUE ENTEROCOCCUS DURANS STRAIN 141-1
-----
```

```
SEA ENTEROCOCCUS DURANS STRAIN 152
-----
```

```
L4      QUE ENTEROCOCCUS DURANS STRAIN 152
-----
```

```
SEA ENTEROCOCCUS DRANS 141-1
-----
```

```
L5      QUE ENTEROCOCCUS DRANS 141-1
-----
```

```
SEA ENTEROCOCCUS DURANS 141-1
```

```

-----
L6      2    FILE USPATFULL
        QUE ENTEROCOCCUS DURANS 141-1
-----

FILE 'USPATFULL' ENTERED AT 16:36:57 ON 16 DEC 2008
L7      2 S L6

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:37:29 ON 16 DEC 2008
        SEA ENTEROCOCCUS DURANS 152
-----
        1    FILE AGRICOLA
        1    FILE BIOENG
        1    FILE BIOSIS
        1    FILE CABA
        2    FILE CAPLUS
        1    FILE FROSTI
        1    FILE FSTA
        1    FILE HEALSAFE
        1    FILE LIFESCI
        1    FILE MEDLINE
        1    FILE PASCAL
        1    FILE SCISEARCH
        2    FILE USPATFULL
L8      QUE ENTEROCOCCUS DURANS 152
-----

FILE 'AGRICOLA, BIOENG, BIOSIS, CABA, CAPLUS, FROSTI, FSTA, HEALSAFE,
LIFESCI, MEDLINE, PASCAL, SCISEARCH, USPATFULL' ENTERED AT 16:38:26 ON 16
DEC 2008
L9      15 S L8
L10     3 DUP REM L9 (12 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:40:04 ON 16 DEC 2008
        SEA LACTOCOCCUS LACTIS C-1-92
-----
        1    FILE CAPLUS
        11   FILE GENBANK
        1    FILE PROMT
        2    FILE USPATFULL
L11     QUE LACTOCOCCUS LACTIS C-1-92
-----

FILE 'CAPLUS, GENBANK, PROMT, USPATFULL' ENTERED AT 16:41:04 ON 16 DEC
2008
L12     15 S L11
L13     14 DUP REM L12 (1 DUPLICATE REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:47:33 ON 16 DEC 2008
        SEA LACTOCOCCUS LACTIS C-1-152
-----
        7    FILE GENBANK
        2    FILE USPATFULL

```

1 FILE WPIDS  
1 FILE WPINDEX  
L14 QUE LACTOCOCCUS LACTIS C-1-152  
-----

FILE 'GENBANK, USPATFULL' ENTERED AT 16:49:45 ON 16 DEC 2008  
L15 9 S L14  
L16 9 DUP REM L15 (0 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:55:03 ON 16 DEC 2008  
SEA FOOD(P)PROCESS? AND INHIBIT? (P)PATHOGEN? AND SURFACE  
-----

0\* FILE ADISNEWS  
11 FILE AGRICOLA  
2\* FILE ANTE  
1\* FILE AQUALINE  
4 FILE AQUASCI  
11\* FILE BIOENG  
32 FILE BIOSIS  
11\* FILE BIOTECHABS  
11\* FILE BIOTECHDS  
12\* FILE BIOTECHNO  
13 FILE CABA  
15 FILE CAPLUS  
0\* FILE CEABA-VTB  
0\* FILE CIN  
1 FILE CROPU  
6 FILE DISSABS  
12 FILE EMBASE  
16\* FILE ESBIODBASE  
0\* FILE FOMAD  
0\* FILE FOREGE  
20\* FILE FROSTI  
45\* FILE FSTA  
1 FILE GENBANK  
1 FILE HEALSAFE  
39 FILE IFIPAT  
0\* FILE KOSMET  
13 FILE LIFESCI  
12 FILE MEDLINE  
0\* FILE NTIS  
1\* FILE NUTRACEUT  
18\* FILE PASCAL  
1\* FILE PHARMAML  
24 FILE PROMT  
14 FILE SCISEARCH  
16 FILE TOXCENTER  
2042 FILE USPATFULL  
5 FILE USPATOLD  
620 FILE USPAT2  
1\* FILE WATER  
32 FILE WPIDS  
1 FILE WPIFV  
32 FILE WPINDEX  
L17 QUE FOOD(P) PROCESS? AND INHIBIT? (P) PATHOGEN? AND SURFACE  
-----  
SEA L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)  
-----  
0\* FILE ADISNEWS

```

0* FILE ANTE
0* FILE AQUALINE
0* FILE BIOENG
0* FILE BIOTECHABS
0* FILE BIOTECHDS
0* FILE BIOTECHNO
1 FILE CAPLUS
0* FILE CEABA-VTB
0* FILE CIN
1 FILE DISSABS
0* FILE ESBIODBASE
0* FILE FOMAD
0* FILE FOREGE
0* FILE FROSTI
0* FILE FSTA
0* FILE KOSMET
0* FILE NTIS
0* FILE NUTRACEUT
0* FILE PASCAL
0* FILE PHARMAML
92 FILE USPATFULL
15 FILE USPAT2
0* FILE WATER

```

L18 QUE L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)

-----

FILE 'CAPLUS, DISSABS, USPATFULL' ENTERED AT 17:00:10 ON 16 DEC 2008

FILE 'DISSABS, USPATFULL, USPAT2' ENTERED AT 17:00:27 ON 16 DEC 2008

FILE 'CAPLUS, DISSABS, USPATFULL, USPAT2' ENTERED AT 17:00:43 ON 16 DEC 2008

```

L19      109 S L18
L20      46 S L19 AND TREAT?(P)SURFACE
L21      3 S L20 AND INHIBIT(P)PATHOGEN(P)?ORGANIS?
L22      3 S L21 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)
L23      0 S L22 AND INHIBIT?(P)FIRST POPULATION OF MICROORGANISM
L24      3 S L22 AND (C-1-152 OR C-1-92 OR 152 OR 141-1)
L25      3 S L24 AND STRAIN
L26      0 S L25 AND STRAIN 152
L27      0 S L25 AND STRAIN 141-1
L28      0 S L25 AND STRAIN C-1-152
L29      0 S L25 AND STRAIN C-1-92

```

=> logoff

ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF

LOGOFF? (Y)/N/HOLD:y

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	113.40	311.64

STN INTERNATIONAL LOGOFF AT 17:08:01 ON 16 DEC 2008

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:ssspt189dxw

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

\* \* \* \* \* Welcome to STN International \* \* \* \* \*

NEWS 1 Web Page for STN Seminar Schedule - N. America  
NEWS 2 DEC 01 ChemPort single article sales feature unavailable  
NEWS 3 JAN 06 The retention policy for unread STNmail messages  
will change in 2009 for STN-Columbus and STN-Tokyo  
NEWS 4 JAN 07 WPIDS, WPINDEX, and WPIX enhanced Japanese Patent  
Classification Data  
NEWS 5 FEB 02 Simultaneous left and right truncation (SLART) added  
for CERAB, COMPUAB, ELCOM, and SOLIDSTATE  
NEWS 6 FEB 02 GENBANK enhanced with SET PLURALS and SET SPELLING  
NEWS 7 FEB 06 Patent sequence location (PSL) data added to USGENE  
NEWS 8 FEB 10 COMPENDEX reloaded and enhanced  
NEWS 9 FEB 11 WTEXTILES reloaded and enhanced  
NEWS 10 FEB 19 New patent-examiner citations in 300,000 CA/Caplus  
patent records provide insights into related prior  
art  
NEWS 11 FEB 19 Increase the precision of your patent queries -- use  
terms from the IPC Thesaurus, Version 2009.01  
NEWS 12 FEB 23 Several formats for image display and print options  
discontinued in USPATFULL and USPAT2  
NEWS 13 FEB 23 MEDLINE now offers more precise author group fields  
and 2009 MeSH terms  
NEWS 14 FEB 23 TOXCENTER updates mirror those of MEDLINE - more  
precise author group fields and 2009 MeSH terms  
NEWS 15 FEB 23 Three million new patent records blast AEROSPACE into  
STN patent clusters  
NEWS 16 FEB 25 USGENE enhanced with patent family and legal status  
display data from INPADOCDB  
NEWS 17 MAR 06 INPADOCDB and INPAFAMDB enhanced with new display  
formats  
NEWS 18 MAR 11 EPFULL backfile enhanced with additional full-text  
applications and grants  
NEWS 19 MAR 11 ESBIODBASE reloaded and enhanced  
NEWS 20 MAR 20 CAS databases on STN enhanced with new super role  
for nanomaterial substances  
NEWS 21 MAR 23 CA/Caplus enhanced with more than 250,000 patent  
equivalents from China  
NEWS 22 MAR 30 IMSPATENTS reloaded and enhanced  
NEWS 23 APR 03 CAS coverage of exemplified prophetic substances  
enhanced  
NEWS 24 APR 07 STN is raising the limits on saved answers  
  
NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,  
AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.  
  
NEWS HOURS STN Operating Hours Plus Help Desk Availability  
NEWS LOGIN Welcome Banner and News Items  
NEWS IPC8 For general information regarding STN implementation of IPC 8

Enter NEWS followed by the item number or name to see news on that  
specific topic.

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for software development or design, implementation of commercial

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\* \* \* \* \* STN Columbus \* \* \* \* \*

FILE 'HOME' ENTERED AT 13:45:18 ON 09 APR 2009

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
0.22	0.22

FULL ESTIMATED COST

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 13:45:46 ON 09 APR 2009

68 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0\* with SET DETAIL OFF.

=> s (Enterococcus duras or Lactococcus lactis) and (PTA-4759 or PTA-4758 or PTA-4760 or PTA-4761)

1 FILE IFIPAT  
54 FILES SEARCHED...  
2 FILE USPATFULL  
1 FILE WPIDS  
1 FILE WPINDEX

4 FILES HAVE ONE OR MORE ANSWERS, 68 FILES SEARCHED IN STNINDEX

L1 QUE (ENTEROCOCCUS DURAS OR LACTOCOCCUS LACTIS) AND (PTA-4759 OR PTA-4758 OR PTA-4760 OR PTA-4761)

=> file ifipat uspatfull

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
4.76	4.98

FULL ESTIMATED COST

FILE 'IFIPAT' ENTERED AT 13:49:59 ON 09 APR 2009

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FILE 'USPATFULL' ENTERED AT 13:49:59 ON 09 APR 2009

CA INDEXING COPYRIGHT (C) 2009 AMERICAN CHEMICAL SOCIETY (ACS)

=> s l1

L2 3 L1

=> rem dup l2

DUP IS NOT VALID HERE

The DELETE command is used to remove various items stored by the system.

To delete a saved query, saved answer set, saved L-number list, SDI request, batch request, mailing list, or user-defined cluster, format, or search field, enter the name. The name may include ? for left, right, or simultaneous left and right truncation.

Examples:



DELETE BIO?/Q	- delete query names starting with BIO
DELETE ?DRUG/A	- delete answer set names ending with DRUG
DELETE ?ELEC?/L	- delete L-number lists containing ELEC
DELETE ANTICOAG/S	- delete SDI request
DELETE ENZYME/B	- delete batch request
DELETE .MYCLUSTER	- delete user-defined cluster
DELETE .MYFORMAT	- delete user-defined display format
DELETE .MYFIELD	- delete user-defined search field
DELETE NAMELIST MYLIST	- delete mailing list

To delete an ordered document or an offline print, enter its number.

Examples:

DELETE P123001C	- delete print request
DELETE D134002C	- delete document order request

To delete an individual L-number or range of L-numbers, enter the L-number or L-number range. You may also enter DELETE LAST followed by a number, n, to delete the last n L-numbers. RENUMBER or NORENUMBER may also be explicitly specified to override the value of SET RENUMBER.

Examples:

DELETE L21	- delete a single L-number
DELETE L3-L6	- delete a range of L-numbers
DELETE LAST 4	- delete the last 4 L-numbers
DELETE L33-	- delete L33 and any higher L-number
DELETE -L55	- delete L55 and any lower L-number
DELETE L2-L6 RENUMBER	- delete a range of L-numbers and renumber remaining L-numbers
DELETE RENUMBER	- renumber L-numbers after deletion of intermediate L-numbers

Entire sets of saved items, SDI requests, batch requests, user-defined items, or E-numbers can be deleted.

Examples:

DELETE SAVED/Q	- delete all saved queries
DELETE SAVED/A	- delete all saved answer sets
DELETE SAVED/L	- delete all saved L-number lists
DELETE SAVED	- delete all saved queries, answer sets, and L-number lists
DELETE SAVED/S	- delete all SDI requests
DELETE SAVED/B	- delete all batch requests
DELETE CLUSTER	- delete all user-defined clusters
DELETE FORMAT	- delete all user-defined display formats
DELETE FIELD	- delete all user-defined search fields
DELETE SELECT	- delete all E-numbers
DELETE HISTORY	- delete all L-numbers and restart the session at L1

To delete an entire multifile SDI request, enter DELETE and the name of the request. To delete a component from the multifile SDI, enter DELETE and the name of the component.

```
=> dup rem l2
PROCESSING COMPLETED FOR L2
```

L3 2 DUP REM L2 (1 DUPLICATE REMOVED)

=> d 13 1-2

L3 ANSWER 1 OF 2 IFIPAT COPYRIGHT 2009 IFI on STN DUPLICATE 1  
AN 11124117 IFIPAT;IFIUDB;IFICDB  
TI Composition and method for inhibition of microorganisms  
IN Doyle Michael P; Zhao Tong  
PA Unassigned Or Assigned To Individual (68000)  
PPA Georgia, University of Research Foundation Inc (Probable)  
PI US 20060073129 A1 20060406  
AI US 2003-535357 20031124  
WO 2003-US37526 20031124  
20050518 PCT 371 date  
20050518 PCT 102(e) date  
PRAI US 2002-428863P 20021125 (Provisional)  
FI US 20060073129 20060406  
DT Utility; Patent Application - First Publication  
FS CHEMICAL  
APPLICATION  
ED Entered STN: 10 Apr 2006  
Last Updated on STN: 10 Apr 2006  
CLMN 35  
GI 1 Figure(s).  
FIG. 1 illustrates the results of analyzing four probiotic isolates for their DNA fingerprinting by pulsed field-gel electrophoresis; lane 1 Lambda ladder DNA standard, lane 2 C-1-92 [*L. lactis* subsp. *lactis*], lane 3 C-1-152 [*L. lactis* subsp. *lactis*], lane 4 141-1 [*E. durans*], and lane 5 152 [*E. durans*].

L3 ANSWER 2 OF 2 USPATFULL on STN  
AN 2006:79924 USPATFULL  
TI Foaming composition of competitive exclusion microbes and method of using same  
IN Podtburg, Teresa C., Waconia, MN, UNITED STATES  
Schmidt, Bruce, Apple Valley, MN, UNITED STATES  
Cords, Bruce, Inver Grove Heights, MN, UNITED STATES  
Grab, Lawrence A., Dusseldorf, GERMANY, FEDERAL REPUBLIC OF  
Halsrud, David A., Minneapolis, MN, UNITED STATES  
PI US 20060067915 A1 20060330  
AI US 2005-233922 A1 20050922 (11)  
PRAI US 2004-612882P 20040924 (60)  
DT Utility  
FS APPLICATION  
LN.CNT 1878  
INCL INCLM: 424/093.400  
INCLS: 435/243.000  
NCL NCLM: 424/093.400  
NCLS: 435/243.000  
IC IPCI A01N0063-00 [I,A]  
IPCR A01N0063-00 [I,A]; A01N0063-00 [I,C]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d hist

(FILE 'HOME' ENTERED AT 13:45:18 ON 09 APR 2009)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 13:45:46 ON 09 APR 2009

SEA (ENTEROCOCCUS DURNAS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

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1 FILE IFIPAT  
2 FILE USPATFULL  
1 FILE WPIDS  
1 FILE WPINDEX

L1 QUE (ENTEROCOCCUS DURNAS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

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FILE 'IFIPAT, USPATFULL' ENTERED AT 13:49:59 ON 09 APR 2009

L2 3 S L1

L3 2 DUP REM L2 (1 DUPLICATE REMOVED)

=> logoff

ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF

LOGOFF? (Y)/N/HOLD:y

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

6.95

11.93

STN INTERNATIONAL LOGOFF AT 13:50:26 ON 09 APR 2009